Homo sapi Human DNA

AX300942 Sequence
BX449247 Zebrafish
AC121795 Mus muscu
AC130668 Mus muscu
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AC087504 Homo sapi
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AC087136 Homo sapi
AC097363 Rattus no
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AC121878 Human DNA

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Roesl, F., Soto, U., Coy, J., Finzer, P., Delius, H., Poustka, A., zur Hausen, H. and Patzelt, A. Regulatory sequences of the human mcp-1 gene Patent: EP 1170372-A 1 09-JAN-2002; DEDTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OBFFENTLICHEN RECHTS (DE)
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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100.0%; Pred. No. 1.7e-142;
ive 0; Mismatches 0;
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Sequence 1 from Patent BP1170372.
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AC130668
AC137730
AC134681
AC021336
AC097363
AC097363
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BD110729
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AC123884
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AL359183
AX300942
BX649247
AC120369
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Best Local Similarity 100.
Matches 600; Conservative
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7.0 194946
7.0 210525
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AUTHORS
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AL713839 Mus muscu
AC073824 Mus muscu
AC17824 Rattus no
AC128200 Rattus no
AC129672 Rattus no
AC095987 Rattus no
AC096469 Rattus no
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AF519531 Homo sapi
Y18933 Homo sapien
AC005549 Homo sapien
X60001 H.sapiens 9
AC123203 Rattus no
AC114440 Rattus no
AC16494 Sequence 14
AC022299 Mus muscu
                                                                                                                      August 3, 2005, 21:53:02 ; Search time 2411.66 Seconds (without alignments) 12055.236 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                    4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
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AL626807
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HSY18933
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AC123203
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AC022299
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Post-processing:

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Searched:

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Perfect score:

Sequence:

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Run on:

PAT 01-FEB-2002

linear

DNA

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Gaps

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Length 600; 0, Indels 120

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AC129672 AC095987 AC127001 AC098469

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239429 243299

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Result Š

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Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Best Local Similarity 100.0%; Pred. No. 9.4e-143;
Matches 600; Conservative 0; Mismatches 0; Indels
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Homo sapiens MCP-1 gene and enhancer region.
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Birren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N.,

Birren, B., Easman, K., Linton, L., Barna, N., Beckerly, R.,

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Boutwell, C., Brown, A., Cooke, P., Corliss, D., Depayre, E.,

Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E.,

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Ve, W. J., Zhao, J. and Zody, M.

Direct Submission

AL Submitted (27-AUG-1998) Whitehead Institute/MIT Center for Genome submitted (27-AUG-1998) Whitehead Institute/MIT Center for Genome submitted (27-AUG-1998) Whitehead Losting, M., Stone, S.,

Research, 320 Charles Street, Cambridge, MA 02141, USA

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Anderson, M., Baker, J., Baldwin, J., Berkerly, Beckerly, R., Grant, G., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E.,

Burren, B., Fasman, K., Linton, L., Horton, L., Howland, J. C.,

Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J. C.,

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Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J. C.,

Hagos, B., Marquis, N., Molman, P., McGwan, P., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC005549 147416 bp DNA linear PRI 22-SEP-1998
Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
AC005549
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1. (bases 1 to 147416)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone hRPK.215_E_13

Outpublished
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                                                                                                   2 (bases 1 to 11793)
Roesl, F.
Blacet Submission
Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKF2
(German Cancer Research Institute), Im Neuenheimer Feld 506, 69120
non-tumorigenic HPV 18 positive cells: the role of the chromatin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 TAGAAATGGTGATGATGTACATCAAGCAGGAGAAAAACCAATGAACCAGATGCGAATT
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/513. 7517

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100.0%; Pred. No. 8.9e-143;
ive 0; Mismatches 0;
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Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vasailiev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M.

L. Submitted (12-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

4 (Dases 1 to 147416)

Birch, B., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Barran, M., Baker, J., Baldwin, J., Barna, M., Beckerly, R., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collymore, A., Coorliss, D., Depayre, B., Devon, K., Dewar, K., Dones, C., Kann, L., Horton, L., Howland, J. C., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., Meckeran, K., Maddrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Vas, W.J., Zhao, J., Chon, J., Wann, D., Ye, W.J., Zhao, J., Chon, J., Wheeler, J., Wu, Y., Wyman, D., Ve, W.J., Zhao, J., Chon, J., Wheeler, J., Wu, Y., Wyman, D., Dirett, Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Ye, W.J., Zhao, J., Chon, J., Wheeler, J., Wu, Y., Wyman, D., Dirett, Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Ye, W.J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Dirett, Subramanian, A., Tesfaye, S., Tichovolsky, N., Yo, W., Wyman, D., Dirett, Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, N., Ye, W.J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Dirett, Subramanian, A., Tesfaye, S., Tichovolsky, N., Yo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Dirett, Subramanian, A., Tesfaye, S., Tichovolsky, N., Yo, A., Wagner, S., Wu, J., Wu, Y., Wyman, D., Dirett, Subraman, M., Wallish, M., Wallish, W., Wallish, W., Wallish, W., Wallish, W., Wallish, W., Wallish,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (2.5EP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA NO Sep 13, 1998 this sequence version replaced gi:3581743. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Only the first 147416 bases of this clone are being submitted. Bases 145417-155040 overlap accession number AC004147 (WICGR project L228). The first 2Kb of the overlapping region are submitted to confirm overlap.

Location/Qualifiers

1. .147416
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/rpt family="FLAM C"
complement (5941. .6051)
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Ratura.

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Ruzny, D.Marie., Metzker, M.Lee., Abramzon, S., Adams, C., Alder, J.,

Allan, C., Alebrooks, S., Amin, A., Anguiano, D.,

Allan, C., Alebrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswalo, K., Blair, J., Blankehuurg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

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Clackeland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

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Delgado, O., Denson, S., Deramo, C., Dinn, H., Divya, K.,

Bran, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,

Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Poster, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC123203 242335 bp DNA linear HTG 09-NOV-2002
Rattus norvegicus clone CH230-28P9, WORKING DRAFT SEQUENCE.
AC123203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission S. Schwarz, Albert Einstein College of Submitted (16-MAY-1991) B. Schwarz, Albert Einstein College of Medicine, Dept of Microbiology & Immunology, Forchheimer Bldg Room 411, 1300 Morris Park Avenue, Bronx NY 10461, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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AC123203.4 GI:24818687
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JE protein; secretory protein.
Homo sapiens (human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58554 TATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTCCCTGAAACCAGAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAACTTATAGATTTTATACATACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AATGTTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                    1 TAGGAAATTTATAGGATCATTAAGAAAGGAGGAAGGAAGAGGAGGAGGAATTACCTGGAGG
                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                    Length 147416;
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                                                                                                                                                                                                                                                                                       ; Score 600; DB 9; L; Pred. No. 5.3e-143; 0; Mismatches 0;
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/rpt_family="MLTIG"

complement (48165. 48209)
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ON NOV 9, 2002 this sequence version replaced gi:23265933.
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas sassembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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Direct Submission

Submitsed (19-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
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------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 236664 bases at least Q40
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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Direct Submission
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                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                185 TTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAG 244
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                                                                                                                                         Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                189111 inanciciación de confector de contra contra na contra de co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 CCCACACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATG
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Consensus quality: 238611 bases at least Q30
Consensus quality: 239758 bases at least Q20
Estimated insert size: 245041; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                     is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 24235: contig of 242335 bp in length.
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Pred. No. 4.8e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
|mol_type="genomic DNA"
|db_xref="taxon:10116"
|clone="CH230-28P9"
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/note="clone boundary
clone_end:Sp6
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complement(240270..24:
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                                                                                                                                                                                RS MARIATO, MARIATION, LEB., Abramacon, S., Adams, C., Alder, J., Allen, H., Alsbrooks, S., Amin, A., Anguinno, D., Allen, L., Alsen, H., Alsbrooks, S., Amin, A., Anguinno, D., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguinno, D., Allen, L., Alsen, H., Alsbrooks, S., Amin, A., Anguinno, D., Anguisher, D., Barder, M., Barder, M., Barder, M., Bander, D., Chang, S., Barber, M., Barnstead, M., Benhad, F., Barder, D., Chang, S., Chang, S., Chang, S., Chang, S., Chang, C., Burch, P., Burrell, K., Calderon, E., Chardens, V., Carter, A., Chang, C., Burch, P., Burrell, K., Chang, C., Day, B., Baves, C., Day, B., Baves, C., Day, Carroll, L., De, And, C., Dederich, D., Detager, M., Dugan, Roche, D., Dinh, H., Duyan, Roger, P., Fraser, C., M., Gabis, A., Gang, R., Carroll, L., Dinh, H., Duyan, R., Bayan, A., Elagan, A., Elagan, A., Elagan, A., Elagan, A., Elagan, M., Riagan, M., Guerra, W., Guerra, W., Guerra, W., Guerra, M., Guraz, M., Havlak, P., Haves, A., Hanler, S., Hamil, C., Hamilton, C., Karpethy, S., Kellys, S., Hune, J., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Marchan, C., March, C., Mince, G., Mince, M., March, M., March, M., March, M., March, C., March, C., Mince, G., Mince, G., Mince, G., Mince, G., Mince, G., Mince, G., March, C., March, M., March, C., March, M., Ma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (20-NOV-2002) Human Genome Sequencing Center, Department Submitted (20-NOV-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On NOV 20, 2002 this sequence version replaced gi:23195167. The sequence in this assembly is a combination of BAC based reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (109-MAR-2002) Human Genome Sequencing Center, Department Submitted (109-MAR-2002) Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 3 (bases 1 to 245808)

Rat Genome Sequencing Consortium.
                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
AC114440.4 GI:25138837
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 245808)
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                                                                                           Rattus norvegicus
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REFERENCE
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      VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                           REFERENCE
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130404 CAGCGIGIATGICAAAGAAIGGGGITTİTICAAAAGGAAGGIGAATACAGGGITİTİTAATG 130463
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65 AATGGTGATGATGTGTACATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATTCGGG 124
and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold' by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    data.html)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: GSAR
Center clone name: GSAR
Center clone name: CH230-121P3
Assembly program: Phrap; version 0.990329
Consensus quality: 226189 bases at least Q40
Consensus quality: 22817 bases at least Q30
Consensus quality: 229460 bases at least Q30
Estimated insert size: 230674; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTAGGGTGAAAAGTTACTAACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 CCCACACCATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.h. NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 245808;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tch 11.9%; Score 71.6; DB 2; Length 24: al Similarity 57.0%; Pred. No. 4.7e-08; 203; Conservative 0; Mismatches 129; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 3901: contig of 3901 bp in length
2 4001: gap of unknown length
12 245808: contig of 241807 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                         Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .24580B
/organism="Rattus norvegicus"
/mol type="genomic DNA"
/db xref="taxon:10116"
/clone="CH230-121P3"
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1. .1014
/note="wgs_contig"
^^no2. .5165
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5719. .7604
/note="wgs_contig"
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δ 셤 δ 셤 166494/c LOCUS DEFINITION

RESULT 8

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS TITLE JOURNAL FEATURES

ORIGIN

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REFERENCE

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E I (Dases I to leuses).

Metzker,M.L., Lewis,L.R., Hume,J., Edwards,C., Harris,C.,
Dederich,D., Thomas,S., Okwuonu,G., Carlock,C., Garner,T.,
Addison,S., Pacc,A., Williams,G., Bonnin,D., Brooks,A., Brown,J.,
Buhay,C., Bunac,C., Burkett,C., Chacko,J., Chen,G., Chen,Z.,
Cox,C., Davis,C., Delgado,O., Ding,Y., Dugan-Rocha,S.,
Fernandez,C., Ferraguto,D., Forcum-Tansey,J., Gill,R.,
Gorrell,J.H., Gunaratne,P., Haller,G., Hernandez,J., Hogues,M.,
Hosae,H., Hou,X., Huber,J., Jackson,L., Jia,Y., Kelly,S.,
Kovar,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Martin,R.,
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B.,
Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S.,
Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A.,
Warley,K. and Gibbs,R. Scherer,S., Sodergren,E., Weinstock,G.,
Direct Subalssion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (29-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this sequence version replaced gi:11079355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is
Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will he are definitely agreence as soon as it is available and the accession number will
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of 5923 bp in length
unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bom.tmc.edu
Contact: hgsc-help@bom.tmc.edu
Center project Information
Center project name: MAAU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center: Baylor College of Medicine Center code: BCM
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gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
2 (bases 1 to 160869)
Worley, K.C.
                           Mammalia, Eutheria, Ro
1 (bases 1 to 160869)
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55306
                                                REFERENCE
AUTHORS
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AUTHORS
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                                                                   130524 CCCAATGAAGAGGGGATGTGTTCCATTCAGAGGCTCAGAGGTGAGCTTCAGTAAATA 130583
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Mus musculus clone RP23-433D8, *** SEQUENCING IN PROGRESS ***, 32
unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PAT 28-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        245 TCCAATGA----GGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 125 CCCACACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            245 TCCAATGAGGAGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTAAC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    305 TTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGGTCC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           185 TTAGGGTGAAAAGTTACTACTCCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAG 244
                                                                                                                                                        AATGGTGATGATGTACATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATTCGGG
                                                                                                                       301 TAACTTATAGATTTTATACATACAGAGAAATACGGACTAGTGAGAAGCTATTGC 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 6; Length 7218;
                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unclassified.

1 (bases 1 to 7218)

Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11.8%; Score 70.6; DB 6; Jlarity 3.3%; Pred. No. 1.8e-07; Conservative 237; Mismatches 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREARRERRERRERRERRERRERRER 1067
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                                                                                                                                                                                                                                                                                                     I66494 7218 bp D
Sequence 14 from patent US 5670367.
I66494 GI:2724471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="unassigned DNA'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="unknown"
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HTG; HTGS PHASE1.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                       Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown
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RESULT 9 AC022299/c DEFINITION

ORGANISM

ACCESSION

VERSION KEYWORDS SOURCE

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Direct Submission

AL Submitted (12-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 222121)

RS Birren, B. Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barra,N. Bastien,V. Bloom,T., Boquslavkiy,L., Anderson,S., Barra,N. Bastien,V. Bloom,T., Campoplanch,A., Cangoplanch,A., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Gook,A., Gooke,P., Petralugh,W., Gage,D., Galagan,J., Gardyna,S., Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Faro,S., Gord,S., Goyette,M., Graham,L., Cand-Pierre,N., Hagos,B., Horton,L., Hullm,W., Iliev,I., Johnson,R., Jones,C., Macdonald,P., Malor,J., Lindblad-Toh,K., Liu,G., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLan,C., Macdonald,P., Major,J., Marquis,N., Mathews,C., Macdonald,P., Major,J., Marquis,N., Mathews,C., Macdonald,P., Major,J., Maylor,J., Mouven,C., Norman,C.H., O'Connor,T., O'Donnell,P., Pollara,V., Schupback,R., Stere,R., Rieback,M., Santos,R., Schauer,S., Schupback,R., Stenan,S., Severy,P., Spencer,B., StangerThoman,N., Stojanovic,N., Stanow,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Zainner,A., Wallan,B., Wu,X., Wyman,D., Ye,W.J., Young,G.
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129077 AATAGGAAGGTGAGAACATGGTATTCCCTCGGACCTATAATTTAAAGGATAAGTTGAAAC 129018
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Mus musculus chromosome 11, clone RP23-328G11, complete sequence.
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Sciurognathi; Muridae; Murinae; Mus.
                                                    rctrcagrccaarga----ggagggargrgccargrrragagarrcagagaracag
                                                                                                                                               294 G-GAAATGTAACTTATAGATTTTATACACAGAGAAATACGGACTAGTGAGAAGCTA
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Birren, B., Linton, L., Nusbaum, C. and Lander, E. Unpublished
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27737. 28052
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77809. 27813
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           **Rebearch**, 320 Charles Street, Cambridge, MA U2141, USA
Anderson, 5.0 Enailes Street, Cambridge, MA U2141, USA
Anderson, S., Barna, N., Bastlen, V., Bloom, T., Boguslavkiy, L.,
Boukhgalter, B., Brown, A., Calamarata, J., Campopiano, A., Chang, J.,
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Saman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
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Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
Direct Submission
L. Submitted (127-MAR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 25, 2002 this sequence version replaced gi:19683729.
All repeats were identified using RepeatMasker: html
Center: Whithehead Institute/ MIT Center for Genome Center
Center: Code: WIRR
Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpt family="LIME" complement (2080. ..
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6718. .6747
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                   REFERENCE
AUTHORS
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AL713839.1 GI:19682818
SeM1-SP6; DI1Bhm140; DI1Mit354; DI1Mit66; DDK syndrome; Mdeg; Ovum
mutant; Scya2,11,7,8,12,1.
Mus musculus (house mouse)
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Submitted (20-MAR-2002) Genoscope - Centre National de Sequencage :
Submitted (20-MAR-2002) Genoscope - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
IMPORTANT: This sequence is unfinished and does not necessarly
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                                                                                                                                                                                                                                                                                                                                                                                                                                           293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Coumailleau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus chromosome 11 region in the Om locus area (D11Mit37-Scya6) clone 149H13 of library Caltech CITB-BAC from Chromosome 11 of Mus musculus (mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    238 TCTTCAGTCCAATGA----GGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 AAIGTTAGGGTGAAAAGTTACTACTCAACT---CTGTAGGTTAAAAGGAAACGTTGAGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9452 TAGGAAAAAACACAAAAGCATTAAGGAAAACTGGTAGGTGGGGAAATTATCCAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                               61 TAGAAATGGTGATGATGTGTACATCAAGCAGGAGAAAAACCAATGAACCAGATGCGAATT
                                                                                                                                                                                                                                                                                                                   1 TAGGAAAATTATAGGATCATTAAGAAAGGAGAAGGAAGAGGAGGAGGAAATTACCTGGAGG
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Cohen-Tannoudji M., Vandormael-Pournin S., LeBras S., Coumai F., Babinet C., Baldacci, P.
Unite de Biologie du Developpement, CNRS URA 1960, Institut Unite de Biologie du Dr Roux, 75724 Paris cedex 15, France.
Location/Qualifiers
                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                        Length 223726;
                                                                                                                                                                                                                                                                           11;
                                                                                                                                                                                                                             Score 60.4; DB 10; Length
Pred. No. 3.5e-05;
0; Mismatches 151; Indels
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TITLE
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VERSION
KEYWORDS
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CNS07YOT
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Direct Submission

Direct Submission

Direct Submission

Submitted (04-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Submitted (04-APR-2002) Wellcome requests: clonerequestgeanger.ac.uk

Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Nov 30, 2001 this sequence version replaced gi:17065774.

During sequence assembly data is compared as variations
Where differences are found these are annotated as variations

Where differences are found these are annotated as variations

Variation annotation may not be found in the sequence submission

variation annotation may not be found, in the sequence submission

only a small overlapping clone, as we submit sequences with

only a small overlapping clone, as we submit sequence with

regions were either double-stranded or sequenced with an alternate

regions were either double-stranded or sequenced with an alternate

chemistry or covered by high quality data (i.e., phred quality) =

chemistry or covered by high quality data (i.e., phred quality)

as compressions and repeats; all regions were covered by at least

as compressions and repeats; all regions were covered by at least

one plasmid subclone or more than one M13 subclone; and the

one plasmid subclone or more than one M13 subclone; and the

abbreviations are used to associate primary accession numbers given

abbreviations are used to associate primary accession numbers given

abbreviations are used with their source databases: Em:, EMBL; Sw:,

in the feature table with thair source databases: Em:, EMBL; Sw:,

http://www.sanner.ac.uk/Projects/C elecans/wormpep RP23-350Gl is
                                                                                                                                                                                                                                                                                                                           100157 GAĞCTGCATGTATAİCAAGAĞATGGĞGATTİTTCAAGAĞGAAĞCİCAAİACAĞĞĞTİTĞ 100098
                                                                                                                                                                                                                                                                                                                                                                                                                         100097 AATAGGAAGGTGAGAACATGGTATTCCCTCGGACCTATAATTTAAAGGATAAGTTGAAAC 100038
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                                                                                                                                    100274 TAGGAAAAAAACACAAAAGCATTAAGGAAAACTGGTAGGTGGGGAAATTATCCAAAAA 100215
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223726 bp DNA linear ROD 05-APR-2002
Mouse DNA sequence from clone RP23-350G1 on chromosome 11, complete
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     294 G-GAAATGTAACTTATAGATTTTATACACAGAGAAATACGGACTAGTGAGAAGCTA 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            293
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                AATGTTAGGGTGAAAAGTTACTCAACT---CTGTAGGTTAAAAGGAAACGTTGAGAA 237
                                                                                           9
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                                                                                         61 TAGAAATGGTGATGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATT
                                                Gaps
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                           55.5%; Pred. No. 3.5e-05;
tive 0; Mismatches 151; Indels
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DOE Joint Genome Institute.

Direct Submission

Submitted (29-JUN-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

-----Genome Center

Center: Joint Genome Institute
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Sciurognathi; Muridae; Murinae; Mus
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Consensus quality: 143665 bases at least Q40
Consensus quality: 160562 bases at least Q30
Consensus quality: 164105 bases at least Q30
                                                                                                                  Score 60.4; DB 10;
Pred. No. 3.5e-05;
0; Mismatches 151;
/db_xref="taxon:10090"
/chromosome="11"
/clone="149H13"
/clone_lib="Caltech CITB-BAC"
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Center clone name: RPCI-23_92G22
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ACO73824.1 GI:8810441
HTG; HTGS PHASE1; HTGS DRAFT.
Mus musculus (house mouse)
Mus musculus (house mouse)
Eukaryota; Metazoa; Chordata; Ci
Mammalia; Eutheria; Rodentia; Sci
1 (bases 1 to 180944)
DOE Joint Genome Institute.
                                                                                                                  Query Match
Best Local Similarity 55.5%;
Matches 202; Conservative
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Estimated insert size: 194000; pulse field gel estimation
Estimated insert size: 176244; sum-of-contige estimation
Quality coverage: 6.92 in Q20 bases; pulse field gel estimation
Quality coverage: 7.62 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 48 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* trus of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1: gap of unknown length
8: gap of unknown length
7: contig of 8667 bp in length
7: contig of 875 bp in length
7: gap of unknown length
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| organism="Mus musculus"
| mol Lype="genomic DNA"
| db_xref="texon:10090"
| clone="RP23-92G22"
| /clone_lib="RPCI mouse BAC library 23"
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106443 ACIOSEGUE C 255772 bp DNA Illnear HTG 08-OCT-2002

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KEYWORDS
SOURCE
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                                                      AL SUBMILTERIOR OF COTT-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77010, USA

On Sep 14, 2002 this sequence version replaced gi:21737094.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using described in the feature table below represents a scaffold in the Atlas assembly (a 'contig scaffold'). Within each contig-scaffold, individual sequence contrigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: Estimated insert size may differ from sequence length

* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)

* NOTE: This sequence may represent more than one clone.

* NOTE: This is a 'working draft' sequence. It currently

* consists of 1 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* This sequence will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Assembly program: Phrap; version 0.990329
Consensus quality: 233717 bases at least Q40
Consensus quality: 236719 bases at least Q30
Consensus quality: 236622 bases at least Q30
Estimated insert size: 252037; sum-of-contigs estimation
Quality coverage: 4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7.9%; Score 47.4; DB 2; Length 259772; il.2%; Pred. No. 0.071; ve 0; Mismatches 106; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center: Baylor College of Medicine Center code: BCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center clone name: CH230-36G6
                               Genome Sequencing Consortium.
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/db_xref="taxon:10116"
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3446. .6094
/note="wgs_contig"
254751. .255855
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258597. .259772
/note="wgs_contig"
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AUTHORS
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TGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTAACTTATAGATTTTATACAT 321

0; Gaps

51.2%;

Best Local Similarity 51.29 Matches 111; Conservative

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Muzny, D. Marte., Marker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allan, C., Allan, H., Alsprooks, S., Amin, A., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Anguiano, D., Bandaranaike, D., Barber, M., Baratesed, M., Benshmed, F., Bladwin, D., Bandaranaike, D., Barber, M., Baratesed, M., Benshmed, F., Blatwain, D., Blante, M., Cree, A., D'Guere, M., Carter, K., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Carter, M., Davis, C., Davy, Carroll, L., De Anda, C., Dederich, D., Delado, O., Denson, S., Derson, S., Derson, C., Duing, Y., Dinh, H., Divya, K., Denson, S., Derson, C., Duing, Y., Duin, B., Duin, H., Duyan, Rocker, M., Erane, C.A., Folls, T., Fang, M., Gerran, M., Gerran, M., Gerran, M., Gerrander, M., Gerran, M., Gerrander, M., Gerran, M., Gerran, M., Gerrander, M., Gerran, M., Gerrander, M., Harlak, P., Hander, M., Hamilton, C., Hamilton, K., Handler, M., Harlak, M., Handler, M., Hamilton, K., Hangum, A., Jackben, J., Jacob, L., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Karter, C.L., Lebow, H., Jewan, T., Lewis, L., Lill, J., Lill, M., Lill, Y., London, P., London, P., London, P., London, P., London, P., London, P., London, P., London, P., London, P., Martin, R., Martin, R., Martin, R., Martin, R., Martin, K., Mangum, A., Mandhan, M., Morris, S., Milosa, M. P., Martin, R., Martin, R., Martin, R., Martin, R., Martin, S., Mores, S., Morgan, M., Morris, S., Morlock, M. P., Mordon, M., Morris, S., Morlock, M. P., Mordon, M., Morris, S., Morton, M., Morris, S., Morton, M., Morris, S., Morton, M., Morris, S., Morton, M., Morris, S., Morton, M., Morris, S., Paul, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morris, M., Morr
119950 AGTTTATACAATTTGTCAGCCAGACAGGAAAAAGGATACACCGTTCCCAAGGTCAACACT 119891
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Rattus norvegicus clone CH230-33A7, WORKING DRAFT SEQUENCE, 4
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                               382 GGCCTAAATATGGAGCCAAAGGGCAGCAATGAAGAATGAGCCATGCAGGGTGAAATGCT
                                                                                                                                                                                                                                                                                                                                                                    119890 ccarcracacceracarccacacaccrcraraarrca 119854
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DRAFT; HTGS_FULLTOP
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unpublished

2 (bases 1 to 239429)

Norley, K.C.

2 (bases 1 to 239429)

Norley, K.C.

Direct Submission

Submitted (19-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

CE Rat Genome Sequencing Consortium.

Direct Submission

Nov. 2002 Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

ON Nov 15, 2002 this sequence version replaced gi:23267649.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas and thep://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas and individual sequence contigs are ordered and orienced, and separated individual sequence contigs are ordered and orienced, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contigs-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence conly contigs will be indicated in the feature table.
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NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Assembly program: Phrap, version 0.990329
Consensus quality: 220063 bases at least Q40
Consensus quality: 223393 bases at least Q30
Consensus quality: 225574 bases at least Q30
Estimated insert size: 225962; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.
Direct Submission
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3408: gap of unknown length
157094: contig of 153686 bp in length
157194: gap of unknown length
23986: contig of 80792 bp in length
239086: gap of unknown length
239429: contig of 1343 bp in length.
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Center adde: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: project Information
Center project name: GYB1
Center clone name: GYB1
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/organism="Rattus norvegicus"
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clone_end:T7"
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/db_xref="taxon:10116"
/clone="CH230-33A7"
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/note="clone_boundary
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7.4%; Score 44.6; DB 2; Length 239429;
Best Local Similarity 53.1%; Pred. No. 0.38;
Matches 95; Conservative 0; Mismatches 84; Indels 0;
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                                         end sequence: BH351359" 3409. .5768
                                                                                /note="wgs_contig"
clone_end:T7
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August 3, 2005, 15:09:47; Search time 397.652 Seconds (without alignments) 8932.047 Million cell updates/sec
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1 taggaaaattataggatcat......cctggaatcatccatttaaa 600
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                            4390206 seqs, 2959870667 residues
                                                                               OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqn2003cs:* geneseqn2003ds:* geneseqn2004as:* geneseqn1980s:* geneseqn1990s:* geneseqn2000s:* geneseqn2001as:* geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* geneseqn2003as:* geneseqn2003bs:* N_Geneseq_16Dec04:* geneseqn2004bs 10: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

						SUMMARIES	
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Ž	No.	Score	Match	Match Length DB	DB	DI	Description
] 	-	600	100.0	909	9	ADH13938	Adh13938 Human mon
	0	009	100.0	11793	12	AD003803	Ado03803 Human Cc1
	m	41.2	6.9	78268	11	ACN44342	Acn44342 Human gen
υ	4	40.8	6.8	2000	8	ADA71938	Ada71938 Rice gene
υ	S	39.4	9.9	126974	12	ADN30166	Adn30166 Hepatocyt
υ	9	39.4	9.9	144035	11	ACN44062	Acn44062 Human gen
U	7	38.8	6.5	1768	13	ADR64667	Adr64667 Cotton cD
	æ	38.8	6.5	7340	9	AAD28378	Aad28378 Human che
	6	38.4	6.4	8943	9	ABK39967	Abk39967 .Human che
	10	38.2	6.4	52302	σ	ADA02738	Ada02738 Human CCN
. •	11	38.2	6.4	52302	10	ADB72476	Adb72476 Human CCN
. •	12	38.2	6.4	52302	10	ADC85218	Adc85218 Human Ccn
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	14	37.4	6.2	2000	œ	ADA71938	Ada71938 Rice gene
. •	15	37	6.2	2646	13	ADR07244	Adr07244 Full leng
	16	37	6.2	7261	4	AAS46669	Aas46669 Tumour su
	17	37	6.2	101616	11	ACN44934 3	Continuation (4 of
	18	37	6.2	110000	11	ACN44934_2	Continuation (3 of
υ	19	36.6	6.1	201143	9	ABK83568 _	Abk83568 Human DNA
	20	36.4	6.1	3364	9	ABL45715	Ab145715 Human mat

1 Adl13771 Osteoarth	Aas30497 DNA encod	Aal06277 Human rep		2 Adb63552 Human cDN	Aav88382 EST clone	1 Adc08421 Rice DNA	5 Adj41665 Plant cDN	6	Ada31548 DNA encod		7	Acc72421 Human ova	2 Adr72882 Human ove		5 Continuation (6 of		ď	1 Adh71331 Human ger		Aca30251 Prokaryot	Aas69830 DNA encod	Aas72863 DNA encod		
ADL13771	AAS30497	AAL06277	AAK71730	ADB6355	AAV88382	ADC08421	ADJ41665	ABD33599	ADA31548	ABQ76227	ACC72422	ACC72421	ADR72882	ADC86636	ABQ74964	ACN44126	ABT08488	ADH7133	AD009837	ACA30251	AAS69830	AAS72863	ABL33155	
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36.4	36.2	36.2	36.2	36	35.8	35.8	35.8	35.4	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35.2	35	35	35	34.8	34.8	34.8	34.8	,
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ALIGNMENTS

RESULT 1

ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:1. Poustka A; Delius H, Finzer P, (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. BP. 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. ADH13938 standard; DNA; 600 11-MAR-2004 (first entry) Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A; Homo sapiens. EP1170372-A1. 09-JAN-2002. ADH13938; ADH13938

Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer. WPI; 2002-165895/22.

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoatrractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosoclarotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A Disclosure; SEQ ID NO 1; 30pp; English.

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16-OCT-2003;
                                30-OCT-2002;
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 pharmaceutical composition of the invention is useful for the of diseases associated with dysregulation of MCP-1 expression, atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                          Length 600;
                                                                                      Sequence 600 BP; 213 A; 101 C; 150 G; 136 T; 0 U; 0 Other;
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                                                                                                                        ; Score 600; DB 6; I
; Pred. No. 2.3e-173;
0; Mismatches 0;
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               240
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                                                                                                                                                                                                                                                                                                                                                                      This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular Ccl2-deficient, Ccr2-deficient and/ or a Ccl2-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lippfuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polynucleotide sequence is the human Ccl2 gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                    Testing candidate drug for treating age-related macular degeneration, by administering drug to Col2-deficient, Cor2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGAGAAAAAGACCTGTGACTTCAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAACTTATAGATTTTATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        aatgitagggtgaaaagttactactcactctgtaggttaaaaaggaaacgttgagaatct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCAGTCCAATGAGGAGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 IAGAAATGGTGATGATGTACATCAAGCAGGAAAAACCAATGAACCAGATGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10039 TAGAAATGGTGATGATGTGTACATCAAGGAGAAAAACCAATGAACCAGATGCGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 11793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 600; DB 12;
100.0%; Pred. No. 9.1e-173;
rative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                           Disclosure; SEQ ID NO 4; 64pp; English.
                                                                                       KENTUCKY RES FOUND
                                              2002US-0422096P.
2003WO-US032933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                    accumulation in eye.
                                                                                                                                                                                 WPI; 2004-400512/37.
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Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant
                                                                                     Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 27; SEQ ID NO 5263; 899pp; English
                                                                                                                                                                                                                                                                                                                                                    (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                         22-JUN-2001; 2001WO-IB001105
                                                                                                                                                                                                                                                                                                                  22-JUN-2001; 2001WO-IB001105
          20-NOV-2003 (first entry)
                                                 Rice gene, SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                       Katagiri F, Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-175290/17
                                                                                                                                                                                        WO2003000898-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene expression
                                                                                                                                                   Oryza sativa.
                                                                                                                                                                                                                                03-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                 Chang H,
                                                                                                               gene;
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9409 AGGCACAAGGAACAGCAGGTACAAAGGCTCGGAGGTCGGAATGAACTTAATGTTCTACA 9468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating (x) for inhibiting the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma or a propensity to carcinoma; (vi) for determining Carcinoma Associated (CA) gene copy number. In addition, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 AAGGAGAAGGAAGGAGGAAATACCTGGAGGTAGAAATGGTGATGATGTACATC 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent US2002182586A1, for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 78268 BP; 20402 A; 18203 C; 18818 G; 20845 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       6.9%; Score 41.2; DB 11; Length 78268; 62.7%; Pred. No. 0.55; Live 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                               88
                                                                                                                                                                                                                                                                                        Cytostatic; carcinoma; lymphoma; cancer; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 742; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        nucleotide sequence.
                                                                                                                                                                                                                                                  Human genomic sequence hCG17932.
                                                                                                                          ACN44342 standard; DNA; 78268
                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-FEB-2003; 2003WO-US006235
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                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                  ACN44342;
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                                                                                     RESULT 3
                                                                                                           ACN44342
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Hou Y; T, Zou

Goff SA, Hors 2, Zhu T,

Glazebrook J, G Whitham S, Xie

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Cooper 1 S, Tao

Chen W,

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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is bacterial, fungal or viral infection. The present sequence to a plant to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 TAGAAATGGTGATGATGTGTACATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                866 MAKHYMATGWATHMWRYTHYTYYYYACYAMTCAKCKYKMAMTKWWTTWACAWRATSWRWRAM 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GMRWKRYKOKKRAYWWKWWRCWKAGWARWMKSRYRWKWKKYATRYYWKMWAMTWWWSWRRW 747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     421 AGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGAGAAAAAACACCTGTGACTTCAGA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               346 KSYRMWSGMGRMRWSAWRYCSRMKCAKTKYASSARWTKRAKRSYRYRRRWYWKRKGWTYR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           926 ISCMWWKYWRIWSCWYIMWWGAMRYAYYAMRRRRWTYKWSWRRMYWIMIKWAWIWMICMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  686 YRYWRSCRMTRARMSKRRKWAGASMKSCWMYWRGARSMWYSKYSCSAKCCKKTRYMTSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AATGTTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 TCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TAACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 GTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCCAATGAAGAATG
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                                                                                                                                                                                                                                                                                                                              Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                                                                                                         Length 2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   IndelB
                                                                                                                                                                                                                                                                                                                                                                                  6.8%; Score 40.8; DB 8;
10.6%; Pred. No. 0.14;
ive 228; Mismatches 255;
                                                                                                                                                                                                                                                                                                                                                                                                                    10.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      57; Conservative
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δ 셤 ઠે g ADA71938 standard; DNA; 2000

ADA71938

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Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                    407 AGCAATGAAGAATGAGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGAGAAAGA
                                                                                                                                                                                                                                                                                                                                                                                               Cytostatic; carcinoma; lymphoma; cancer; human; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 322; Opp; English.
                                                                                                                                                                                                                                                           ACN44062 standard; DNA; 144035 BP.
                                                                                                                                                                                                                                                                                                                                                                 Human genomic sequence hCG38705.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2002; 2002US-00087192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-2003; 2003WO-US006235
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Best Local Similarity
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                                                                                                                                                                            88077 CATAT 88073
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                                                                                                                                           CCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
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                                                                                                                                            467
                                                                                                                                                                                                                                                                                                      ACN44062;
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Matches
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                                                                                                                                                                                                                                     RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention describes a new compound 8-80 nucleobases in length targeted to a nucleic acid molecule encoding hepatocyte growth factor receptor, where the compound specifically hybridises with the nucleic acid molecule encoding hepatocyte growth factor receptor comprising a acid molecule encoding hepatocyte growth factor receptor comprising a sequence of 4586 bp (SEQ ID NO: 4) and inhibits the expression of hepatocyte growth factor receptor in inhibiting the expression of hepatocyte growth factor receptor in cells inhibiting the expression of hepatocyte growth factor receptor or receptor; a diagnostic method for identifying a disease state; a kit or assay device compitaing the compound; and treating an animal having a disease or condition associated with hepatocyte growth factor receptor. The compound and methods are useful in diagnosing and treating hyperproliferative discorder. This sequence represents a human, hepatocyte hyperproliferative discorder. This sequence represents a human, hepatocyte hyperproliferative discorder.
                                                                                                                                                541 GITICCCICCATIACTAIACCCCCCAICCCAATCTCAGGCACCTGGAATCATCATTIAAA 600
                                                                                                                                                                     CWYYYYGMYMKCSYMWRYGYCKACKKCCYAMCWKAAYSGMMYWYRKYSKWMRMSTKYMW 447
                                                                                                 566 MRKRKYMRYMKWKCTWRRCMCYRWGYTWYTGRSRMMYTGRYKRRYMWYKYRKY 507
                        626 MSTGMYGMYSSYKSMSWTSKMSYMGKMTCTMYTSMKGSTRRSKMGRMSGMSRNYMRWWKK 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88257 Aartacacaaaataatatataaccictgaaaaaaaatacaaaaaaaaccaaactaaacra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seguence 126974 BP; 38160 A; 25346 C; 24426 G; 39042 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New compound targeted to a nucleic acid molecule encoding hepatocyte growth factor receptor, useful in diagnosing and treating
                                                                             481 TATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTCCCTGAAACCAGAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 39.4; DB 12; Length 126974;
Pred. No. 2.5;
0; Mismatches 91; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                 cytostatic; hepatocyte growth factor receptor; human; ds. hyperproliferative disorder; antisense technology; human; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               growth factor receptor associated polynucleotide
                                                                                                                                                                                                                                                                                                                                                                                Hepatocyte growth factor receptor associated DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 15; SEQ ID NO 12; 116pp; English.
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                                                                                                                                                                                                                                                                                  ADN30166 standard; DNA; 126974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23-NOV-2002; 2002US-00304019
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hyperproliferative disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bennett CF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                           12-AUG-2004
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Best Local Si
Matches 94,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dean NM,
                                                                                                                                                                                                 909
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96700 TTGTTGCTAGACTGATAGAGTAACGAAACAAGGAAGTTGAACTGGGTCCGAATGAGAT 96641
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              287 AGTITCAGGAAATGTAACTTATAGATTTTATACATACACAGAAATACGGACTAGTGGG
                                    The present inventious interacts to mover with any entire present inventious interacts. The sequences are useful for: (i) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (CAP); (iii) for screening of binding to Carcinoma Associated Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for diagnosing evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vii) for reating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochib; (x) for diagnosing carcinoma associated (CA) gene copy number: In addition, the determining Carcinoma Associated (CA) gene copy number: In addition, the carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This parent is an equivalent to basic patent upsached is an equivalent to basic patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     347 AAGCTATTGCCATGGTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGG
The present invention relates to novel DNA and protein sequences which
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 144035 BP; 43371 A; 28888 C; 27578 G; 44198 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 39.4; DB 11; Length 144035;
Pred. No. 2.6;
0; Mismatches 91; Indels 0; G
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347 AAGCTATTGCCATGGTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGC 406

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a recombinant polymucleotide comprising any of the 58798 Cotton plant cDNA sequences mentioned in the specification.

CC the 58798 Cotton plant cDNA sequences mentioned in the specification.

CC sequences mentioned in the specification and producing a plant having an improved property.

CC comprises transforming a plant with a recombinant construct comprising a promucer region functional in a plant cell operably joined to a promoter region functional in a plant cell operably joined to a promoterty, and growing the transformed plant. The polypetide associated to polymucleotide comprising a coding sequence for a polypeptide associated to plant cells by modification of the cell cycle pathway, improving plant coll tolerance, manipulating growth rate in plant tolerance, providing increased resistance to plant disease, producing galactomannan (or lignin or plant growth regulators), improving plant tolerance to herbicides, increasing the rate of homologous recombination in plants, improving plant tolerance to extreme commoting conditions or to pathogens or pests, improving yield by modification of photosynthesis, modifying seed oil or protein yield by modification of photosynthesis, modification of carbohydrate, introgen corpus, improving yield by modification of photosynthesis, modification of carbohydrate, introgen corpus, improving yield by providing improved plant growth and development under at least one stress condition. The polymucleotide and polypeptide may also be used in recombinant DNA
                                             407 AGCAATGAAGAATGAGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAAGA 466
                                                                                                                                                                                                                                                                                                                                                                                                                                               Cotton, ss. plant, cold tolerance; growth rate, cell cycle pathway, drought tolerance; plant disease resistance; galactomannan, lignin, plant growth regulator; heat tolerance; herbicide tolerance; homologous recombination; extreme osmotic condition tolerance; pathogen resistance; pest resistance; yield; photosynthesis; seed oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New recombinant nucleic acid molecules and polypeptides from Gossypium hirsutum, useful for producing plants with improved biological characteristics (e.g. improved plant cold or drought tolerance).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 5448; 14pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                         Cotton cDNA sequence, SEQ ID 5448.
                                                                                                                                                                                                                                                                 ADR64667 standard; cDNA; 1768 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-JAN-2004; 2004US-00767795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-MAY-2001; 2001US-00849529
12-DEC-2001; 2001US-00021323
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                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                 96580 CATAT 96576
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ZHOU Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gossypium hirsutum.
                                                                                                      CCTGT 471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance.
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                                                                                                      467
                                                                                                                                                                                                                                                                                                              ADR64667;
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1402 ATAAGAAAGGAAACATAAGAGAAGACGAAATAAAAAATAGATGGTGGAAGTGATAAAA 1343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1283 AAAGAAGAGAGAAAAGAATATTAATAATAAACATAGATAAAACAGAGAGAAATGAACATA 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1223 ACAAAGTATACAATACATATAAAAAAAAGTCACAAGGAAAAATAAAAGTACTAGAAACA 1164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                128 ACACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTA 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 GGGTGAAAAGTTACTACTCCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAGTCC 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 AATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTAACTTA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               308 TAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGGTCCAAG 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; cytostatic; antidepressant; neuroleptic; nootropic; antiaddictive; adrenergic alpha-1C-receptor; cytosine methylation; therapy; alcoholism; behavioural disorder; neurological; psychiatric; cancer; schizophrenia; Tourette's syndrome; smoking; human immunodeficiency virus dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATGAGCCATG 427
constructs, in physical arrays of molecules, as plant breeding markers, or in computer-based storage and analysis systems. The present sequence is a Cotton plant cDNA of the invention. NOTE: The sequence data for thi patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence is commat directly from USPTO at sequence.html?Doc1D=20040181810. However only 6585 polymucleotide sequences were available, the remaining 52213 polymucleotides and all 58798 protein sequences were not present.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38.8; DB 13; Length 1768; Pred. No. 0.53;
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1768 BP; 390 A; 329 C; 277 G; 772 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 6.5%;
Best Local Similarity 47.4%;
Matches 147; Conservative
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1103 AAAGCTTCAA 1094
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428 CAGGGTGAAA 437
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Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1182 ĠGTAĠTŤſTĀĠŤGGĀAARŢĠĞPGĀŤĞĞŤPĀĠĠŤPĀĠĀĀŢŤĀĠĠĀŢŦĀĀĀŢŢŦĀĠĠ 1241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1242 tiraratakarahakitrokakirasakarararitrakarriskirrarikasakaksi 1301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                     The invention relates to nucleic acids comprising a segment of chemically pretreated DNA of adrenergic alpha-IC-receptor gene. The invention also relates to oligonucleotides or peptide nucleic acid (PNA) oligoners useful for detecting cytosine methylations. The pretreated DNA is useful useful for detecting cytosine methylations. The pretreated DNA is useful disorders and cancer, in particular major depressive disorder. Tourette's disorders and cancer, in particular major depressive disorder; Tourette's syndrome, schizophrenia, psychiatric and neurological disorders, smoking, syndrome, schizophrenia, metaricular major depressive disorders, smoking, and schizoaffective patients, and suicidal behaviours in patients with and schizoaffective patients, and suicidal behaviour in patients with schizophrenia. The nucleic acid is useful for detecting the methylation state of all CpG dinucleotides and/or single nucleotide polymorphisms (SNPS). The present sequence is human chemically treated genomic DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ggaaggijgagicaaggaitigaaigiragggigaaaagijactacicaacicigiagg 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    218 TTAAAAGGAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTGCCATGTTAGAGAT 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; ds; bisulphite treatment; CpG; DNA methylation; cancer; tumour; cytostatic; ALDH6; CYPIAA; CYPIBA; CYPIAA; DPYD; BFHX2; OCLN; TXNRD1; UGT8; MRP; pharmacogenomics; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
      Novel nucleic acid useful for diagnosis and therapy of behavioral disorder, neurological disorder and cancer, comprises a sequence of segment of chemically pretreated DNA of adrenergic alpha-1C-receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7340 BP; 1725 A; 249 C; 1982 G; 3384 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 7340;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human chemically pretreated gene sequence #24 strand 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6.5%; Score 38.8; DB
54.1%; Pred. No. 1;
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           278 TCAGAGATAAGTTTCAGGAAATGTAA 303
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                                                                                                                Claim 1; Page 94-98; 190pp; English.
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.5
Best Local Similarity 54.1
Matches 79; Conservative
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The invention relates to a nucleic acid comprising a sequence at least 18 conservation in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the sequences of the associated with pharmacogenomics according to one of the sequences of the genes ALDIE (NM 000693), CYP11A (NM 000761), CYP11B1 (NM 000497), CYP3A3 (NM 000776 and NM 01990), NM 01990), NM 01990, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900, NM 019900
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3198 haritgereadaadarritarritritritritaaaeeeaaaaareraaaatstaa 3257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            243 AGTCCAATGAGGAGGAATGTGTGTTTAGAGATTCAGAGATAAAGTTTCAGGAAATGTA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; carcinoma associated; oncogene; carcinoma; cancer; breast;
prostate; lymphoma; leukaemia; cytostatic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 rgithagagrapapartactactcaacrcraftagartaaaagaaacartaaaaaarcrtc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 8943 BP; 2415 A; 42 C; 1943 G; 4543 T; 0 U; 0 Other;
pharmacogenomics and for therapy of diseases e.g. cancer.
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                                                                                               Claim 1; SEQ ID NO 48; 24pp; English.
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tes 84; Conservative
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Morris

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50950 AGCAGAAGGAACAGAGAATGCAAAAGATCCGGAGGTAGGAATGAGCATGACGTGGTCTACG 51009
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                                                                                                                                                                                                                                                                                                               The invention relates to a novel recombinant nucleic acid comprising a nucleotide sequence salected from any of the 600 sequences fully defined in the specification. A polymucleotide of the invention has cytostatic activity, and may have a use in gene therapy, or in a vaccine. The recombinant nucleic acids and polymptides are useful for treating carcinomas, e.g. lymphomas, cancers, neoplasm, adenocarcinoma, and sarcomas. The present sequence represents a human gene of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 AGGAGAAGGAAGGTGGGAGCAAATACCTGGAGGTAGAAATGGTGATGTGTACATCA 86
                                                                                                                                                                                            recombinant nucleic acid, useful for treating carcinomas, lymphomas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New recombinant nucleic acid comprising a nucleotide sequence of any of the carcinoma-associated (CA) genes, useful for screening for drug candidates for diagnosing or treating carcinomas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 52302 BP; 13145 A; 12501 C; 12728 G; 13888 T; 0 U; 40 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ch 6.4%; Score 38.2; DB 10; Length 52302; Similarity 69.3%; Pred. No. 3.8; 52; Conservative 0; Mismatches 23; Indels 0;
                                                                                                                                                                                                                     cancers, neoplasm, adenocarcinoma, or sarcomas.
                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 304; 2304pp; English.
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20-DEC-2001; 2001US-00034650.
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                                              (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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                                                                                                                                             WPI; 2003-239337/23
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                                                                                               Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Morris DW,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to recombinant carcinoma associated (CA) nucleic acid sequences from mouse and human (ADA01482-ADA03094), and to recombinant carcinoma associated proteins (CAP) encoded by them. The invention also encompasses expression vectors and host cells comprising a CA nucleic acid, a polypeptide (especially an antibody) that specifically finds to the protein, and a blochip comprising CA nucleic acid or fragments thereof. The sequences of the invention were identified using oncogenic retroviruses, which insert into the genome of the host organism at random. Many of these do not carry transduced host oncogenes or pathogenic trans-acting viral genes, meaning that cancer incidence is a direct consequence of the effects of proviral integration into host protonnocegenes. The CA nucleic acid sequences can be used to diagnose
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carcinoma (especially breast cancer, prostate cancer, lymphoma or leukaemia) or a propensity to carcinoma by determination of the sequence of a CA gene, or by determination of CA gene expression in particular tissues. CA nucleic acids, proteins and antibodies are also useful as therapeutic agents and in screening and evaluating drug candidates. The present sequence of the invention. Note: The complete sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 52302 BP; 13145 A; 12501 C; 12728 G; 13888 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                 recombinant nucleic acid encoding carcinoma associated protein, ful for preparing compositions for treating carcinomas.
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6.4%; Score 38.2; DE
1 Similarity 69.3%; Pred. No. 3.8;
52; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                      Claim 1; SEQ ID NO 1256; 245pp; English.
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; 2001US-00052482.
; 2001US-00997722.
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                                                             WPI; 2003-587068/55.
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23-OCT-2001;
08-NOV-2001;
30-NOV-2001;
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Katagiri F,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to new recombinant nucleic acids. The invention also relates to a host cell comprising a recombinant nucleic acid or also relates to a host cell comprising a recombinant nucleic expression vector, an expression vector comprising a recombinant nucleic acid, a recombinant protein, a method of screening for drug candidates, a acid, a recombinant protein, a method of screening for a bioactive agent capable of binding to a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a carcinoma associated protein (CAP) encoded by a nucleotide sequence, a method of evaluating the effect of a candidate carcinoma drug, a method of diagnosing carcinoma, a method of the activity of a CAP, a method of treating carcinoma, a method of capable of carcinoma or neutralising the effect of a CAP and a method of evaluating the effect of a candidate propensity to carcinoma. A method of evaluating the effect of a candidate carcinoma drug comprises administering the drug to a patient, removing a carcinoma drug comprises administering alterations in the
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associated (CA) genes from the 50 tables given in the specification. The CA proteins are secreted, transmembrane or intracellular proteins. The recombinant nucleic acids are useful for screening for drug candidates for diagnosing or treating carcinomas. Sequences given in ADC85215-ADC85514 represent CA genes of the invention.
                                                                                                                                                                                                                        27 AGGAGAAGGAAGAGGAGGAAATACCTGGAGGTAGAAATGGTGATGATGTGTATACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; carcinoma associated nucleic acid; CA nucleic acid; gene; ds; carcinoma associated protein; CAP; carcinoma; leukaemia; lymphoma;
                                                                                                              Sequence 52302 BP; 13145 A; 12501 C; 12728 G; 13888 T; 0 U; 40 Other;
                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New carcinoma associated gene or protein, useful for preparing a composition for diagnosing or treating carcinoma e.g., leukemia
                                                                                                                                                6.4%; Score 38.2; DB 10; Length 52302; 9.3%; Pred. No. 3.8; o, Mismatches 23; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human carcinoma associated (CA) nucleic acid #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 4; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADM74333 standard; DNA; 52302 BP.
                                                                                                                                                                                                                                                                                                                                            51010 AACAGAGAGAGGCCC 51024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-NOV-2001; 2001US-00997722.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-DEC-2000; 2000US-00747377.
02-MAR-2001; 2001US-00798586.
                                                                                                                                                                                                                                                                                                         87 AGCAGGGAGAAAACC 101
                                                                                                                                                                            ilarity 69.3%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MORR/) MORRIS D W.
(ENGE/) ENGELHARD E K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-328562/30.
                                                                                                                                                  Query Match
Best Local Similarity
.....heg 52; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US2004072154-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15-APR-2004.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cytostatic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADM74333;
                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
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expression or activation of a gene comprising the nucleotide sequence. A method of diagnosing carcinoma comprises determining the expression of method of diagnosing carcinoma comprises determining the expression of the cone or more genes comprising the nucleic acid sequence in a first tissue con or mate genes comprising the expression of the gene from the first individual conformation of the gene from the first individual, where a difference in the expression indicates conformation of the first individual has carcinoma. A method of inhibiting the carcinomas comprises binding an inhibitor to the CAP. Treating a cutivity of a CAP comprises binding an inhibitor of CAP.

C carcinomas comprises administering to a patient an inhibitor of CAP.

C carcinomas comprises administering to a patient an inhibitor of CAP.

C carcinomas comprises an antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acid. The nucleic acid. The nucleic acid. The nucleic acid. The polypoptide and antibody that specifically binds to the protein encoded by the nucleic acid. The nucleic acid of the invention. Note: The sequence data associated (CA) nucleic acid of the invention. Note: The sequence data associated (CA) nucleic acid of the invention. Note: The sequence data conformed an electronic format directly from USPTO at the print of the print of the printed specification but was compared to the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care of the printed specification but man care 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identifying at least one gene involved in plant resistance or response pathogenic infection for conferring resistance or tolerance to a plant bacterial, fungal or viral infection by determining or detecting plant gene expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a method (M1) for identifying genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 AGGAGAAGGAAGAGGAAGCAAATACCTGGAGGTAGAAATGGTGATGATGTGTACATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 52302 BP; 13145 A; 12501 C; 12728 G; 13888 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant; bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 52302;
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Z, Zhu T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23;
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Whitham S, Xie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6.4%; Score 38.2; DB
59.3%; Pred. No. 3.8;
ve 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADA71938 standard; DNA; 2000 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  segdata.uspto.gov/sequence.html.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        51010 AACAGAGAGAGCCC 51024
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S, Tao Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-JUN-2001; 2001WO-IB001105.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 AGCAGGGAGAAAACC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62..
Best Local Similarity 62..
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-NOV-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen W, Cor
F, Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-175290/17.
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comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or viral infection. The present sequence was used to instract the invention.
                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                              62 AGAAATGGTGATGATGTACATCAAGCAGGAGAAAACCAAATGAACCAGATGCGAATTC 121
                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                       327 KKMYWYRGYKGMKRGWWAGRMMRSMCRWSKACYYWRWRWRWRWTRRRRWAKKSSRTSRRK 386
                                                                                                                                                                                                                                                                                                                                                                                                                                         241
                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 KRKWCMRKRKYKRWRGYSRWRSCKRARWMKRCRSGRAWKWGCKGCWICRMKSYGWMRWKS 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         626 KRSSAKRYAMMGGMISGSRMSRWKSYICYWRKWGSMKSTCTWMYYMSKYIYAKYGSYWRY 685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RYRAWCMYMWRWYYYRYRSYMTYMAWYTSSTRMAMTGMKYSGRYWTSWYKYCKCSWKYRS 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               302 AACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        482 ATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTCCCTGAAACCAGAATGTG 541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Full length human cDNA useful for treating neurological disease Seq 750.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene; 88; human; oligo-capping method; diagnostic marker; gene therapy; osteoporosis; neurological disease; Alzheimer's disease; Parkinson's disease; dementia; short memory; cancer; sense or motor function; emotional reaction; fear response; panic; osteopathic; neuroprotective; nootropic; antiparkinsonian; cytostatic;
                                                                                                                                                                                                                                                                                                                     267 RKMRWSRSYGWYSWSYKMMCTAYKKSYYSRWCYMYRGGGWRGATRYWGRGYMSRMAMYY
                                                                                                                                                                                                                                                                                                                                                                 CAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATGTTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     422 GCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAAGACCTGTGACTTTCAGAT
                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                        Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                             DB 8; Length 2000;
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                                                                                                                                                                                                                                      Best Local Similarity 8.4%; Pred. No. 1.5;
Matches 43; Conservative 237; Mismatches 228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADR07244 standard; cDNA; 2646
                                                                                                                                                                                                                         6.2%;
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This invention relates to novel, isolated full length human cDNA molecules and the encoded proteins thereof. Specifically, it refers to constant obtained by an oligo-capping method, where none of these clones are identical to any known human mRNAs. The present invention describes an immunoassay to identify agonists and antagonists, as well as cartibodies, antisense molecules and siRNAs that can all be used to bind to and modulate expression of the CDNA molecules. As such, these conditions diseases or morbid states. In particular, they are useful in gene therapy for treating osteoporosis, neurological disease, Alabeimer's disease, Parkinson's disease, dementia, short memory and various cancers, as well as for maintening equilibrium of sense or motor function, and for treating emotional reaction, fear response and panic. Accordingly, they exhibit osteopathic, neuroprotective, nootropic, antiparkinsonian, cyfostatic and tranquiliser activities. This solymucleotide is a full langth human cDNA sequence of the invention. NOTE: This sequence is not given in the sequence listing of the specification but can be obtained on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1800 TATTAAGAAATGATAGGAACATTGACACTAATGTGGAGGAATTTGCCAAATATTTTATTT 1859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278
                                                                                                                                                                                                                                                                                                                              New 1995 cDNA, useful for treating osteoporosis, neurological diseases, Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219 TAAAAGGAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATT
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                                                                                                                                                                                                      Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2646 BP; 845 A; 450 C; 495 G; 856 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                45; Indels
                                                                                                                                                                                                   Nishikawa T, Isono Y,
Nagai K, Irie R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 750; 2686pp; English.
                                                                                                                                                             (REAS-) RES ASSOC BIOTECHNOLOGY
                                                                                                14-FEB-2003; 2003JP-00102207.
09-MAY-2003; 2003JP-00131452.
                                                          12-FEB-2004; 2004EP-00003145.
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58.7%;
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Best Local Similarity 58.77
Matches 64, Conservative
                                                                                                                                                                                                   Yamamoto J,
, Ishii S,
                                                                                                                                                                                                                                                                  WPI; 2004-583265/57.
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                                                                                                                                                                                                                           Wakamatsu A,
                 18-AUG-2004.
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Search completed: August 4, 2005, 08:30:58 Job time : 406.652 secs

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Perfect score:

Sequence:

OM nucleic

Run on:

Total number

Searched:

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tigr-gss dog-17000363267544 Dog Library Canis familiaris genomic,
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USB
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/organism="Canis familiaris"
/organism=Canis familiaris"
/mol type="genomic DNA"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db xref="taxon:9615"
/db xref="taxon:9615"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
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The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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llarity 72.3%; Pred. No. 3.4e-47;
Conservative 0; Mismatches 114;
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AG429637
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CC063247
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Class: shotgun.
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Canis familiaris
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage.

BP 191 91006 ENTRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of Determination with the Berkeley Diroscophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Dirosophila The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Razutoyo Goscegawa and melanogaster BAC library was prepared by Razutoyo Goscegawa and melanogaster BAC library was prepared by Razutoyo Goscegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, isogenic strain v2; cn bw sp, the same strain used for the BDGP's isogenic strain v2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or and how to order individual BAC clones, the entire library, or found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Quallifiers

Location/Quallifiers
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                      177
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
TAGAAATGGTGATGATGTGTACATCAAGCAGGAGAAAACCAATGAAACTGCGAATT
                                                                                121 CGGCCCACCAATGTCAAGGGA---TGACAATTAGAAAGGAAGGTTGAGTCAAGGGAT
                                                                                                                      melanogaster"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGAATGAGCCATGCAGGGTGAAATGCTGCATGTTG 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    480 AGAATGAAATAGGTAGAATGAAATGCTGTGCGTTG 514
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/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone="BACR12X2"
/clone lib="RPCI-98"
/note="end : TET3"
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Direct Submission

Direct Submission

Direct Submission

Submitted (02-UNN-1999) Genoscope - Centre National de Sequencage:

Submitted (02-UNN-1999) Genoscope.

Bp 191 91006 EVRY cedex - FRANCE (E-mail: seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a petermination of this BAC-end sequence was carried out as part of a petermination of this BAC-end sequence project (BDGP).

Collaboration with the Berkeley Drosophila Gromer constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila Drosophila melanogaster BAC library was prepared by Kazutoyo Osocgawa and melanogaster BAC library was prepared by Kazutoyo Osocgawa and Anyr The library is named RPCI-99 and was constructed by patrial NY. The library is named RPCI-99 and was constructed by patrial CORI digestion of Drosophila DNA provided by the BDGP from the BCORI digestion of Drosophila DNA provided by the BDGP from the BCORI digestion of Drosophila DNA provided by the BDGP from the BCORI digestion of Drosophila DNA provided by the BDGP from the BCORI digestion of corder individual BAC clones, the entire library, or and how to order individual BAC clones, the entire library, or found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACROIM22 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              302 AACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           362 TCCAAGCAAGAATGAAGGCCTAAATATGGAGCCAAAGAGGAGCAGCAATGAAGAATGA
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Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Bukaryota; Metazoa; Arthropoda; Brachycera; Muscomorpha;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                              62 AGAAATGGTGATGTGTACATCAAGCAGGAAAAAACCAATGAACCAGATGCGAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 884 RARARARARAKAARAKGARRRRGKRRRRGKRAKARAKGAGGRAGRRGKGRGKRARAK
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ch
1 Similarity 18.5%; Pred. No. 4.1e-07;
86; Conservative 173; Mismatches 206;
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Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Geoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial BCORI digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2; cn bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
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                                                                                                                                                                                                                                                                                                                                                                                             130 ACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTAGG
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Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha,
Ephydroides, Drosophilidae, Drosophila.
                                                                                                                                                                                                                                                      Length 1101;
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                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                          Mismatches 133;
                                                                                                                                                                                                                                                 8.3%; Score 49.6; DB 9;
19.5%; Pred. No. 0.015;
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/organism="Drosophila m
/mol_type="genomic DNA"
/db_xref="taxon:7227"
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                                                                                                          /clone lib="DrosBAC"
/plasmid="pBeloBAC11"
/note="end : T7"
                                                                                   /clone="BACN03K20"
                                                                                                                                                                                                                                                                                                          Conservative 144;
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Droscophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - . This Droscophila malanogaster BAC library (Dros BAC) was made by Alain Billaud at CBFH (Centre d'Ettude du Polymorphisme Humain) with funding provided by a MRC paroject grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                             65 AATGGTGATGATGTGTACATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATTCGGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  125 CCCACACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATG 184
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
I (bases 1 to 1101)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 365 AAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATGA
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                                                                                                                                                                                                                                                                             Length 1101;
                                                                                                                                                                                                                                                                             9.5%; Score 57; DB 9; Length 110 ilarity 24.7%; Pred. No. 0.00012; Conservative 128; Mismatches 186; Indels
                                                         melanogaster"
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Drosophila melanogaster
                                  1. .110]
/organism="Drosophila mel/organism="Drosophila mel/mol type="genomic DNA"
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/clone="backolus2"
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AG287979 171 bp DNA linear GSS 02-JUN-2004 TALS musculus molossinus DNA, clone:MSMg01-061N22.TJ, genomic survey
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Mus musculus molossinus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus
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Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial NY. The library is named RPCI-98 and was constructed by partial in EcoRI digestion of Drosophila DNA provided by the BDGP from the Engentic strain y2. On bw sp, the same strain used for the BDGP's in and how to order individual BAC clones, the entire library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          182 AIGTIAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTT
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2 (bases to 771)

4 thattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Pl
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAATGGTGATGTGTACATCAAGCAGGAGAAAAACCAATGAACCAGATGCGAATTC
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BAC end Sequences of Library MSMg01
Unpublished
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| sarrgrrrarragagarrgarrrarragrragrragara 574
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Local Similarity 22.5%; Pred. No. 0.045;
Les 91; Conservative 121; Mismatches 193; Indels
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/organism="Drosophila melanogaster"

/organism="Drosophila"

/db_xref="taxon:7227"

/clone="BARCH0516"

/clone lib="RPCI-98"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNSO0418 10 0 0NA linear GSS 03-JUN-1999 Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR09CIG of RPCI-98 library from Drosophila melanogaster (fruit fluit ell)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 CCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATGAG 422
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                                                                                                                                                                                                                                                                                                                                                                                                                                       63 GAAATGGTGATGATGTGATCATCAAGCAGGAGAAAAACCAATGAACCAGATGCGAATTCG 122
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/mol_type="genomic DNA"
/db_xref="texon:7227"
/clone="BACRO8K10"
/clone lib="RRCI-98"
/note="end : TET3"
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1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institude, Bio Resource Center, The Institude, Physical and Chemical Research (RIKBN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (B-mail: seqref@genoscope.cns.fr.
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Barkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Gsoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 AGAAATGGTGATGATGTGTACATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATTC 121
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="mixture of kidney and spleen" clone_{1b}=msmg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                             organism="Mus musculus molossinus"
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                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                  e-mail: abe@rtc.riken.jp
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CNS0182P 1101 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37D10 of DrosBAC library from Drosophila melanogaster (fruit
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.ut - . This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 ATGTTAGGGTGAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTT 241
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NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the Esogenic strain y2; cn bw sp, the same strain used for the BDGP sp and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                              /.organism="Drosophila melanogaster"
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Pred. No. 0.29;
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Drosophila melanogaster
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Best Local Similarity 14.1%;
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CNSOOEMH Linear GSS 04-JUN-1999
Drosophila melanogaster genome survey sequence T7 end of BAC:
BACR29MG of RPCI-98 library from Drosophila melanogaster (fruit
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Submitted (02-UU1-1999) Genoscope - Centre National de Sequencage :
Submitted (02-UU1-1999) Genoscope - FRANCE (E-mail : segref@genoscope.cns.fr
Bp 191 91006 EWRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
Web : www.genoscope.cns.fr)
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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/organism="Sorghum propinguum"
/organism="Sorghum propinguum"
/olox taref="teaxon:132711"
/clone="SP_Ba0082111"
/clone="SP_Ba"
/note="Woctor: pBeloBAC11; Site_1: HindIII; Site_2: HindIII; Paterson lab BAC library (HindIII)"
                                                                                                                                                                                                                                                                                                                                                            Length 1181;
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7.4%; Score 44.4; DB 8; 1
Best Local Similarity 44.4%; Pred. No. 0.43;
Matches 185; Conservative 0; Mismatches 231;
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                                                     PCR PRIMERS
FORWARD: atc agc ggc cgc gat cc
BACKWARD: gta aaa cga cgg cca gtg
Plate: 0082 row: I column: 11
Seq primer: atc agc ggc cgc gat cc
Class: BAC ends.
Tel: 520 626 3967
Fax: 520 621 9288
Email: http://genome.arizona.edu
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                                                                                                                                                             Location/Qualifiers
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Sorghum.

(bases 1 to 1181)

Wing, R., Yu, Y., Kim, H.R., Collura, K., Pries, G., Currie, J.,

Sequencing of Sorghum BAC ends.

http://genome.arizona.edu/stc/sorghum

Unpublished (2003)
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University of Arizona
Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
85721-0088, USA
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/note="end : SP6"
                                                                                                                                                                                                                                    Query Match 7.5%; Score 44.8; DB 9; L
Best Local Similarity 26.3%; Pred. No. 0.33;
Matches 121; Conservative 129; Mismatches 209;
                                   Location/Qualifiers
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                     pBeloBAC11
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecorl digestion of Drosophila DNA provided by the BDGP from the isogenic strain v2: cn bw 8p, the same strain used for the BDGP's PI and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Mus musculus molossinus DNA, clone:MSMg01-271024.TJ, genomic survey
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Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 ATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTAGGGTGAAAGTTACTA
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
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29.3%; Pred. No. 1;
tive 77; Mismatches 167; Indels
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                                                                                                                                                                                                                                                                                                                                      /organism="Drosophila melanogaster"
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BAC end Sequences of Library MSMg01
Unpublished
                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic DNA"
/db_xref="taxon:7227"
/dlone=lab="RROI-98"
/note="end : T7"
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Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-15-503-9170)
Clones are derived from the mouse BAC library MSNg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Troukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan phone: 81-298-36-9189, fax: 81-298-36-9199
PRIMERS
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etrinopterrygii; Neopterrygii; Teleostei; Neoteleostei; Neoteleostei;
Acanthomorpha; Acanthopterrygii; Percomorpha; Tetraodontiformes;
Tetradontoidea; Tetraodontidae; Tetraodon.
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Saurin, W. and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
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/clone lib="MSMg01 Mouse Male BAC Library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Mus musculus molossinus"
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/sub_species="molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:57486"
/clone="MSMg01-271024.TJ"
/sex="male"
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GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
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: EcoRI
: EcoRT
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Matches 108, Conservative
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Tue Aug

20296633 10835645

PUBMED REFERENCE

AUTHORS

10899143 3 (bases 1 to 893)

TITLE JOURNAL

COMMENT

AUTHORS

REFERENCE

20359837

JOURNAL

TITLE

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AG379935 1065 bp DNA linear GSS 03-JUN-2004 Mus musculus molossinus DNA, clone:MSMg01-189C10.IJ, genomic survey sequence.
                 AG379935
LOCUS
DEFINITION
RESULT 14
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CCATGCAGGGTGA 435 GAAAGGGGAGGGA 539

423 527

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Submitted (IT-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); I-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel:81-45-503-9111, Fax:81-45-503-9170)

Clones are derived from the mouse BAC library MSMg01. For BAC clones are derived from the mouse BAC library MSMg01. For BAC Treukuba Institude, Bio Resource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Bhone: 81-288-36-9189, fax: 81-298-36-9199

e-mail: abe@rtc.riken.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              261 GIGCCAIGITIAGAGAITCAGAGAIAAGITICAGGAAAIGIAACITAIAGAITITAIACA 320
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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/clone_lib="MSMg01 Mouse Male BAC Library"
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BAC end Sequences of Library MSMg01
Unpublished
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/sub_species="molossinus"
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/clone="MSMg01-189C10.TJ"
/sex="male"
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Direct Submission
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R.Site 2
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Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                      ORGANISM
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AUTHORS
TITLE
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AUTHORS
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                  VERSION
KEYWORDS
SOURCE
ACCESSION
                                                                                                                                                                                                                     JOURNAL
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                                                                                                                                                                                                                                                                    Genoscope.

Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 ACTIATAGATITITATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGGT 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              468
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GAAATGGTGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATTCG 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGAAAATTATAGGATCATTAAGAAAGGAGAAGGAAGAGTGGGAGCAAATACCTGGAGGTA 62
                                                                                                                                                                                                                                                                                                                                                 - Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a lar scale clone-end sequencing project of the Tetracdon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetracdon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Tetraodon nigroviridis"
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/db_xref="taxon:99883"
/clone="046011"
/clone lib="G"
/note="Genoscope sequence ID : COBG046AH06LP1~end : T7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 AGGGGAAAGAGARAGGGGGC----GAGAAGGGAAGAAGAGAAARAAGAAARAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       363 CCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCCAAAAGAGGCAGCAATGAAGAATGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 TGTTAGGGTGAAAAGTTACTACTCCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           419 GGAAAAAAAGGAAANACAAAGAARGAARGGGAAGAAAAAAGAGGGA------
                                                          Rocet Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C., Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J. Characterization and repeat analysis of the compact genome of Ereshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9; Length 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20; Mismatches 207; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.0%; Score 42; 43.9%; Pred. No.
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Query Match Best Local Similarity 43.99 Matches 190; Conservative

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FEATURES

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811

80

871

Job time : 2839.9 secs

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Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the Buropean Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.ur. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                 Drosophila melanogaster genome survey sequence SP6 end of BAC BACNOSCO7 of DrosBAC library from Drosophila melanogaster (fruit ALI), genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          589 AGAAAAATAAAAAAAAWAGAAAGRAGAARAAAGGAAARARAAWAWAAAAAWAAWAAA 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             65 AATGGTGATGATGTGTACATCAAGCAGGGAGAAAACCAATGAACCAGATGCGAATTCGGG 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             125 CCCACACCAATGTCAAGGGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATG 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            185 TTAGGGTGAAAAGTTACTACTCCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAG 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            409 AGAAAAAAATAATATATATATAAATTAAATTAGWAGRATARATAAWTGAAATAAAAGAAAR 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               245 TCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTAAC 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                349 AAAAAAAAATWAAAWRAAAACATAATRWGWGTAAAACAAAAAAAAAAAAAAAAAAAAAAAA 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TTATAGATTTTATACATACATAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGGTCC 364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 AAAATTATAGGATCATTAAGAAAGGAGAAGAAGAAGTGGGAGCAAATACCTGGAGGTAGA
                                                                                                                                                                                                                 Drosophila melanogaster (fruit fly)
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Drosophila melanogaster"
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/db xref="texon:7227"
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/clone lib="DrosBAC"
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/note="end : SP6"
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6.94; Score 41.6; DB 9;
Best Local Similarity 34.24; Pred. No. 2.5;
Matches 143; Conservative 37; Mismatches 238;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                       AL102403.1 GI:5614014
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RESULT 15
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                                                                   DEFINITION
                                                                                                                                                                                                                                             ORGANISM
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Search completed: August 4, 2005, 14:31:57

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Sequence 135585, Sequence 145580, Sequence 14558, A Sequence 15858, A Sequence 15546, A Sequence 1546, A Sequence 44, Appl Sequence 44, Appl Sequence 2268, A

Sequence Sequence Sequence

2, Appli 15273, A 68086, A

Sequence Sequence Sequence

Sequence:

Run on:

Searched:

Database

Result

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Length 7218;
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US-09-509-712B-56

US-09-509-112B-56

US-09-949-016-13585

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US-09-949-016-14580

US-09-949-016-14580

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US-09-949-016-14580

US-09-949-016-18580

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US-09-949-016-16073

US-09-949-016-16073

US-09-270-767-8286

US-09-270-767-8286

US-09-270-767-8286

US-09-270-767-8286

US-09-270-767-8286

US-09-270-767-8286

US-09-949-016-18073

US-09-949-016-18073

US-09-949-016-18073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 14, Application US/08232463
Sequence 10, 5670367
GENERAL INFORMATION:
APPLICANT: SCHEIFLINGER, F.
APPLICANT: PALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDERSS:
ADDERSSEE: FOley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: ALAxandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 22313-0229
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEFAX: R001/
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 26-AUG-1991
ATTONNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11.8%; Score 70.6;
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INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
    277
3857
3857
3857
3955
40117
145320
1193303
1193303
3851
8851
86573
6601
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STRANDEDNESS: single
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 1
US-08-232-463-14/c
       Query Match
       Sequence 16268, A Sequence 16268, A Sequence 16281, A Sequence 16431, A Sequence 16431, A Sequence 17, Appl Sequence 2813, Ap Sequence 2813, Ap Sequence 2813, Ap Sequence 2813, Ap Sequence 2835, Ap
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Sequence 32, Appl
Sequence 32, Appl
Sequence 3, Appli
                                                                                                                                                      August 4, 2005, 07:01:49; Search time 123.644 Seconds (without alignments) 7940.282 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 14, Appl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                 1 taggaaaattataggatcat.......cctggaatcatccatttaaa 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Description
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                         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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S-09-949-016-18001
S-09-949-016-194028
S-09-949-016-1333
S-09-949-016-1333
S-09-949-016-15956
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US-09-949-016-15841
US-09-621-976-18033
US-09-09-016-15841
US-09-09-016-15841
US-09-244-796-17
US-09-244-796-17
US-09-949-016-15509
US-09-949-016-15509
US-09-949-016-15670
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US-09-949-016-115670
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US-09-949-016-115670
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US-09-949-016-115670
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Maximum Match 100%
Listing first 45 summaries
                                                                                                              OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
Maximum DB seq length: 200000000
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600
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Match Length
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score great
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36.2
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35.22
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Sequence 15841, Application US/09949016
; Sequence 15841, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES
; TITLE OF INVENTION: UNMBER: 2000-04-14
; PRIOR PLILING DATE: 2000-10-20
; PRIOR PLILING DATE: 2000-10-03
; PRIOR PRILING DATE: 2000-10-03
; PRIOR PLILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2007012
; SOFTWARE: FRSESEQ for Windows Version 4.0
; SEQ ID NO 15841
                                                                                                                                                                                                                                                                                              Sequence 16268/C

Sequence 16268, Application US/09949016

Sequence 16268, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, USTORING ET al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TITLE OF INVENTION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,768

PRIOR FILING DATE: 2000-10-20
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE FEASERQ for Windows Version 4.0

SEQ ID NO 16268

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118 WRKKSYRRTRCANAYAWKTKRSYYWCWRWKWKRCMMMMMMAMAYGKTMMMRACWKTRYWR 59
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                                                                                                                                  58 WAAWAAMWEMWITMPOMYYYWYNEAMKERWMWEKWESWSWMWAAWGMITRWAARNWWEW
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Pred. No. 0.48;
0; Mismatches 91; Indels 0;
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1 Similarity 50.8%;
94; Conservative (
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Best Local Similarity
Matches 94; Conserv
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US-09-949-016-16268
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                                                                                                                                                                                                                                   185 TTAGGGTGAAAAGTTACTACTCCAACTCTGTAGGTAAAAGGAAACGTTGAGAATCTTCAG 244
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ilarity 10.5%; Pred. No. 0.024;
Conservative 140; Mismatches 125; Indels
                                                                   Similarity 3.3%; Pred. No. 1.4e-11; Indels 13; Conservative 237; Mismatches 141; Indels
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APPLICANT: JOBERT, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTS and Encoded Human Proteins.
FILE REFERENCE: GENSET.054PR2
CURRENT APPLICATION WUMBER: US/09/621,976
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 19335
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Patent No. 6639063
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Matches 31; Conserve
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US-09-621-976-2813
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NAME/KEY: CDS
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APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12342 AGACAGCAAAACCAAAAAACATGGTTAGAATAAATAAGAATTTTACTTAATGATTGCTA 12301
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                          385 CTAAATATGGAGCCAAAGAGGCAGCAATGAAGAATGAGCCATGCAGGGTGAAATGCTGCA 444
                                                                                                                                    159 GAAGGTTGAGTCAAGGGATTTGAATGTTAGGGTGAAAAGTTACTACTCCAACTCTGTAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                339 CTAGTGAGAAGCTATTGCCATGGTCCAAGCAAGAGATGATGAAGGCCTAAATATGGAGCC
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CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR PILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 16431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.1%; Score 36.4;
46.5%; Pred. No. 1.
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COCATION: (1)...(16741)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-16431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 46.5
Matches 118; Conservative
                                                                                                                                                                                              505 CATTTTAA 512
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76 AAWWWTWA 69
                                                                                                                                                                                                                                                                                                  RESULT 6
US-09-949-016-16431
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US-09-007-005-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTGC 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATGITIAGAGAITCAGAGAIAAGITICAGGAAAIGIAACTIAIAGAITITIAIACAIACA 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              316 RGGKYMRRAARRWTWARRAAMYTWWTYWWKGSCMWKSMMMRKWRKYMWKCCYWWWRKYCC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  256 MRKKRRRGKKRARSYKGSYKGGSYTYYKGGKKGGGTKGCKAMSKKGRRRAMTTTTYYKK 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            87351 TGGGTAAACCAGAGGAGACTGAGAAACACGGCAACACAGAGGGGGGGAATTCATCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AATGTTAGGGTGAAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT
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                                                                                                            Length 177251;
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                                                                                                          Score 39.4; DB 4; Length 1
Pred. No. 0.57;
0; Mismatches 171; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Jobert, S. APPLICANT: Jobert, S. APPLICANT: Giordano, J.Y. TITLE OF INVENTION: ESTS and Encoded Human Proteins. FILE REFERENCE: GENEET.054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
NUMBER OF EQ ID NOS: 19335
SOFTWARE: Patent.pm
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Best Local Similarity 13.3%; Pred. No. 0.18;
Matches 41; Conservative 130; Mismatches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18033, Application US/09621976
Patent NO. 6639063
GRERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
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                                                                                                     Query Match
Best Local Similarity 45.4%;
Matches 142; Conservative
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LOCATION: 16
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US-09-621-976-18033/c
                   ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15841
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LENGTH: 177251
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LENGTH: 474
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RESULT 10
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US-U9-244-/20-1)

Sequence 17, Application US/09244796

Sequence 17, Application US/09244796

Sequence 17, Application US/09244796

GENERAL INFORMATION:
APPLICANT: SCOSTAK, Jack W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS
FILE REFERENCE: 00786/350007
CURRENT FILING DATE: 1999-02-05
CURRENT FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FRESCE for Windows Version 4.0

SEQ ID NO 17

LENGTH: 289
APPLICANT: SZOSTAK, Jack W.
APPLICANT: RODETER, Richard W.
APPLICANT: RODETER, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: FUSIONS
TITLE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-0-1-14
CURRENT FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17
SEQ ID NO 17
LENGTH: 289
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Best Local Similarity 4.6%; Pred. No. 0.22;
Matches 9; Conservative 89; Mismatches 99;
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LCCATION: (1)...(289)

CTHER INFORMATION: n = A,T,C or G

US-09-007-005-17
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208 NRNRSRNRNRSRCRARG 224
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ORGANISM: Artificial Seguence
FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           143 WWKRWKKAMTTWWWKKTYYWAATRYWWMCWTKRWRASWWYCWWWGKARKWSTWRKSRSY 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      203 ASARSAKRCCYSCSWGAMSWKYMWRWRGWATGAGMKAWRASCMMRRKYAGKSKTSYK 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 SMWMCWIRSWKYCYTKARWIGYYCYRKGGMWGKRGRWYASKKYMWKRWWWCWARMYRYST 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                 148 NRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSR 207
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                                                                                                                                                                                                                                                                                                                                                                                  89 NRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSR 147
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                                                                                                                                                                                                                                                                                  28 URUKURARCRARARUKURARCRARARUKGRINRINRSRINRINRSRINRINRSRINRINRSR
                                                                                                                                                                                                                                                      Length 832;
                                                                                                                                                         Query Match 6.0%; Score 36.2; DB 3; Length 289;
Best Local Similarity 4.6%; Pred. No. 0.22;
Matches 9; Conservative 89; Mismatches 99; Indels
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; Sequence 2813, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; FILE REFERENCE: GENSET, 054PR.
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SEQ ID NO 2813
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CTHER INFORMATION: Translation template FEATURE:

NAME/REY: misc_feature

LOCATION: (1)...(289)

OTHER INFORMATION: n = A,T,C or G

US-09-244-796-17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        208 NRNRSRNRNRSRCRARG 224
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: CDS
LOCATION: 235..399
US-09-621-976-2813
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US-09-621-976-2813
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Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 0000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR PRILOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0
                                                              APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/02/1,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASEUSE OF OF WINDOWS Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        199117 TTGAGTCCAGGGAGGTCAAGGCTGCAGTGAGCTATGATTGCACCACTGCACCCCATCTTG 199176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             164 TIGAGICAAGGGATTIGAAIGTTAGGGIGAAAAGTTACTACTCAACTCTGTAGGTTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    224 GGAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              344 GAGAAGCTATTGCCATGGTCCAAGCAAGAGATGATGAAGGCCTAAATATGAGCCA 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 209210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.0%; Score 36; DB 4; Length 209
47.0%; Pred. No. 7.5;
tive 0; Mismatches 125; Indels
Sequence 15094, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: (1)...(209210)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity Tree Matches 111; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 15094
LENGTH: 209210
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LENGTH: 174639
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RESULT 12
US-09-328-352-2835/c
US-09-328-352-2835/c
Sequence 2835, Application US/09328352
Parent No. 6562958
GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION UNDBER: US/09/328,352
CURRENT PILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 2835
LENGTH: 1245
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%20quence 13587, Application US/09949016

%20quence 13587, Application US/09949016

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%20quence 13587, Application US/09949016

%20quence 13587, Application NUMBER: US/09/949,016

%20quence 13587, Application NUMBER: US/09/949,016

%20quence 13587, Casig et al.

%20quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 130quence 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AAAGGAGAAGAGGAGGAGCAAATACCTGGAGGTAGAAATGGTGATGTGTACAT
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ilarity 50.0%; Pred. No. 0.97;
Conservative 0; Mismatches 88;
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; Pred. No. 11;
0; Mismatches
LOCATION: (1)...(174639)
OTHER INFORMATION: n = A,T,C or G
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US-09-328-352-2835
                                                                                                                                                                                                                     Query Match 5.9%;
Best Local Similarity 49.2%;
Matches 93; Conservative
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Best Local Similarity
Matches 88; Conserv
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Patent No. 6650334

GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
TITLE OF INVENTION: THEREOF
FILE REFERENCE: CLOOL167
CURRENT APLICATION NUMBER: US/09/751,389
CURRENT FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENTH:: 786431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 IGCCATGTTTAGAGATTCAGAGATAGATTTCAGGAAATGTAACTTATAGATTTTATACAT 321
                                                                                                                                                                                                                                                                                                                                                                               7305 İGAĞCAAĞĞARĞATGGGİĞİĞGAĞAĞAÇAĞAĞAĞAĞTTĞGAGGTĞGAĞAĞAAAAAÇA 7246
                                                                                                                                                                                                                                                                                                                                                      310 GATTTTATACATACACAGAGAAATACGGACTAGTGAGAAGCTATTGCCATGGTCCAAGCA 369
                                                                                                                                                                                                                                                                                    250 TGAGGAGGATGTGCCATGTTTAGAGATTCAGAGATACAGGAAATGTAACTTATA 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 GGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTAGGGTGAAAAGTTAC
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                                                                                                                                                                                                                    Length 10321;
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                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                          73;
                                                                                                                                                                                                                             DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                7185 AGAGAATGGGGTGGAAAAGAAGAGGGGAGA 7154
                                                                                                                                                                                                                                                                                                                                                                                                                               370 AGAGATGAAGGCCTAAATATGGAGCCAAA 401
                                                                                                                                                                                                                         Ouery Match
S.9%; Score 35.2; DB
Best Local Similarity 52.0%; Pred. No. 2.9;
Matches 79; Conservative 0; Mismatches
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOPTWARE: FRASE FOR Windows Version 4.0
SEQ ID NO 13587
LENGTH: 10321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
LOCATION: (1)...(786431)
CTHER INFORMATION: n = A,T,C or G
US-09-751-389-3
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ORGANISM: Human
                                                                                                                                                                 ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13587
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; sequence lob/s, application os/office.

Patent No. 6812339
; patent No. 6812339
; general INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASESEQ for Windows Version 4.0

LENGTH: 84525
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                          Sequence 16678, Application US/09949016
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Query Match
Best Local Similarity 55.3%;
Matches 68; Conservative C
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Job time : 128.644 secs
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; ORGANISM: Human
US-09-949-016-16678
RESULT 15
US-09-949-016-16678
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Sequence Sequence Sequence Sequence Sequence Sequence

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> Total number Minimum DB Maximum DB

Database

Searched:

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Run on:

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APPLICANT: Roal, Frank
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Coy, Johannes
APPLICANT: Finzer, Patrick
APPLICANT: Finzer, Patrick
APPLICANT: Poustka, Annemarie
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US-10-027-612-2638B1
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 600
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Patent No. US20020106355A1
GENERAL INFORMATION:
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; ORGANISM: Homo sapiens
US-09-899-276-1
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                              GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*
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                                                                                                                                          - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                               IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum Match 100%
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Sequence 144, App Sequence 144, App Sequence 5719, Ap Sequence 17839, A Sequence 155, App Sequence 391, App Sequence 1630, Ap Sequence 190233, Sequence 190233, Sequence 190233,

Sequence 1099, Ap Sequence 2, Appli Sequence 161407, Sequence 161407,

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Gaps

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Length 600; Indels

100.0%; Score 600; DB 9; L 100.0%; Pred. No. 9.6e-167; ive 0; Mismatches 0;

Query Match Best Local Similarity 100. Matches 600; Conservative

Sequence 4, Appli Sequence 112, App Sequence 13, Appl Sequence 170737, Sequence 170737, Sequence 742, App

US-10-685-705-4
US-10-085-117-112
US-10-275-323A-13
US-10-027-632-170737
US-10-087-192-742

408 760 760 78268

Result õ

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48511 GAACTGTGAATCTCCAGGCACAGCAGGAGGGGGGGTCAACCATACAGTGGTAAGAGAT 48452
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                                                                                                                                                                                                                                                                                                                                         GITICCCICCATIACIATACCCCCATCCCAATCTCAGGCACCTCGAATCATCATTAAA
                                                                                                                                                      GTCCAAGGAAGATGATGAAGGCCTAAATATGGAGCCAAAGAGGGAGCAATGAAGAATG
                                                                                                                                                                                                                                                                                          421 AGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGGAGAAAGACCTGTGACTTCAGA
                                                                                                                                       rcagrccaargagagggarggccargrragagarrcagagaraagarrcaggaaarg
ATGTTAGGGTGAAAGTTACTACTCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCT
                                        cegeccoscacosarercascastracastracastracasacertrascasacertre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 112, Application US/10085117
Sequence 112, Application US/10085117
PUBLICANT NO. US20030232334A1
SEMERAL INFORMATION:
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
APPLICANT: Engelhard, Eric K.
APPLICANT: MOYEL COMPOSITIONS AND METHODS FOR CANCER TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER TITLE OF INVENTION: UNDER: 2002-02-77
CURRENT FILING DATE: 2002-02-77
PRIOR PILING DATE: 2010-03-02
NUMBER OF SEQ ID NOS: 361
SOFTWARE: FASTERQ for Windows Version 4.0
SOFTWARE: FASTERQ for Windows Version 4.0
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ORGANISM: Homo sapiens
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US-10-085-117-112/c
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Matches 102
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APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Ambati
APPLICANT: University Ambati
TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular
TITLE OF INVENTION: Degeneration
FILE REFERENCE : 05029-0415
FILE REFERENCE : 05029-0415
CURRENT APPLICATION NUMBER: US/10/685,705
FRIOR PEPLICATION NUMBER: 60/422,096
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
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                                                                                                                                     CGGCCCACACCATGTCAAGGGATGACAATTAGAAAGGTGGGTTGAGTCAAGGGATTTG 180
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                                                                                                                                                                                                                                                                                                      GTCCAAGCAAGAGATGAAGGCCTAAATATGGAGCCAAAGAGGCAATGAAGAATG
                                                                                                   TAGANATGGTGATGTTGTGTACATCAAGCAGGGAGAAAACCAATGAACGAGATGCGAATT
                                                   Length 11793;
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Best Local Similarity 100.0%; Pred. No. 3.7e-166;
Matches 600; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/10685705; Publication No. US20040177387A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
US-10-685-705-4
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US-10-685-705-4
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348 DRRDTWRTRRKDDWYDYYNRDKTDNDWBHDBBBYTRGTRCTGGWGTTYCTWTAATAADKW 289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      288 TRDDHBRHDHRIXHDWYNKKWHDGWHKHKHVRVNDDWDBVWNRDDWRRSRNRWTWDDD 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             228 RNNDGVRRTWDNRDNDDDDWWTDVDDKWDKDDDDKDBKDBRDRDWKAYRHWABRWRDWKK 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   345 AGAAGCTATTGCCATGGTCCAAGCAAGAGTGATGAAGGCCTAAATATGGAGCCAAAGAG 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           405 GCAGCAATGAAGAATGAGCCATGCAGGGTGAAATGCTGCATGTTGTAAATGGAGAGAAAA 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      168 DWWDHWDAWYDGHKRAARWHYDYTGGTTKHRTTYNKDDDKYSYRDRRRWWRYRSWDRRWT 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                465 GACCTGTGACTTCAGATATGAAAACCTCATCTTCAACCCACATTTTAAGGGGGCAGCTTC 524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 GAAACGTTGAGAATCTTCAGTCCAATGAGGAGGGATGTGCCATGTTTAGAGATTCAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: modified base
CACATTON: (406)...(406)
US-10-275-323A-13
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LOCATION: (357)...(357)
OTHER INFORMATION: a, c, g, or
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                                                                                                                                                                                NAME/KEY: modified base
LOCATION: (324)..(324)
OTHER INFORMATION: a, c, g,
                                                                                                                                                                                                                                                                 NAME/KBY: modified base
LOCATION: (330)..(330)
OTHER INFORMATION: a, c, g,
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LOCATION: (364)..(364)
OTHER INFORMATION: a, c, g,
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INFORMATION: a, c, g,
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48 GYGGANRKRRCMWY 35
NAME/KEY: modified base
LOCATION: (253)..(253)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: modified base
LOCATION: (352)..(352)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified base
LOCATION: (355)..(355)
OTHER INFORMATION: a, c,
                                                                                        NAME/KEY: modified base
LOCATION: (269)..(269)
OTHER INFORMATION: a, c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: modified base
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APPLICANT: DONNE-COUSSE, CARCLE
APPLICANT: LAUDET, VINCENT
APPLICANT: LAUDET, VINCENT
APPLICANT: LAUDET, VINCENT
APPLICANT: HANNI, CATHERINE
APPLICANT: HANNI, CATHERINE
TITLE OF INVENTION: MATERIALS DERIVED FROM BIRDS, AND OLIGONUCLEOTIDES FOR CARRYING
TITLE OF INVENTION: MATERIALS DERIVED FROM BIRDS, AND OLIGONUCLEOTIDES FOR CARRYING
TITLE OF INVENTION: MATERIALS DERIVED FROM BIRDS, AND OLIGONUCLEOTIDES FOR CARRYING
TITLE OF INVENTION NUMBER: US/10/275,323A
CURRENT APPLICATION NUMBER: PCT/FR01/01279
FRIOR APPLICATION NUMBER: FR 00/05850
FRIOR FILING DATE: 2000-04-26
NUMBER OF SEQ ID NOS: 96
NUMBER OF SEQ ID NOS: 96
SOFTWARE: PATERIAL VEFSION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: DNA fragment amplified OTHER INFORMATION: from the genome of birds
                              48391 CTATCCTGTTGGCAAAAGAGA 48371
                                                                                                          RESULT 4
US-10-27-323A-13/c
US-10-27-323A-13/c
; Sequence 13, Application US/10275323A
; Publication No. US20050079491A1
; GENERAL INFORMATION:
    206 CAACTCTGTAGGTTAAAAGGA 226
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LOCATION: (134)..(134)
OTHER INFORMATION: a, c, g, or t
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LOCATION: (245)...(245)
OTHER INFORMATION: a, c, g, or t
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OTHER INFORMATION: a, c, g,
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LOCATION: (43)..(43)
OTHER INFORMATION: a, c, g,
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INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c, g,
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OTHER INFORMATION: a, c,
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OTHER INFORMATION: a, c,
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LENGTH: 408
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 GGAGAAAACCAATGAACCAGATGCGAATTCGGGCCCACACCAATGTCAAGGGATGACAAT 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 AAGGAAGAGTGGGAAGCAAATACCTGGAGGTAGAAATGGTGATGATGTGTACATCAAGCAG 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SERNEMAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-20

PRIOR FILING DATE: 2000-03-20

PRIOR FILING DATE: 2000-03-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: FESTEREQ for Windows Version 4.0

LENGTH: 760

LENGTH: 760
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50.2%; Pred. No. 0.13;
tive 0; Mismatches 102;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         736 GAATGAGTTAAGTGAGGAGGTGGGA 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 170737, Application US/10027632 publication No. US20030204075A9 GENERAL INFORMATION:
           ; Sequence 170737, Application US/10027632; publication No. US20020198371A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     7.0
Best Local Similarity 50.2
Matches 103; Conservative
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US-10-027-632-170737
                                                                                                                                                                                                                                                                                                                                                                                                                                                         , ORGANISM: Human
US-10-027-632-170737
RESULT 5
US-10-027-632-170737
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9409 Agicacaladgiakcadciacadarachalaggircdgalgircdgalatgarcrialatgircaca 9468
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                                                                                                                                                                                                                                                                                                                                                                                                          32 AAGGAAGAGTGGGAGCAAATACCTGGAGGTAGAAATGGTGATGATGTGTACATCAAGCAG
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Sequence 742, Application US/10087192

Sequence 742, Application US/10087192

Publication No. US2002018258641

GENERAL INFORMATION:
APPLICANT: MORIAG, Eric K.
APPLICANT: MORIAGE COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: ACANCER
FILE REFERENCE: 5.2945200122
CURRENT APPLICATION NUMBER: US/10/087,192
CURRENT FILING DATE: 2002-03-01
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059

SEQ ID NOS: 2059

SEQ ID NO 742

LINGTHENT FRASESQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                DB 17;
                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.9%; Score 41.2; DF 62.7%; Pred. No. 1.6; tive 0; Mismatches
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-02-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 170737
                                                                                                                                                                                                                                                                                                                                Score 41.8;
Pred. No. 0.1
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                                                                                                                                                                                                                                                                                                                                Query Match 7.0%;
Best Local Similarity 50.2%;
Matches 103; Conservative C
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Best Local Similarity 62.7%
warrhes 64, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA; ORGANISM: Homo sapiens
US-10-087-192-742
                                                                                                                                                                                                                                                  TYPE: DNA
CRGANISM: Human
US-10-027-632-170737
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FEATURE: OTHER INFORMATION: Distance between 3'-terminus of neighbour sequence of OTHER INFORMATION: sequence listing upward to telomere on chrosomal short arm and OTHER INFORMATION: 5'-terminus of this base sequence : 216681
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Publication No. US20040102622A1
GENERAL INFORMATION:
APPLICANT: Nicholas M. Dean
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODILATION OF HEPATOCYTE GROWTH FACTOR RECEPTOR EXPRESSION
FILE REFERENCE: PTS-0043
CURRENT PAPLICANT: 2002-11-23
NUMBER OF SEQ ID NOS: 147
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 AGTTTCAGGAAATGTAACTTATAGATTTTATACATACACAGAGAAATACGGACTAGTGAG 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               82 CATCAAGCAGGAGAAAACCAATGAACCAGATGCGAATTTGGGGCCCACACAATGTCAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                          22 AAGAAAGGAGAAGAAGGAGGAGCAAATACCTGGAGGTAGAAATGGTGATGATGTGTA
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                                                                                                                                           OTHER INFORMATION: Distance between a terminus base of telomere on OTHER INFORMATION: chromosomal short arm and 5'-terminus of this base OTHER INFORMATION: sequence : 28899985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 GGATGACAATTAGAAAGGAAGGTTGAGTCAAGGGATTTGAATGTTAGGGTGAAA 195
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                                                                                                                                                                                                                                                                                                                                                                                              84; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 39.4; DB
; Pred. No. 6.8;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 Score 39.6; DE Pred. No. 0.4; 0; Mismatches
                                                                         FRATURE:
OTHER INFORMATION: Located on chromosome 16
FRATURE:
OTHER INFORMATION: Distance between a termin
                                                   OTHER INFORMATION: HUMUT8173B
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l Similarity 51.7%;
90; Conservative
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Best Local Similarity 50.8
Matches 94; Conservative
         ORGANISM: Homo sapiens
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Best Local Similarity
Matches 90; Conservat
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US-10-304-019-12/c
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LOCATION: 55607-55706, 360227-360326, 363103-363202, 363428, 366093-366192,
LOCATION: 368528, 44732, 45263-452752, 457192, 457207-457306, 461808-461907,
LOCATION: 461921, 461928, 461942
OTHER INFORMATION: n = A, T, C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              512227 AGGTGGTGGTAAGCTATTTGGATTATTAAAGCAAATTGGGCAGCCACTGAAAAAATG 512286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 512287 Gagaagagaaangriarararararararararrararasaaargraacregarricaa, 512346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    196 AGTTACTACTCCAACTCTGTAGGTTAAAAGGAAACGTTGAGAATCTTCAGTCCAATGAGGA 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           256 GGGATGTGCCATGTTTAGAGATTCAGAGATAAGTTTCAGGAAATGTAAC-----TTATA 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 599001;
Sequence 4, Application US/10317869A
Publication No. US20050101000A1
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Kenneth W. Dobie
TITLE OF INVENTION: MODULATION OF PHOSPHODIESTERASE 4B EXPRESSION
FILE REFERENCE: RTS-0429
CURRENT APPLICATION NUMBER: US/10/317,869A
CURRENT FILING DATE: 2002-12-11
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 6.6%; Score 39.8; DB 21; Length Best Local Similarity 48.5%; Pred. No. 10; Matches 144; Conservative 0; Mismatches 147; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 22067, Application US/10674124A Publication No. US20040197797A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: INOKO, Hidetoshi APPLICANT: TAMIYA, Gen
                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-10-674-124A-22067
                                                                                                                                                                                                                                                       LENGTH: 599001
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Sequence 322, Application US/10087192
Publication No. US20020182586A1
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                                                                                                                                        US-11-013-608-12/C
sequence 12, Application US/11013608
sequence 12, Application Wolloof State  
Publication No. US20050153925A1
GENERAL INCRAWATON
APPLICANT: C. Frank Bennett  
APPLICANT: Stream M. Freier  
APPLICANT: Breat P. Monia  
APPLICANT: Breat P. Monia  
APPLICANT: Breat P. Monia  
APPLICANT: Breat P. Monia  
APPLICANT: Breat P. Ward  
APPLICANT: Breat P. Ward  
APPLICANT: Lax M. Gaarde A. Ward  
APPLICANT: Lax M. Cowsert: Main A. Gaarde A. PAPLICANT: Lax M. Wall M. Cowsert M. APPLICANT: COMPOSITIONS AND THEIR USES DIRECTED TO TRANSFERASES FILE REFERENCE: BNDL-000908. Pl
CURRENT FILING DATE: 2004-112-16
PRIOR APPLICANTION NUMBER: 10/309, 294
FRIOR FILING DATE: 2002-11-16
PRIOR APPLICANTION NUMBER: 10/309, 42
FRIOR APPLICANTION NUMBER: 10/309, 42
FRIOR PRILOR DATE: 2002-11-12
PRIOR PRILOR DATE: 2002-11-12
PRIOR PLILOR DATE: 2002-11-12
PRIOR FILING DATE: 2002-11-14
PRIOR FILING DATE: 2002-11-14
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PRIOR PRIOR PRIOR PRIOR PAPPLICATION NUMBER: 10/15/34
PRIOR FILING DATE: 2002-11-14
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Best Local Similarity
Matches 94; Conservat
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RESULT 12 US-10-087-192-322/C

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; Sequence 263881, Application US/10027632
; Publication No. US2020198371A1
; GENERAL INFORMATION:
APPLICATION No. US2020198371A1
; GENERAL INFORMATION:
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: DAID:
FILE REFERENCE: 108827.129
CURRENT PEPLICATION NUMBER: US/10/027,632
CURRENT PEPLICATION NUMBER: US 60/18,006
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-04-20
PRIOR PLILING DATE: 2000-04-20
PRIOR PLILING DATE: 2000-04-20
PRIOR PLILOR DATE: 2000-04-20
PRIOR PLILING DATE: 2000-03-24
PRIOR PLILING DATE: 2000-02-24
PRIOR PLILING DATE: 2000-02-24
PRIOR PLILING DATE: 1999-11-23
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PUBLICATION NO. US20020182586A1

PUBLICATION NO. US20020182586A1

GENERAL INFORMATION:
APPLICANT: MORTIS, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR TITLE OF INVENTION: CANCER;
TITLE OF INVENTION: CANCER;
FILE REFERENCE: 52945200122
FURBERT APPLICATION NUMBER: US 09/747,377

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-12-22

PRIOR FILING DATE: 2000-10-03-03

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50.8%; Pred. No. 7.2;
tive 0; Mismatches 91;
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Best Local Similarity 50.8%
watches 94; Conservative
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CRGANISM: Homo sapiens
US-10-087-192-322
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US-10-027-632-263881/c
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LENGTH: 144035
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Search completed: August 4, 2005, 15:54:10 Job time : 1076.28 secs
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PAPLICATION NUMBER: US 60/218,006
FRIOR PELING DATE: 2000-07-12
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR PILING DATE: 2000-07-20
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 2000-03-29
FRIOR PILING DATE: 1999-11-23
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR APPLICATION NUMBER: US 60/167,363
FRIOR PILING DATE: 1999-11-23
FRIOR PILING DATE: 1999-10-23
FRIOR PILING DATE: 1999-09-28
FRIOR PILING DATE: 1999-09-28
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Publication No. US20030204075A9
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
FITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108027129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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4.1%; Pred. No. 1.6;
ve 0; Mismatches 33; Indels 0;
                                                                                      Length 3918;
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                                                                                 Score 39.2; DB 13;
Pred. No. 1.6;
0; Mismatches 33;
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 263882, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
                                                                              Query Match 6.5%;
Best Local Similarity 64.1%;
Matches 59; Conservative
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Best Local Similarity 64.1
Matches 59; Conservative
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US-10-027-632-263881/c
; ORGANISM: Human
US-10-027-632-263881
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US-10-027-632-263882
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           316 CCTAAATTAGGAAAGCAGTAAGCAATATAGAA 285
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
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PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09-00-09
NUMBER OF SEQ ID NOS: 325720
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US-10-027-632-263881
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LENGTH: 3918
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Scoring table:

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EC009716 Home sapi
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BD195644 70 human
CQ775689 Sequence
AR352699 Sequence
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CQ775688 Sequence
AR352698 Sequence
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G06615 human STS W
A37281 Sequence
AX311515 Sequence
AX311515 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA
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ED195643

CQ775688

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BD195649

AR352937

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AR380620
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ACCESSION
VERSION
KEYWORDS
SOURCE
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CQ15681 Sequence
CQ174058 Sequence
CQ27544 Sequence
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12055.236 Million cell updates/sec
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                         - nucleic search, using sw model
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CQ096880
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AX577974
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                                                                                                                                                                                  Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human hela cells or other human cervical epithelialcells

Patent: WO 0157278-A 5501 09-AUG-2001;
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Score 198.4; DB 9;
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CQ096880/c CQ096880 360 bp DM

LOCUS CQ096880 BATCH W00157272.
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CQ069701
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Location/Qualifiers
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      Query Match
Best Local Similarity 99.5%;
Matches 199; Conservative
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/protein.id="CAC14049.1"
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                                                                                             PRI 18-OCT-2000
                                                                                                                                                                                                                                                 Finzer, P., Soto, U., Delius, H., Patzelt, A., Coy, J.F., Poustka, A., zur Hausen, H. and Roel, F.
Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HTV 18 positive cells: the role of the chromatin structure and AP-1 composition

oncogne 19 (29), 3235-3244 (2000)
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Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKFZ
Submitted (15-APR-1999) F. Roesl, Applied Tumor Feld 506, 69120
(German Cancer Research Institute), Im Neuenheimer Feld 506, 69120
Heidelberg, FRG
Location/Qualifiers
                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/gene="MCP-1"
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9906. 19073

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/ gene="MCP-1"

/ gene="MCP-1"
                                                                                                                                                         MCP-1 gene; monocyte chemoattractant protein-1.
Homo sapiens (human)
Homo sapiens
                                                                                                HSY18933 1793 bp DNA 1:
Homo sapiens MCP-1 gene and enhancer region.
Y18933
Y18933.1 GI:10933860
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1.360
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                                                                         61 AATTTTGTTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                     227 IGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCCCTGTTTTATTTTATAATG
                                                                                             AATTTTGTTTGTTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTAAGTTA
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human heart
Patent: WO 0157274-A 5454 09-AUG-2001;
Aeomica, Inc. (US)
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Sequence 5454 from Patent W00157274.
CQ174058.1 GI:41168794
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/mol_type="unassigned DNA"
/mol_txpe="taxon:9606"
/note="MAP TO AC005549.1~EXPRESSED IN BONE MARROW, SIGNAL
= 2.4"
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                                                    Homo sapiens (human)
Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
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1...36

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

/note="MAP TO AC005549.1-EXPRESSED IN PLACENTA, SIGNAL

2.9"
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 5703 09-AUG-2001;
Aeomica, Inc. (US)
Location/Qualifiers
                                                                                                                                             Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human placenta
Patent: WO 0157222-A 5739 09-AUG-2001;
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Location/Qualifiers
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                   GI:41065906
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CQ096880
CQ096880.1
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Matches 198; Conserv
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TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCTTGTTTATTATTATAATG
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CQ294784
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Location/Qualifiers
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CQ294784/c
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/nore="MAP TO AC005549.1~EXPRESSED IN FETAL LIVER, SIGNAL
= 3.7"
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Location/Qualifiers
1. 360
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
/note="wAP TO AC005549.1~EXPRESSED IN ADULT LIVER, SIGNAL = 2.5"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                        Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR ALLYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVERS130> Be 1004 WO ALLSO US 60/180, 312<151> 04 February 2000 (04.02.00)<150> US 60/207, 456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03 August 2000 (30.08.00)<150> US 60/207, 456<151> 20 Cotober 2000 (03.08.00)<150> US 60/235,550<151> 27 September 2000 (27.09.00)<150> US 60/234,687<151> 27 September 2000 (27.09.00)<150> US 09/608,408<151> 21 September 2000 (27.09.00)<150> US 09/608,408<151> 30 June 2000 (30.06.00)<170> Patent: WO 0157273-A SB16 09-AUG-2001;
Acomica, Inc. (US)
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                                                                                                                                                                                                                                                                                                                                               Gaps
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human fetal liver
Patent: WO 0157277-A 5805 09-AUG-2001;
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  Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                    Length 360;
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Pred. No. 4.3e-26;
0; Mismatches 2;
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Location/Qualifiers
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99.0%;
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CQ257544/c
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PAT 23-JAN-2004
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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               TIGATGITITAAGITITATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA
                                                                                                                                              107 TIGATGITITAAGITTATCITTCAIGGIACIAGIAGITTITITAGAIACAGAGACITGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .360 /organism="Homo sapiens" /mol type="unassigned DNA" /mol type="unassigned DNA" /mol type="taxon:9606" /noce="MAP TO AC005549.1~EXPRESSED IN LUNG, SIGNAL /noce="MAP TO AC005549.1~EXPRESSED IN LUNG, SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human lung
Patent: WO 0186003-A 5889 15-NOV-2001;
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98.4%; Score 196.8; DB 6;
Best Local Similarity 99.0%; Pred. No. 4.3e-26;
Matches 198; Conservative 0; Mismatches 2;
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PAT 08-OCT-2004
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Lyamichev, V., Skrzpczynski, Z., Allawi, H.T., Wayland, S.R., Takova, T. and Neri, B.P.
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Charge tags and separation of nucleic acid molecules
Patent: WO 0.2063030-A 72 15-AUG-2002;
THIRD WAVE TECHNOLOGIES, INC. (US)
Location, Qualifiers
1. 647
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326 IGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCCTGTTTTATTATTATAAATG
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Pred. No. 3.8e-26;
0; Mismatches 2;
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other sequences; artificial sequences.
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Patent: US 6780982-A 72 24-AUG-2004;
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Sequence 72 from patent US 6780982.
AR567996

    647
    /organism="unknown"
    /mol_type="unassigned RNA"

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Sequence 72 from Patent W002063030.
AX698741
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/ord_Lype="unassigned DNA"

/db_xref="texon:9606"

/note="MAP TO AC005549.1-EXPRESSED IN BRAIN, SIGNAL = 2.5"
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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METHODS FOR MONITORING DRUG ACTIVITIES IN VIVO /i
Patent: WO 2004072265-A 294 26-AUG-2004;
Wyeth (US); Burczynski, Michael E. (US); Twine, Natalie C. (US);
Dorner, Andrew J. (US); Trepicchio, William L. (US)
                                                                      for
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33..199
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t, g or c, or contains no nucleotide."
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                                                Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human brain
Patent: WO 0157275-A 5534 09-AUG-2001;
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                                                                                                                      Aeomica, Inc. (US)
Location/Qualifiers
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CQ861661.1 GI:51982650
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1 (bases 1 to 725)
2 (bases 1 to 725)
2 (bases 1 to 725)
2 (continuo-modulating effects of chemokines in DNA vaccination patent: US 6569418-A 3 27-MAY-2003;
2 (contion)Qualifiers
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                                                                                                                                                                                                                                                                             AR337874 725 bp Sequence 3 from patent US 6569418. AR337874 AR337874.1 GI:33724486
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SM Unknown.

Unclassified.

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SG Cocks B.G., Stuart, S.G. and Seilhamer, J.J.

SG Cocks B.G., Stuart, S.G. and Seilhamer, J.J.

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Job time: 807.887 secs
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GenCore version 5.1.6
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August 3, 2005, 15:09:47; Search time 132.551 Seconds Run on:

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US-09-899-276C-2 200

1 tgcagctaacttattttccc.....aattgcttttcctctgtac 200 Perfect score: Sequence:

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4390206 seqs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N_Geneseq_16Dec04:* Database

geneseqn2001as:*geneseqn2001bs:* geneseqn2002as:* geneseqn2002bs:* genesegn1990s:* geneseqn1980s:* geneseqn2000s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2003ds:*geneseqn2004as:*geneseqn2004bs:*

geneseqn2003cs:*

9

geneseqn2003as: * geneseqn2003bs: *

SUMMARIES

		de				
Result No.	Score	Query Match	Query Match Length DB	DB	άı	Description
				-		
-	200	100.0	200	9	ADH13939	Adh13939 Human mon
~	198.4	99.5	489	σ	ACH19135	Ach19135 Human adu
٣	198.4	99.2	772	13	ADS16434	Ads16434 Human cyt
Ω	198.4	99.5	1005	10	ADI02670	Adi02670 Human cDN
0	198.4	99.2	1472	10	ADE25637	Ade25637 Human cDN
9	198.4	99.2	11793	12	AD003803	Ado03803 Human Cc1
7	198	99.0	950	æ	ACF64400	Acf64400 Human MCP
80	197.6	98.8	2775	9	ABK47979	Abk47979 Human sma
o 0	196.8	98.4	360	4	AAI15568	Aai15568 Probe #55
c 10	196.8	98.4	360	4	ABA57500	Aba57500 Human foe
c 11	196.8	98.4	360	4	AA137053	Aai37053 Probe #57
c 12	196.8	98.4	360	4	ABA26988	Aba26988 Probe #54
c 13	196.8	98.4	360	4	AAK31146	Aak31146 Human bon
c 14	196.8	98.4	360	4	AAK05543	Aak05543 Human bra
c 15	196.8	98.4	360	4	ABS30826	Abs30826 Human liv
c 16	196.8	98.4	360	9	ABS05898	Abs05898 Human gen
17	196.8	98.4	508	13	ADR52943	Adr52943 Drug ther
18	196.8	98.4	647	9	ABS68800	Abs68800 Human mon
19	196.8	98.4	725	~	AAQ85370	Aaq85370 Chemoattr
20	196.8	98.4	725	N	AAX80631	Aax80631 Monocyte

Add18494 Human mon Add18494 Human pro Add18419 Farreey1 Add132018 Human cDN Adr05375 Human cDN Adr05375 Human mon Aav10341 CDNA which Aav10341 CDNA which Abv78071 Hypoxia-r Abz34738 Coding se Adf4546 Human vas Add1445 Antipsori Adr24988 Breast ca	Ada34899 Human ade Aaf21021 Human low Ab296715 Human low Ad31819 Human nuc Ad31819 Human cDN Ad20564 Human cDN Ad003801 Human CC1 Ad10266 Human CC1 Ad014996 Human CC1 Ad095635 Human BEC Ad095635 Human BEC Ad095631 Human BEC Ad076313 Human SCY Adq76211 Chemokine
10 AADS8817 10 ADD18494 11 ADD18499 11 ADD132018 13 ADR05375 2 AAV10341 6 ABV78071 8 ABZ34738 8 ABZ34738 12 ADN04745 12 ADN04745	3 AAA34899 3 AAA51021 10 AB2966115 11 ABD20564 11 ABD20569 10 ADD14996 10 ADD14996 11 AD099635 12 AD078911
725 725 725 725 739 739 739	7477 7441 7441 757 757 757
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ALIGNMENTS

ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:2. ADH13939 standard; DNA; 200 BP. 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. 11-MAR-2004 (first entry) EP1170372-A1. Homo sapiens 09-JAN-2002. ADH13939; RESULT 1

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Delius H, Finzer P, Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A;

Poustka A;

WPI; 2002-165895/22.

Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer.

Disclosure; SEQ ID NO 2; 30pp; English.

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention mas cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A

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09-MAY-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to an isolated polynucleotide comprising any one of 38043 cDNA sequences, appearing as ACH12789-ACH350811, whose sequence was determined by the technique of SBH (sequencing by hybridisation). Also included is a purified polypeptide comprising a sequence corresponding to a reading frame of the novel polynucleotide. The nucleic acid sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New polynucleotide sequences obtained from various cDNA libraries, useful as hybridization probes, as oligomers for PCR, for chromosome and gene mapping, in the recombinant production of protein, or in generating
                                                                                  ö
                                                                                                                                        120
                                                                                                                                                                                     TIGATGITITAAGTITATCTITCAIGGTACTAGTGITTTITAGATACAGAGACTIGGGGA 180
                                                                                                                                                                                                                                                                                                                                                        expressed sequence tag; EST;
                                                                                                                      9
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pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                     61 AATTTTGTTTGTTGAAGCATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA
                                                                                    ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jones
                                                                 Length 200;
                                                                                    Indels
                                                Sequence 200 BP; 48 A; 29 C; 31 G; 92 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dickson MC,
                                                                 ; Score 200; DB 6;
; Pred. No. 1.5e-30;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                          Human; ss; sequencing by hybridisation; SBH; e>
genome mapping; biodiversity; genetic disorder.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 6347; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stache-Crain B,
                                                                                                                                                                                                                    AATTGCTTTTCCTCTTGTAC 200
                                                                                                                                                                                                                                    AATTGCTTTTCCTCTTGTAC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-JUL-2001; 2001US-00918995.
                                                                  vuery match 100.0%;
Best Local Similarity 100.0%;
Matches 200; Conservative 0
                                                                                                                                                                                                                                                                                    ACH19135 standard; cDNA; 489
                                                                                                                                                                                                                                                                                                                                          Human adult lung cDNA #138
                                                                                                                                                                                                                                                                                                                         13-OCT-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DEMANAC R T.
LABAT I.
STACHE-CRAIN B.
DICKSON M C.
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                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                        ACH19135;
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(LABA/)
(STAC/)
(DICK/)
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bacterial infection; viral infection; anaemia; B cell deficiency;
T cell deficiency; vulnerary; antibacterial; virucide; gene; ss.
are useful in diagnostics as expressed sequence tags (EST) for identifying expressed genes or for physical mapping of the human genome, in forensics, in assessing biodiversities, or in identifying mutations responsible for genetic disorders and other traits. The nuclectide sequences are also useful as hybridisation probes, as oligomers for for chromosome and gene mapping, in the recombinant production of protein, or in generating antisense DNA or RNA. The purified polypeptide is useful for generating antisense DNA or RNA. The purified polypeptide is useful for generating antibodies specific for it. The present sequence is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from USPTO at sequence. Large sequence. Large L
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     139 IGCAGCTAACTITITICCCCTAGCITICCCCAGACACCTIGITITATITATIATAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTITGITITGITIGAIGIGAAACATIAIGCCTIAAGIAAIGITAAITTITAAGIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       199 AAITITGIIIGIIGAAGAAACAITAIGCCITAAGIAAIGIIAAITCITAITAAGITA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 489 BP; 147 A; 95 C; 75 G; 165 T; 0 U; 7 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.2%; Score 198.4; DB 99.5%; Pred. No. 3.1e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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160. .369
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73...141
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Best Local Similarity 99.5
Matches 199; Conservative
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The invention relates to a new combination which comprises cDNAs or their complements not given in the specification that are differentially expressed in vascular endothelium. The combination of cDNAs is useful for preparing a composition for diagnosing or treating vascular disorder, comprising atherosclerosis, haemangioma, haemangioendothelioma, oedema, diabetic retinopathy, warts, pyogenic granulomas, Kaposi's sarcoma, scar keloids, allergic oedema, neoplasms, psoriasis, ulcers, follicular cysts, endometriosis, periconeal sclerosis or obesity. The present sequence represents a cDNA differentially expressed in the vascular endothelium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180
                                                                                                                                                                                       New combination comprising cDNAs that are differentially expressed in vascular endothelium, useful for preparing a composition for diagnosing or treating vascular disorder, e.g., atherosclerosis, psoriasis, ulcers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; 88; differential expression; foam cell; LPS; lipopolysaccharide; cardiovascular disease; atherosclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          347 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCTTGTTTTATTATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1005 BP; 318 A; 183 C; 178 G; 326 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA differentially expressed in foam cells #41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 198.4; DB 10
Pred. No. 3.1e-30;
0; Mismatches 1
                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 211; 28pp; English.
                                                                                                       BG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTGCTTTTCCTCTTGTAC 200
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ADE25637 standard; cDNA; 1472 BP.
                                                                                                          Cocke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99.24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.5
Matches 199; Conservative
                                                                                                          Bandman O,
                   (ASTR/) ASTROMOFF A. (BAND/) BANDMAN O. (COCK/) COCKS B G.
                                                                                                                                                 WPI; 2003-898115/82
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                                                                                                          Astromoff A,
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                                                                                                                                                                                                                                                       obesity
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                                                                                                                                                                                                                                                                      New isolated human JE cytokine DNA and polypeptide, useful for treating bacterial and viral infections, anemia, or B cell or T cell deficiencies, or in wound healing and related tissue repair.
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                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a nucleic acid sequence encoding human cytokine, JE. JE sequence is useful in pharmaceutical preparations for stimulating and/or enhancing immune responsiveness, wound healing and related tissue repeatr. It is also useful for treating bacterial and viral infections, anaemia or B/T cell deficiencies. The present sequence is human JE cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          458 AATTTTGTTTGTTGAAGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTAAGTTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 772 BP; 239 A; 175 C; 134 G; 224 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 99.2%; Score 198.4; DB 13; Length Best Local Similarity 99.5%; Pred. No. 3.1e-30; Matches 199; Conservative 0; Mismatches 1; Indels
                                                                                          (DAND ) DANA FARBER CANCER INST INC
(GEMY ) GENETICS INST INC
                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1; 8pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATIGCTTTTCCTCTTGTAC 200
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89US-00351008.
91US-00701515.
93US-00003136.
94US-00228931.
                                                                                                                                                                     Wong
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                                                                                                                           ) GENETICS INST INC
                                                                                                                                                                   Rollins BJ, Stiles CD,
                                                                                                                                                                                                         WPI; 2004-632933/61
                                                                                                                                                                                                                                 P-PSDB; ADS16435
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                 16-MAY-1991;
12-JAN-1993;
13-APR-1994;
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ADI02670, RESULT

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The invention relates to a combination comprising several polymucleotides convaving any one of 127 sequences (51) such as the sequence of human call-and any one of 127 sequences (51) such as the sequence of human call-and beat as a called any one of 127 sequences. However, and their complements. The cDNAs are differentially expressed in LPS (lipopolysaccharide-treated foam cells. Also included are in LPS (lipopolysaccharide-treated foam cells. Also included are in LPS (lipopolysaccharide-treated foam cells. Also included are containing an extended or full length gene from a library of mucleic acid obtaining the vector, a purified polypeptide appearing as ADE25750 and containing the vector, a purified polypeptide appearing as ADE25750 and composition comprising a protein by culturing the host cell, and a ADE25751, producing a protein by culturing the host cell, and a ADE25750 and composition comprising a putified antibody that specifically binds to the proteins. The foam cell-expressed nucleic acids are useful for a high throughput detection of differential expression of one or more throughput secreening of a library of molecules or compounds to comparison with a standard defines early, with throughput screening of allbrary of molecules or compounds to identify a ligand which binds a polynucleotide. The library is chosen consecular disorder. The foam cell-expressed nucleic acids are useful for diagnosing to protein, for purifying a ligand from a sample for making a antibody. The proteins or microarray which can be used for detecting related as emple, diagnosing cardiovascular disorder. The foam cell-expressed nucleic acids are useful cardiovascular disorder. The foam cell-expressed nucleic acide are useful cardiovascular disorder. The foam cell-expressed nucleic and beach or a microarray which can be used for detecting related in LPS treated foam cells.
                                                                                                                                                                   Combination containing several polymucleotide that are differentially expressed in foam cells and complements of the polymucleotides, useful for diagnosing cardiovascular disease or atherosclerosis.
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Kaser MR;
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 41; 37pp; English.
          Porter JG,
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                     Shiffman
                                                                                                            WPI; 2003-875398/81.
                                Mikita T,
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288
                                                                                               121 TTGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180
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                                                           347 igcagciaacitariticccciagciticcccagacaccitgititaritarialaarg
                                                                                 AATTITGITTGTTGTGATGTGAAACAITATGCCTTAAGTAATGTTAATTCTTAITTAAGTTA
                                         TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCTTGTTTTATTATAATG
                       Gaps
Score 198.4; DB 10; Length 1472;
Pred. No. 38-30;
0; Mismatches 1; Indels 0;
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        99.2%;
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Human Cc12 gene and enhancer region DNA SeqID 4.
            AD003803 standard; DNA; 11793
                                               12-AUG-2004 (first entry)
       AD003803
RESULT
                  SXXXXXXXX
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This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular CC12-deficient, Ccr2-deficient and/ or a Cc12-deficient (Ccr2-deficient dual workockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipotuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and account be used for gene therapy purposes. This polynucleotide sequence is the human Cc12 gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                              Testing candidate drug for treating age-related macular degeneration, by administering drug to Col2-deficient, Cor2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 198.4; DB 12; Length 11793;
Pred. No. 3e-30;
0; Mismatches 1; Indels 0; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen; lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 4; 64pp; English.
                                                                                                                                                                                                                                                                                                           (KENT ) UNIV KENTUCKY RES FOUND.
                                                                                                                                                                                                                                                                    30-OCT-2002; 2002US-0422096P.
                                                                                                                                                                                                                              16-OCT-2003; 2003WO-US032933.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              analyzing developmen
accumulation in eye.
                                                                                                                                                        WO2004041160-A2
                                                                                                                      Homo sapiens
                                                                                                                                                                                                 21-MAY-2004.
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9278
                                           9159 AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 9218
120
                                                                TIGATGITITIAAGITITATCITTCATGGTACTAGTGTTTTTTAAGATACAGAGACTTGGGGA 180
                          61 AATTITGTITGTITGATGTGAAGATTATGCCTTAAGTAATGTTAATTTTAAGTTA
                                                                            Human MCP1 nucleotide sequence >MCP1_03.
                                                                                                                               AATTGCTTTTCCTCTTGAAC 9298
                                                                                                             181 AATTGCTTTTCCTCTTGTAC 200
                                                                                                                                                                                ACF64400 standard; DNA; 950
                                                                                                                                                                                                                          13-OCT-2003
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                                                                                                                                                                                                                                                                           The present invention describes an isolated polynucleotide (PN) comprising: (a) a sequence comprising at least 15 contiguous nucleotides of a sequence comprising variant sequences (A) from Table 4 given in the specification; or (b) a sequence that is complementary to (A). Also described: (1) an array of (PN) s comprising two or more of the isolated storage medium, where each record has a field identifying a base occupying a (PN) site and a location of the polymorphic site; and (4) a signal carrying data for access by an application program having executed on a data processing system. The (PN) can be used for detecting loci associated with multiple sclerosis. ACF64025 to ACF64424 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTTTGTTTGTTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTTTTAAGTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TIGATGITITAAGITITATCITICATGGIACIAGIGITITITAGAIACAGAGACITGGGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
         detection; computer-readable storage medium; polymorphic site; carrying data; data processing system; multiple sclerosis; gene;
                                                                                                                                                                                                                             polynucleotide, useful for detecting loci associated with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCTTGTTTTATTATAATG
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                                                                                                                                                                                     Natsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                    99.0%; Score 198; DB 8; Length 950; 99.0%; Pred. No. 3.7e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 950 BP; 255 A; 220 C; 184 G; 290 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human small inducible cytokine A2 (SCYA2) genomic DNA
                                                                                                                                                                                     Jin W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Mismatches
                                                                                                                                                                                     Rienhoff HY,
                                                                                                                                                                                                                                                           Disclosure; Page 75; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTGCTTTTCCTCTTGTAC 200
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                                                                                                                                  07-AUG-2001; 2001US-0310741P.
24-SEP-2001; 2001US-0324790P.
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                                                                                                              07-AUG-2002; 2002WO-US025268
                                                                                                                                                                                    White R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       02-JUL-2002 (first entry)
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Matches 198; Conservative
                                                                                                                                                                                                       WPI; 2003-268196/26.
                                                                                                                                                               (DNAS-) DNA SCI INC
                                                                                                                                                                                    Jones HB, Xu H,
                                                                     WO2003014319-A2
                                                  Homo sapiens.
                                                                                          20-FEB-2003
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The invention relates to single nucleotide polymorphisms in the gene encoding human small inducible cytokine A2 (SCYA2) polypoptide. A method for haplotyping the SCYA2 gene in a individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the SCYA2 haplotypes given in the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a trait and a haplotype or haplotype pair of the SCYA2 gene can be contained by comparing the frequency of the haplotype pair in a population exhibiting the trait with the frequency of the haplotype or haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype haplotype h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New genetic variants having polymorphisms in the small inducible cytokine A1 (SCYA2 ) gene, useful for studying the function of SCYA2 , and for treating disorders affected by expression or function of the SCYA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120
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haplotyping, atherosclerosis, antiarteriosclerotic, gene therapy; single nucleotide polymorphism; genotyping; drug screening; chromosome 17q11.2-q21.1.
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Pred. No. 4.3e-30;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kumar AM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "Human SCYA2"
                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GENA-) GENAISSANCE PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-AUG-2001; 2001WO-US026899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-AUG-2000; 2000US-0228496P
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98.5$;
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Best Local Similarity 98.5
Matches 197; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anastasio AE, Finkel K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human SCYA2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-339655/37.
P-PSDB; AAU77179.
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                                                                                                                                                                                                                                                Homo sapiens
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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention relates to human single exon nucleic acid probes (SENP). The present sequence is one such probe. The SENPs are derived from human HeLa cells. The SENPs can be used to produce a single exon microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix. notably cervical cancer. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human cervical epithelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTTTGTTTGTTGAAGACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA
                                                                                                                                       for gene expression analysis in human cervical cell sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; microarray; gene expression; cervical epithelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match

98.4%; Score 196.8; DB 4;

Best Local Similarity 99.0%; Pred. No. 6.4e-30;

Matches 198; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 25; SEQ ID NO 5501; 487pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Rank
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2286 AATTGCTTTTCCTCTTGAMC 2305
                                                                                                                                                                                                                                                                                                                ; 2000US-0180312P.
; 2000US-0204456P.
; 2000US-0069408
; 2000US-00632366.
; 2000US-023468TP.
; 2000US-023468TP.
                                                                                                                                                                                                                                                                                                                                                                                                                       (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                               Chen W,
                                                                                                                                                                                                                                                                                        30-JAN-2001; 2001WO-US000670
                                                                AAI15568 standard; DNA; 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-488901/53
                                                                                                                     (first
                                                                                                                                                                                      cervical cancer; ss
                                                                                                                                                                                                                                        WO200157278-A2.
                                                                                                                                                                                                                                                                                                                                26-MAY-2000;
30-JUN-2000;
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27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                           03-AUG-2000;
                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                 Probe #5501
                                                                                                                                                                                                                                                                  09-AUG-2001
                                                                                                                      12-OCT-2001
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                                                                                              AA115568
                                                        AAI15568/c
                                            RESULT 9
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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting, measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human fetal liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                       probe; ss.
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0
                                                                                                                                                                                                                                                                       Human; foetal liver; gene expression; single exon nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 196.8; DB 4; Length 360;
Pred. No. 6.4e-30;
0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 5805; 639pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                 Human foetal liver single exon nucleic acid probe #5805.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTGCTTTTCCTCTTGTAC 200
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632468.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234587P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                       BP.
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Best Local Similarity 99.0%;
Matches 198; Conservative
47 AATTGCTTTTCCTCTTGAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                          30-JAN-2001; 2001WO-US000669
                                                                                                                         DNA; 360
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                                                                                                                                                                                                      (first
                                                                                                                       ABA57500 standard;
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                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                      01-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SG,
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ABA26988 standard; DNA; 360

(first entry)

23-JAN-2002

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                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTAGATACAGAGACTTGGGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to single exon nucleic acid probes (SENP). The present sequence is one such probe. The probes are useful for producing a microarray for predicting, measuring and displaying gene expression in samples derived from human placenta. The probes are useful for antenatal diagnosis of human genetic disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTGATGTTTTAAGTTTTATCTTTCATGGTACTAGTGTTTTTTTAGATACAGAGACTTGGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AATITIGITIGITIGATGAGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA
                                                                                     Probe #5739 used to measure gene expression in human placenta sample.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 4; Length 360;
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                                                                                                       microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.4%; Score 196.8; 99.0%; Pred. No. 6.4
                                                                                                                                                                                                                                                                                                                                                              Claim 25; SEQ ID NO 5739; 654pp; English.
                                                                                                                                                                                                                                                                                                  Chen W, Rank DR;
                                                                                                                                                                                                                                                                                                                                              gene expression in human placenta.
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                                AAI37053 standard; DNA; 360 BP.
                                                                                                                                                                                                                                                                                (MOLE-) MOLECULAR DYNAMICS INC
                                                                                                                                                                                                       2000US-0180312P.
2000US-0207456P.
2000US-00608408.
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; 2000US-0234687P.
; 2000US-0236359P.
; 2000GB-00024263.
                                                                                                                                                                                       30-JAN-2001; 2001WO-US000663
                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 99.0
Matches 198; Conservative
                                                                                                                genetic disorder, ss.
                                                                                                                                                                                                                                                                                                 Hanzel DK,
                                                                                                                                                                                                                                                                                                                  WPI; 2001-488897/53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                   WO200157272-A2.
                                                                                                                                                                                                       04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                  Homo sapiens
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                                                                    17-0CT-2001
                                                                                                                                                                     09-AUG-2001
                                                  AAI37053;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                 Penn SG,
                                                                                                       Probe;
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ABA26988/c
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The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular eg. cardiovascular disease, hypertension, cardiac arrhythmias and eg. cardiovascular disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AATTTTGTTTGTTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Single exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               227 recaectrartritccccraectriccccaeacaccccrertrartrartrarare
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Probe #5454 for gene expression analysis in human heart cell sample.
                                              Human, gene expression; heart, microarray, vascular system; probe; cardiovascular disease; hypertension; cardiac arrhythmia; congenital heart disease; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7
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99.0%; Pred. No. 6...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rank DR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTGCTTTTCCTCTTGTAC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOLE-) MOLECULAR DYNAMICS INC
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2000US-00632366.
2000US-0234687P.
2000US-0236359P.
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2000US-0207456P.
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                                                                                                                                                                                                                        WO200157274-A2
                                                                                                                                                                                                                                                                                                                                                                                        04-FEB-2000;
26-MAY-2000;
30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                            09-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              167
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AAK05543 standard; DNA; 360
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                                                                                                                                                                                                                                                                                                                                      The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bonc marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of the probes of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 TIGATGITTTAAGTTTATGTTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                               120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  108
                                                                                                                                                                                                                                                                                                Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human bone marrow.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                             Human; bone marrow expressed exon; gene expression analysis; probe; microarray; cancer; leukaemia; lymphoma; myeloma; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                   ..
                                                                                                                                                                                                                                                                                                                                                                                                                   Score 196.8; DB 4; Length 360;
                                                                              Human bone marrow expressed single exon probe SEQ ID NO: 5703.
                                                                                                                                                                                                                                                                                                                           Example 4; SEQ ID NO 5703; 658pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. 6.4e-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-006632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000US-02346359P.
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                                   BP
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                                                                                                                                                                                          2000US-0180312P
                                   AAK31146 standard; DNA; 360
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198; Conservative
                                                                   (first entry)
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                                                                                                                                           WO200157276-A2
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                                                    AAK31146;
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                     RESULT 13
AAK31146/c
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RESULT 14 AAK05543/c

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATTITGITIGITGAIGIGAACAITAIGCCITAAGIAATGITAAITCTIAITTAAGITA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            probes which are derived from genomic sequences expressed in the human probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                         Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Single exon nucleic acid probes for analyzing gene expression in human brains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCAGCTAACTTATTTCCCCTAGCTTTCCCCCAGACACCTTGTTTTATTATTATAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention provides a number of single exon nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; SBQ ID NO 5534; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                               expressed single exon probe SEQ ID NO: 5534.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rank
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                                                                                                                                                                                                                                                                                                                                                                                 04-FEB-2000; 2000US-0180312P.
26-MAX-2000; 2000US-0207456P.
30-JUN-2000; 2000US-00608408.
03-AUG-2000; 200US-00632366.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-0234687P.
04-OCT-2000; 2000GB-00024263.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
ABS30826/c
ID ABS30826 standard; DNA; 360
                                                                                                                                                                                                                                                                                                                                     30-JAN-2001; 2001WO-US000667
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hanzel DK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-483446/52
                                                                                                                                                                                                                                              WO200157275-A2.
                                                                                                                                                                                                    Homo sapiens.
  05-NOV-2001
                                                 Human brain
                                                                                                                                                                                                                                                                                             09-AUG-2001
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The invention relates to a single exon nucleic acid probe (SENP) (I) for measuring human gene expression in a sample derived from human adult liver. Comprising one of 13109 defined nucleotide sequences given in the specification (or complements/ fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. (I) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is sesociated with coronary heart disease. ABS25011-ABS51005 represent human liver single exon nucleic acid probes of the invention. Note: The sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 227 TGCAGCTAACTTATTTTCCCCTAGCTTTTCCCCAGACACCCTGTTTTATTTTTTATAATG 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       167 AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTTCTTATTTTAAGTTA 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCTTGTTTTATTATTATAATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                      Human, single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 4; Length 360;
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99.0%; Pred. No. 6.4e-30;
iive 0; Mismatches 2;
                                                                                      Human liver single exon probe, SEQ ID No 5816.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 5816; 658pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen W, Rank DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MOLE-) MOLECULAR DYNAMICS INC.
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2000US-0234687P.
2000US-0236359P.
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2000US-0207456P.
2000US-00608408.
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                                                  (first entry)
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Best Local Similarity 99.0
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30-JUN-2000;
03-AUG-2000;
21-SEP-2000;
27-SEP-2000;
                                                                                                                                                                                                  Homo sapiens
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4, 2005, 08:31:05 Search completed: August Job time: 139.551 secs

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A1927247 wn24c03.x AA47235 zk74a08.9 AA429323 zw07b05.r BU5.2858 AGENCOURT AA804854 off44g07.8 AA57653 nm62b07.8 BU077671 im36d12.y

AA024754 ze76609.8 A1927356 wr49902.x BE466610 br23a10.x W52063 zc90802.81 A1086784 oz77c03.x A109809 gm91d11.x A1075862 ozz5b08.x A1298305 gm92d03.x BU49323 nadz6d10.

Scoring table:

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University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
Tel: 319 315 9266
Fax: 319 315 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com).
The following repetitive elements were found in this cDNA
sequence: 1-36, >AT rich#Low_complexity (matched compliment)
Seg primer: M13 FORWARD
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UI-E-CLI-afe-p-03-0-UI.sl UI-E-CLI Homo sapiens CDNA clone
UI-E-CLI-afe-p-03-0-UI 3', mRNA sequence.
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/organism="Homo sapiens"
/organism="Homo sapiens"
/db xref="taxon:9606"
/clone="UI-E-CL1-afe-p-03-0-UI"
/tissue type="human retina"
/dev tagage="adult"
/lab host="DH10B (Life Technologies) (Tl phage resistant)"
/clone lib="UI-E-CL1"
/note="Organ: eye; Vector: pT7T3-Pac (Pharmacia) with a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryorgium, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Bukammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. I (bases I to 424)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
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CA477924 UI-H-DH0-
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BF224310 7975a08.x
CD673147 fg21d04.y
BF065923 7h90601.x
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AV717017 AV717319
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                  GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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modified polylinker; Site_1: ECOR I; Site_2: Not I; ul-E-CLI is a normalized CDNA library confaining the UI-E-CLI is a normalized CDNA library confaining the following tissue(s): retina. The library was constructed following tissue(s): retina. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, e191-806, 1996. First strand CDNA synthesis was primed e191-806, 1996. First strand cDNA was ligated to an ECOR I adaptor, digested stranded cDNA was ligated to me ECOR I adaptor, digested with Not I, and cloned directionally into pT713-Pac vector. The oligonalectide used to prime the synthesis of vector. The oligonalectide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The located for the program, Gene Discovery in the Visual System, supported by National Eye Institute (NEI).

TAG_IISUE-human retina
TAG_LIB-UI-E-CII
TAG_SEQ-CCGGG"
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1 (bases 1 to 450)

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1 Hillier, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Thaising, B., White, Y., Wylie, T., Waterston, R. and Wilson, R. Unpublished (1997)

Contact: Wilson RK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (infc@image.llnl.gov) for further information.
Seq primer: -40UP from Gibco.
Location/Qualifiers
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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/mol_type="mRNA"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrini; Hominidae; Homo.

1 (bases 1 to 456)

NGI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

RS NCI-CGAP http://www.ncbi.nlm.nih.gov/
Tumor Gene Index

Unpublished (1997)

AL Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Fissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.

Emmert-Buck, M.D., Ph.D.

CONA Library Preparation: M. Bento Soares, Ph.D.

CONA Library Preparation: M. Bento Soares, Ph.D.

CONA Library Preparation: M. Catago Clone distribution information can be cloud distribution: NGI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Insert Lengh: 618 & Std Error: 0.00
                                      AI818813 456 bp mENA linear EST 07-MAR-2000 wk91f09.xl NCI CGAP Lu19 Homo sapiens cDNA clone IMAGE:2422793 3' similar to gb: W24545 MONOCYTE CHEMOTACTIC PROTEIN 1 PRECURSOR
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Seq primer: -400P from Gibco
High quality sequence stop: 4
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HUMAN);, mRNA sequence.
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AI818813.1 GI:5437892
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Homo sapiens
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDN Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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NCI-CAAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 IGCAGCTAACTITATTITCCCCTAGCTITCCCCCAGACACCTIGITTATTATTATAAATG
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                                                                          tissue_type="Metastatic Chondrosarcoma"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.2%; Score 198.4; DB 6; Best Local Similarity 99.5%; Pred. No. 3.8e-31; Matches 199; Conservative 0; Mismatches 1;
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TAG_LIB=UI-H-DH0
TAG_SEQ=AGATCATTGC"
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DEFINITION
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VERSION
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                                                                                                                                                                        "Gev stages" adult"

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[Ala_host="nH10B (phage-resistant)"

[Ala_host="nH10B (phage-resistant)"

[Ala_host="nto-resistant and the stage of the modified polylinker; lst strand cDNA was prepared from pooled lung tumor tissue, and was then primed with a Not I oligo(dT) primer. Double-stranded cDNA was ligated to ECO RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and ECO RI sites of the modified pTT3 vector. Library went through one round of normalization, Library constructed by Bento Soares and M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution inforwation can be obtained
from Dr. M. Bento Soares, bento-soares@uiowa.edu
The following repetitive elements were found in this cDNA
sequence: 1-36, AT_rich#Low_complexity (matched compliment)
FOLYA=Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CA437924 462 bp mRNA linear EST 08-NOV-2002 UI-H-DHO-aur-l-19-0-UI.81 NCI CGAP DHO Homo sapiens cDNA clone UI-H-DHO-aur-l-19-0-UI 3', mRNA sequence.
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                                   /clone="IMAGE:2422793"
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differentiated (4 pooled tumors, including primary and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 456;
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Pred. No. 3.8e-31;
0; Mismatches 1;
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Best Local Similarity 99.5%;
Matches 199; Conservative
                                                                                                                                                    metastatic)"
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Homo sapiens
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Unpublished (1997)
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g ò 셤 RESULT 4 CA437924/c DEFINITION

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE

JOURNAL

COMMENT

FEATURES

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Gapa

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FEATURES

ORIGIN

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Memanla; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mamanla; Eutheria; Primates; Catarrhini; Hominidae; Homo. Wistow,G., Bernstein,S.L., Ray,S., Wyatt,M.K., Behal,A., Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K. Expressed sequence tag analysis of adult human iris for the NEIBank Project: steroid-response factors and similarities with retinal pigment epithelium.
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fg21d04.yl Human Iris CDNA (Normalized): fg Homo sapiens CDNA Clone
fg21d04.5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fadil graeme@helix.nih.gov
Emali graeme@helix.nih.gov
Plate: 21 row: d column: 04
Seq primer: MI3RP1 reverse primer (ABI).
Location/Qualifiers
1. 506
                                     organism="Homo sapiens"
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22103462
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Location/Qualifiers
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Homo sapiens
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Best Local Similarity 99.5
Matches 199; Conservative
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CD673147
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                                                                                                               Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Email: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCT-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
Alifo@inage.llnl.gov
High quality sequence stop: 416.
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NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
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99.5%; Pred. No. 3.8e-31;
iive 0; Mismatches 1
                  www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 541 Std Error: 0.00
Seg primer: -40m13 fwd. BT from Amersham
High quality sequence stop: 447.
Location/Qualifiers
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Matches 199, Conservative
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/tissue_type="color tumor, RER+"
/lab_host="nulus"
/lab_host="nulus"
/clone_lib="NCI_CGAP_Col6"
/note="Organ: colon" Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Col0 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 114484-1145351).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BUS80378 601 bp mRNA linear EST 17-SEP-2002
in33b12.x1 Human Fetal Pancreas 1B Homo sapiens cDNA 3' similar to
SW:SY02_HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2 PRECURSOR ;, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 601)

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Endocrine Pancreas Consortium
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99.5%; Pred. No. 3...
                                                                                                   /organism="Homo sapiens"
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Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
                                                                                                                       /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3323256"
  Seq primer: -40UP from Gibco
High quality sequence stop: 4
Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
1 (bases 1 to 562)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
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0
                                                                                           /tissue_type="Iris"
/dev kage="Adult"
/db_host="EMDH108"
/clone_lib="Human Iris cDNA (Normalized): fg"
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Pred. No. 3.8e-31;
0; Mismatches 1;
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Matches 199; Conservative
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p mRNA linear EST 16-OCT-2000 clone DCBBXB06 5', mRNA sequence.
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/lab_host="BM25.8"
/clone llb=DCB"
/note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
                                                             61 AAITITIGITTIGITTGAAGGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA
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ilarity 99.5%; Pred. No. 3.8e-31;
Conservative 0; Mismatches 1;
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                                          /organism="Homo sapiens"
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/clone="DCBBXB06"
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AV717017 DCB Homo sapiens CDNA
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AV717017.1 GI:10814169
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// organism="MRNA"
// organism="MRNA"
// db_xref="taxon:966"
// tissue type="Fetal Pancreas" (4 Pooled Donors, 18 - 20
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// dev_stage="Fetal Pancreas"
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1 (bases 1 to 634)

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2 (bay, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Song, H., Gu, Y., Yang, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Cheng, Z. and Han, Z.

Homo sapiens CDNA DCB clones
Unpublished (2000)
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Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919 (ex.45)
Fax: 86-21-50801922
Email: hanag@chgc.gh.cn
    Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue
findingate.wistl.edu)
Seq primer: -40UP from Gibco
High quality sequence stop: 454.
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Best Local Similarity 99.2%; Score 198.4; DB 5; Length 601;
Best Local Similarity 99.5%; Pred. No. 3.8e-31;
Matches 199; Conservative 0; Mismatches 1; Indels 0.
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This clone is available at CHGC in Shanghai.
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/urganism="Homo sapiens"
// mol type="mRNA"
// db_xref="txxxxn:9606"
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   515 TIGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases I to 637)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
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Coordinated Laboratory for Computational Genomics
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Pred. No. 3.8e-31;
0; Mismatches 1;
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Best Local Similarity 99.5%;
Matches 199; Conservative
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I. (bases I to 637)

Xu,X., Gu,J., Liu,F., Qu,J., Zhao,M., Li,Y., Huang,Q., Zhou,J., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Li,N., Qian,B., Gao,X., Lu,G., Cheng,Z., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Homo sapiens CDNA DCB clones
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Zeguing Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Eax: 86-21-508019192
Email: hansg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
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/note="Vector: pTriplBx2; Site_l: sfilA; Site_2: sfilB"
                                                                                                                                                                                                                                                                                                                          515 TTGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA
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Score 198.4; DB 1;
Pred. No. 3.8e-31;
0; Mismatches 1;
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llarity 99.5%; Pred. No. 3.8e-31;
Conservative 0; Mismatches 1;
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/clone="DCBBXC09"
/cell_type="dendritic cells"
/dev_stage="mature"
/lab_host="BM25.8"
/clone_lib="DCB"
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/organism="Homo sapiens"
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   Query Match
Best Local Similarity 99.5%;
Matches 199; Conservative
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Homo sapiens
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184 AATTGCTTTTCCTCTTGAAC 165
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University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa Med Labs, Iowa City, IA 52242, USA
2024 University of Iowa
2024 University of Iowa
Tel: 319 356 4866
Fax: 319 356 7171
Email: paul-mcrayeuiowa.edu
Email: paul-mcrayeuiowa.edu
Tissue Procurement: Dr. M. J. Welsh, University of Iowa
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CLOMA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: Researchers may obtain clones from Research
Clone Distribution: A.A.T. rich#Low_complexity (matched compliment)
Seq primer: M13 PORWARD
POLYA=Yes.
                                                                                                                                                                                                                                                                                                                                           BU681561 640 bp mRNA linear EST 07-0CT-2002
UI-CF-ECI-acj-k-08-0-UI.s1 UI-CF-EC1 Homo sapiens cDNA clone
UI-CF-ECI-acj-k-08-0-UI 3', mRNA sequence.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                           121 TTGATGTTTTAAGTTTATGTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180
                                                                                                                                                             284 TIGRIGITITAAGITTATCITICAIGGTACTAGIGTTITITAGATACAGAGACTIGGGGA 343
                                                                     AATTITGITTGITGATGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTA
                                                                                                       224 AAITTIGITIGITIGAIGIGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 283
                 1 (bases 1 to 640)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
recaectaactratriticcccraectriccccaeacaccraetritarrary
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BU681561.1 GI:23531598
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BU681561/C
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MEDLINE
PUBMED
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AUTHORS
TITLE
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KEYWORDS
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Tumor Gene Index
Tumor Gene Index
Unpublished (1997)
Conteat: Robert Strausberg, Ph.D.
Conteat: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
Tissue Procurement: Dr. Jose Mercuende
Tissue Procurement: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
Clone Distribution: Clone distribution information can be found
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UI-H-DHO-aun-d-15-0-UI.sl NCI CGAP_DHO Homo sapiens cDNA clone
IMAGE.5871710 3', mRNA sequence.
BM996167
Not I site. Double stranded cDNA was ligated to an ECOR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligomoufsotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the contains Into sequence tag for this library is
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(Dases 1 to 642)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Gancer Institute, Cancer Genome Anatomy Project (CGAP);
                                                                                                                                                                                                                                                                                                                                   AAGTGCTTAC.
AAGTGCTTAC.
AAGTICSUBENORMAL Lung Epithelial Cells Tissue nos 369-371
and 380-383
TAG_LIB=UI-CF-ECI.
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="texon:9606"
/clone="TMAGE:5871710"
/tissue_type="Metastatic Chondrosarcoma"
/dev_stage="Adult"
/lab_host="PH108 (Life Technologies)"
/clone_lib="NCI_CGAP_DH0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 640;
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99.2%; Score 198.4; DB 5; Length
Best Local Similarity 99.5%; Pred. No. 3.8e-31;
Batthes 199; Conservative 0; Mismatches 1; Indels
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/note="Organ: Lung; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI_CGAP_DHO is a cDNA ibrary containing the following tissue(s): vS-8 cell line from Metastatic Chondrosarcoma in Lung. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-86, 1966, 1966, 1961 strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and clonned directionally into pT7T3-Pac vector. The oligonucleoride used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this TAG_LIBSUE-H-DHO TAG_LIB-UH-H-DHO TAG_SEQ=AGATCATTGC.
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ORIGIN

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0; Gaps Query Match 99.2%; Score 198.4; DB 5; Length 642; Best Local Similarity 99.5%; Pred. No. 3.8e-31; Matches 199; Conservative 0; Mismatches 1; Indels 0.

304 AATTIGITIGITIGITIGAGAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 245

121 TTGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180

244 TTGATGTTTTAAGTTTATCTTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 185

181 AATTGCTTTTCCTCTTGTAC 200

AATTGCTTTTCCTCTTGAAC 165 184 Search completed: August 4, 2005, 14:32:05 Job time : 951.968 secs

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August 4, 2005, 07:01:49; Search time 41.2146 Seconds (without alignments) 7940.282 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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200
1 tgcagctaacttattttccc......aattgcttttcctcttgtac 200
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/cgm2 6/ptodata/1/ina/5B_COMB.seq:*
/cgm2 6/ptodata/1/ina/6A COMB.seq:*
/cgm2 6/ptodata/1/ina/6B_COMB.seq:*
/cgm2 6/ptodata/1/ina/pcTUS COMB.seq:*
/cgm2 6/ptodata/1/ina/bcTUS COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                     OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                         IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents NA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                      Sequence:
                                                                                                                                                           Run on:
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		عد		,	SUMMARIES	
Regult No.	Score	Query Match	Query Match Length	DB	8	Description
1	198.4	99.2	772	4	US-08-437-306-1	Sequence 1, Appli
7	196.8	98.4	647	4	US-09-777-430C-72	72,
m	196.8	98.4	725	4	US-09-591-992-3	'n
4	196.8	98.4	725	4	US-09-023-655-1344	
S	196.8	98.4	741	٣	US-07-927-391-25	
9	196.8	98.4	741	4	US-09-023-655-1165	116
7	196.8	98.4	752	9	5212073-1	Patent No. 5212073
8	196.8	98.4	752	9	5212073-1	Patent No. 5212073
6	196.8	98.4	1712	4	US-09-148-545-106	Sequence 106, App
10	196.8	98.4	1822	4	US-09-148-545-105	105,
11	195.2	97.6	661	4	US-09-814-915A-104	104,
12	45.2	22.6	840	4	US-09-016-434-1033	1033,
c 13	43.6	21.8	612	4	US-09-902-540-1357	1357,
14	43.2	21.6	585	4	US-09-328-352-761	Sequence 761, App
15	43.2	21.6	346112	4	US-09-949-016-13165	1316
c 16	42.2	21.1	6124	m	US-08-213-419B-3	m
•	41	20.5	1738	4	US-09-918-909A-27	N
18	40.8	20.4	285478	4	US-09-949-016-13362	H
19	40	20.0	396	4	US-09-640-173-10	Н
20	40	20.0	396	4	US-09-713-550-10	10,
21	40	20.0	396	4	US-09-825-294-10	10,
22	40	20.0	396	4	US-09-970-966-10	10,
c 23	39.4	19.7	6409	4	US-09-967-908A-1	1, 7
•	39.4	19.7	6409	4	US-10-159-151-1	1
25		19.6	49440	4	US-09-949-016-14150 '	
c 26	39	19.5	601	4	US-09-949-016-182221	Sequence 182221,
27	39	19.5	133358	4	US-09-949-016-16964	Sequence 16964, A

Sequence 12651, A Sequence 1280, App Sequence 3, Appli Sequence 135, Appli Sequence 135, Appli Sequence 15546, A Sequence 1, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Appli Sequence 98, Ap
US-09-949-016-12651 US-09-302-540-1280 US-09-303-708-3 US-09-083-7-3 US-09-08-31 US-09-08-31 US-09-949-016-135597 US-09-949-016-135597 US-09-949-016-13546 US-09-949-016-12106 US-09-949-016-12106 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10 US-09-31-10
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US-08-437-306-1
; Sequence 1, Application US/08437306
; Patent No. 6787645
; GENERAL INFORMATION:
; APPLICANT: Stiles, Charles D.
; APPLICANT: Stiles, Charles D.
; APPLICANT: Wong, Gordon G.
; TITLE OF INVENTION: No. 6787645el Human Cytokine
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
STREET: Two Militia Drive
CITY: Lexington
STRATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER NO. 62173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURSERIATION NUMBER: US/08/437,306
FILING DATE: 09-MAY-1995
CLLASIFICATION NUMBER: US 08/228,931
FILING DATE: 13-APE-1994
FILING DATE: 13-APE-1994
FILING DATE: 13-APE-1994
FILING DATE: 12-APA-1993
PRIOR APPLICATION NUMBER: US 07/701,515
FILING DATE: 16-MAY-1991
PRIOR APPLICATION NUMBER: US 07/701,515
FILING DATE: 16-MAY-1991
FILING DATE: 16-MAY-1991
FILING DATE: 16-MAY-1991
FILING DATE: 16-MAY-1991
FILING DATE: 16-MAY-1991
FILING DATE: 12-MAY-1999
ATTORNEY/AGENT INFORMATION:
NAME: BEOOK, DATA:
NAME: BEOOK, DATA:
NAME: REGISTRATION NUMBER: 25-592
PREDEDENTY NUMBER: 25-592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 772 base pairs TYPE: nucleic acid STRANDEDNESS: single
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yeaquence 72, Application US/09777430C
patent No. 6780982
yeatence 72, Application US/09777430C
yeapticANT: Lyamichev, Victor
yeapticANT: Allawi, Hatim T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98.4%; Score 196.8; DB 4;
ilarity 54.0%; Pred. No. 2.3e-38;
Conservative 90; Mismatches 2;
                                                                                                                                                                             DB 4;
                                                                                                                                                                          Query Match 99.2%; Score 198.4; DB 4. Best Local Similarity 99.5%; Pred. No. 9.6e-39; Matches 199; Conservative 0; Mismatches 1.
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AAUUGCUUUUCCUCUUGAAC 525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 AATTGCTTTTCCTCTTGTAC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: RNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) OTHER INFORMATION: Synthetic US-09-777-430C-72
TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                        73..369
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Best Local Simil
Matches 108; C
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US-09-777-430C-72
                                                                          NAME/KEY:
LOCATION:
US-08-437-306-1
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US-Uy-Dyl-By2-3
; Sequence 3, Application US/09591992
; Patent No. 6565418
; Patent No. 6565418
; GENERAL INFORMATION:
; APPLICANT: Gallo, Robert C.
; APPLICANT: Gallo, Anthony L.
; APPLICANT: Garlo, Alfedo
; TILE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
; TILE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
; TILE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
; TILE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
; FILE REFERENCE: 4115-109 CUP.
; CURRENT APPLICATION NUMBER: US/09/591,992
CURRENT FILING DATE: 1998-12-11
; PRIOR FILING DATE: 1998-12-11
; PRIOR FILING DATE: 1997-12-11
; PRIOR FILING DATE: 1997-12-11
; RIOR FILING DATE: 1997-12-11
; SEQ ID NOS: 7
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 3
; LENGTH: 725
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COMPUTER READBLE FORM:
MEDIUW TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
CUSPITARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SUGRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
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Pred. No. 2.3e-38;
0; Mismatches 2
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3174 PORTER DRIVE
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US-003-655-1344
Sequence 1344, Application US/09023655
Fatent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
TITLE OF INVENTION: COMPOSITION
TITLE OF INVENTION: EXPRESSION
TOWNERS OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AATTGCTTTTCCTCTTGTAC 200
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Best Local Similarity 99.0%;
Matches 198; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
US-09-591-992-3
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395 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCCTGTTTTATTTTATTATAATG 454
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Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Offirey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSES: INCTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Propy disk
COMPUTER: Propy disk
COMPUTER: Propy disk
COMPUTER: Propy disk
SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 196.8; DB 3;
Pred. No. 2.3e-38;
0; Mismatches 2;
            FILING DATE: 19920929
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: SANE, Bernhard D
REGISTRATION NUMBER: 28,665
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECHONE: (703) 836-9300
TELEFRY: (703) 683-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 AATTGCTTTTCCTCTTGTAC 200
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                                                                                                                                                                                                                                          TELEX: 899149
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
LENGTH: 74 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-07-927-391-25
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CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 99.0°
Matches 198; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
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Patent No. 6001649

GENERAL INFORMATION:
APPLICANT: CAUT, Daniel
APPLICANT: PERRARA, Pascual
APPLICANT: WILLOW, Brigitte
APPLICANT: WINTY, Adrian
APPLICANT: WINENTION: Protein having a cytokin type
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: Action
TITLE OF INVENTION: Action activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: Action activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: Action activity, and recombinant DNA, expression vector and hosts
CORRESPONDENCE ADDRESS:
ADDRESSEE: RANG Street Station, Suite 500,1800 Diagonal
STREET: Radd, PO. Box 299
CONTRY: ALEXANDRIA
STATE: VIRGINIA
CONTRY: USA

ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 AATTITGTIGTIGATGTGAAACATTAIGCCTTAAGTAAIGTTAATTCTTATTTAAGTTA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 196.8; DB 4;
Pred. No. 2.3e-38;
0; Mismatches 2;
                                                                    APPLICALION:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Scaller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: 97,071
REPERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPAX: (650) 845-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1344:
SEQUENCE CHARACTERISTICS:
LENGTH: 725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AATTGCTTTTCCTCTTGTAC 200
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Best Local Similarity 99.0
Matches 198; Conservative
FILING DATE: HEREWITH
                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GENBANK
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US-09-023-655-1344
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98.4%; Score 196.8; DB 6; Length 752;
Best Local Similarity 99.0%; Pred. No. 2.3e-38;
Matches 198; Conservative 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                         Length 741;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5212073
APPLICANT: ROLLINS, BARRETT; STILES, CHARLES; WONG, GORDON G.
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                       Score 196.8; DB 4;
Pred. No. 2.3e-38;
0; Mismatches 2;
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMUNICATION INFORMATION:
TELEPAN: (650) 845-0555
INFORMATION FOR SEQ ID NO: 1165:
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/351,008
FILING DATE:12-MAY-1989
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                                                                                                                                                                 , CLONE: GENBANK
; CLONE: 9187434
US-09-023-655-1165
                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 198; Conserv
                                                                                                                                                             IMMEDIATE SOURCE:
LIBRARY: GENBA
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                                                                                                                                                                                                                                                                                                                                                                                    Length 752;
5212073-1
;Patent No. 5212073
;Patent No. 5212073
;APPLICANT: ROLLINS, BARRETT;STILES, CHARLES;WONG, GORDON G.
;TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
;NUMBER OF SEQUENCES: 1
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/07/351,008
;FILING DATE:12-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
TITLE OF INVENTION: 70 Human Secreted Proteins
TITLE OF INVENTION: 70 Human Secreted Proteins
CURRENT APPLICATION NUMBER: US/09/148.545
CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,334
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-03-07
EARLIER FILING DATE: 1997-03-03-07
EARLIER FILING DATE: 1997-03-03-07
EARLIER FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                    Score 196.8; DB 6;
Pred. No. 2.3e-38;
0; Mismatches 2;
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R FILING DATE: 1997-05-23

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,502

R APPLICATION NUMBER: 60/047,583

R APPLICATION NUMBER: 60/047,583

R PILING DATE: 1997-05-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 106, Application US/09148545
Patent No. 6590075
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99.0%;
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Best Local Similarity
Matches 198; Conserv
                                                                                                                                                                                                                                                                                                  LENGTH: 752
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R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,500

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,587

R APPLICATION NUMBER: 60/047,587

R APPLICATION NUMBER: 60/047,492

R APPLICATION NUMBER: 60/047,492

R APPLICATION NUMBER: 60/047,598

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,598

R APPLICATION NUMBER: 60/047,598

R APPLICATION NUMBER: 60/047,598

R APPLICATION NUMBER: 60/047,592

R APPLICATION NUMBER: 60/047,592

R APPLICATION NUMBER: 60/047,592 R PLING DATE: 1997-05-23

R APPLICATION NUMBER: 60/047,632

R APPLICATION NUMBER: 60/047,601

R FILING DATE: 1997-05-23

R APPLICATION NUMBER: 60/043,580

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,568

R FILING DATE: 1997-04-11

R APPLICATION NUMBER: 60/043,314

R FILING DATE: 1997-04-11 RELING DATE: 1997-04-11
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RAPPLICATION NUMBER: 60/043,671
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RELING DATE: 1997-04-11
REPLING DATE: 1997-04-11
REPLING DATE: 1997-04-11
REPLING DATE: 1997-04-11
REPLING DATE: 1997-04-11 R FILING DATE: 1997-04-11
R APPLICATION NUMBER: 60/048,974
R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/056,886
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,877 APPLICATION NUMBER: 60/047,618
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592 APPLICATION NUMBER: 60/043,313 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,672 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,315 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,581
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,584 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,612 FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/043,312 FILING DATE: 1997-04-11 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,889 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,630 FILING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,872 APPLICATION NUMBER: 60/047,617 APPLICATION NUMBER: 60/056,893 FILING DATE: 1997-08-22 LING DATE: 1997-08-22 FILING DATE: 1997-05-23 EARLIER EARLIE EARLIER
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R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,903

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,888

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,889

R PILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,880

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,894

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,994

R FILING DATE: 1997-08-22

R APPLICATION NUMBER: 60/056,994

R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/056,874
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,910
R APPLICATION NUMBER: 60/056,864
R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,631 ER APPLICATION NUMBER: 60/057,761
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ER PILING DATE: 1997-05-23
ER FILING DATE: 1997-05-23
ER PILING DATE: 1997-05-23
ER PILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,585
ER RILING DATE: 1997-05-23
ER APPLICATION NUMBER: 60/047,586
ER APPLICATION NUMBER: 60/047,586
ER PILING DATE: 1997-05-23 R APPLICATION NUMBER: 60/056,632
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,664
R APPLICATION NUMBER: 60/056,876
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,816
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,909
R RILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,909
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,909
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,909
R FILING DATE: 1997-08-22 R APPLICATION NUMBER: 60/047,593
RR FILING DATE: 1997-05-23
RR APPLICATION NUMBER: 60/047,614
RR FILING DATE: 1997-05-23
RR FILING DATE: 1997-04-11
RR FILING DATE: 1997-04-11 PLICATION NUMBER: 60/056,882 LING DATE: 1997-08-22 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,845 FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11 APPLICATION NUMBER: 60/056,637 APPLICATION NUMBER: 60/056,636 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/056,892 FILING DATE: 1997-08-22 APPLICATION NUMBER: 60/047,595 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,590 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,594 FILING DATE: 1997-05-23 APPLICATION NUMBER: 60/047,589 LING DATE: 1997-05-23 LING DATE: 1997-08-BARLIER BARLIE EARLIER I EARLIER I EARLIER I EARLIER I EARLIER I EARLIER I EARLIER I EARLIER BEAR

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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,630
FILING DATE: 1997-08-22
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APPLICANT: ROSEN et al.
APPLICANT: ROSEN et al.
TITLE OF INVENTION: 70 Human Secreted Proteins
FILLE REFERENCE: PSOOLPI
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-05-23
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Pred. No. 2.6e-38;
0; Mismatches 2;
EARLIER APPLICATION NUMBER: 60/056,862
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,887
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/048,964
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EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-06-06
EARLIER FILING DATE: 1997-09-05
EARLIER FILING DATE: 1997-09-22
NUMBER OF SEQ ID NOS: 280
SEQTHARE: PATENTING VATE: 1997-08-22
NUMBER OF SEQ ID NOS: 20
SEQTHARE: PATENTING VATE: 2.0
SEQTHARE: PATENTING VATE: 2.0
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; Sequence 105, Application US/09148545
partent No. 6590075
; Partent INFORMATION:
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Best Local Similarity 99.0%;
Matches 198; Conservative
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R. FILING DATE: 1997-04-11

R. APPLICATION NUMBER: 60/043,669

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R. APPLICATION NUMBER: 60/043,312

R. FILING DATE: 1997-04-11

R. RAPLICATION NUMBER: 60/043,313

R. PILING DATE: 1997-04-11

R. APPLICATION NUMBER: 60/043,315

R. FILING DATE: 1997-04-11

R. APPLICATION NUMBER: 60/043,315

R. FILING DATE: 1997-04-11

R. APPLICATION NUMBER: 60/048,974

R. FILING DATE: 1997-06-06

R. FILING DATE: 1997-06-06

R. PALING DATE: 1997-06-06

R. APPLICATION NUMBER: 60/056,886
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RAPPLICATION NUMBER: 60/043,568
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APPLICATION NUMBER: 60/056,877
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BR FILING DATE: 1997-05-23

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APPLICATION NUMBER: 60/043,671
FILING DATE: 1997-04-11
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/047,632
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APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
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APPLICATION NUMBER: 60/043,311
APPLICATION NUMBER: 60/047,633
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,583
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,882
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,637
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,903
                                                                                                                                                                                                                                                                             R APPLICATION NUMBER: 60/056,880
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,894
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,636
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,836
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R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,864
R PILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,631
R R PLING DATE: 1997-08-22
R R PLING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,631
R APPLICATION NUMBER: 60/056,845
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APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,879
FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,578
APPLICATION NUMBER: 60/043,576
APPLICATION NUMBER: 60/043,576
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APPLICATION NUMBER: 60/047,501
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,670
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,876
FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/047,590
FILING DATE: 1997-05-23
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FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,593
      60/056,662
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FILING DATE: 1997-05-23
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                                           APPLICATION NUMBER: 60/056,872
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APPLICATION NUMBER: 60/
FILING DATE: 1997-08-22
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Sequence 104, Application US/09814915A

Sequence 104, Application US/09814915A

Patent No. 6750015

GENERAL INFORMATION:
APPLICANT: Richer, Jennifer
APPLICANT: Richer, Jennifer
APPLICANT: Richer, Jennifer
APPLICANT: Richer, Jennifer
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Progesterone Receptor-Regulated Gene Expression and Methode RelaTITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
FILE REFERENCE: 2848-39
FILE REPERENCE: 2848-39
FILE REPERENCE: 2848-39
FILE REPERENCE: 2848-39
FILE REPERENCE: 2000-06-28
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FILE REPERENCE: 2000-06-28
FILE REPEREN ö 1425 IGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCCTGTTTTATTTTATAATG 1484 61 AATTITGTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120 121 TTGATGTTTTAAGTTTATCTTCATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180 1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCCTTGTTTTATTATAATG 1485 AATTTTGTTGTTGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCTTGTTTTATTATTATATG Gapa ö Length 1822; 97.6%; Score 195.2; DB 4; Length 661; 98.5%; Pred. No. 5.5e-38; ive 0; Mismatches 3; Indels 0 2; Indels 99.0%; Pred. No. 2.6e-38; 0; Mismatches EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,909
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-08-22
EARLIER FILING DATE: 1997-06-06
EARLIER APPLICATION NUMBER: 60/056,908
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PALENTIN VET: 2.0
SEQ ID NO 105
LENGTH: 1822 1605 AATTGCTTTTCCTCTTGAAC 1624 181 AATTGCTTTTCCTCTTGTAC 200 Best Local Similarity 99.0 Matches 198; Conservative Query Match Best Local Similarity 98.5 Matches 197; Conservative Homo sapiens US-09-814-915A-104 US-09-814-915A-104 TYPE: DNA ORGANISM: Query Match a 셤 ò 쉽 ઠ ઠે ઠે ઠે

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                                                                                                                             TIGATGITITAAGITITATGITICATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 180
                                      120
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   AATTTTGTTGTTGATGTGAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA
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Sequence 1033, Application US/09016434

Sequence 1033, Application US/09016434

Sequence 1033, Application US/09016434

PSECONDER No. 650938

APPLICANT: Janice Au-Young

APPLICANT: Janice Au-Young

APPLICANT: Janice Au-Young

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

TITLE OF INVENTION: PATHWAY GENE EXPRESSION

NUMBER OF SEQUENCES: 1490

CORRESPONDENCE ADDRESS:

ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.6%; Score 45.2; DB 4; Length 840; 66.9%; Pred. No. 0.049; ive 0; Mismatches 38; Indels
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM FC Comparible
COMPUTER: IBM FC Comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: HEREUITH
APPLICATION NUMBER: US/09/016,434
FILING DATE: HEREWITH
FILING DATE:
CLASSIFICATION STAR:
APPLICATION NUMBER: APPLICATION:
MAWE: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: 37,071
REGISTRATION NUMBER: BA-0002 US
REGISTRATION NUMBER: PA-0002
REGISTRATION NUMBER: PA-0005
TELECOMMUNICATION INFORMATION:
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3174 PORTER DRIVE
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SEQUENCE CHARACTERISTICS:
LENGTH: 840 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Best Local Similarity 66.9
Matches 79; Conservative
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INMEDIATE SOURCE:
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CLONE: 965517
US-09-016-434-1033
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US-09-328-352-761

j Sequence 761, Application US/09328352

j Sequence 761, Application US/09328352

j Sequence 762, Application US/09328352

j Patent No. 6562958

j GENERAL INFORMATION:

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPBUTICS

TITLE OF INVENTION: UNMBER: US/09/328,352

CURRENT APPLICATION UNMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 761
sequence 1357, Application US/09902540

patent No. 6833447

GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Greegory J.
APPLICANT: Staten C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVERTION: Myxococcus xanthus Genome Sequences and Uses Thereof FILE REFERENCE: 38-10 (15849)
FILE REFERENCE: 38-10 (15849)
FURENT APPLICATION NUMBER: US/09/902,540
CURRENT APPLICATION NUMBER: 06/217,883
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR SPELING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825

LENGTH: 612

TYPE- ...

LENGTH: 612
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Pred. No. 0.14;
0; Mismatches 63; Indels
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54.8%; Pred. No. 0.11;
:ive 0; Mismatches 70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(612)
COTHER INFORMATION: unsure at all n locations
US-09-902-540-1357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA CINETODACTER Daumannii ORGANISM: Acinetobacter baumannii US-09-328-352-761
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Best Local Similarity 56.2%;
Matches 81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Myxococcus xanthus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 21.8°
Best Local Similarity 54.8
Matches 85; Conservative
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Sequence 13165, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; PAPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOPTHARE: FEBSICS for Windows Version 4.0
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| NAME/KEY: misc_feature | LOCATION: (1)...(346112) | OTHER INPORMATION: n = A,T,C or G US-09-949-016-13165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
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			Description		Sequence 2, Appli	Sequence 6347, Ap	Sequence 211, App	Sequence 41, Appl	Sequence 4, Appli	Sequence 5454, Ap	Sequence 294, App
SUMMARIES			ID		9 US-09-899-276-2	US-09-918-995-6347	US-10-133-013-211	16 US-10-247-671-41	US-10-685-705-4	US-09-864-761-5454	19 US-10-775-169-294
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                                                                                                                                                                                                                          Sequence 6447, Application US/09918995
; Sequence 6447, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
APPLICANT: HYSEQ, INC.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT PRILICATION NUMBER: US/09/918,995
CURRENT FILLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILLING DATE: 2001-07-30
PRIOR FILLING DATE: 38054
SOFTWARE: FRASES for Windows Version 3.0
SEQ ID NOS: 38054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AATTGCTTTTCCTCTTGTAC 200
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                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(489)
COTHER INFORMATION: n = A,T,C or G
US-09-918-995-6347
                                                                                                                                                 181 AATTGCTTTTCCTCTTGTAC 200
                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
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hes 199; Conservat
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US-10-133-013-211/c
                                                                                                                                                                                                                             US-09-918-995-6347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCTTGTTTTATTATTATAAATG
                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1472;
                                                                                                                                                                                                                                                                                                       Length 1005;
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; Sequence 41, Application US/10247671
; Publication No. US20030194721A1
; Publication No. US20030194721A1
; GENERAL INFORMATION:
    APPLICANT: Mikita, Thomas
; APPLICANT: Mifitan, Domin, Dow, J.
    APPLICANT: Porter, Gordon, J.
    APPLICANT: RASET, MATCHEW R.
; TITLE OF INTENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; TITLE OF INTENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; TITLE OF INTENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; CURRENT APPLICATION NUMBER: 050/203, 784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL PROGram
; SEQ ID NO 41
: IENNITH: 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature; No. US20030194721A1 989010.6; OTHER INFORMATION: Incyte ID No. US-10-247-671-41
                                                                                                                                                                                                                                                                                                     Query Match 99.2%; Score 198.4; DB 16; Length Best Local Similarity 99.5%; Pred. No. 6.6e-32; Matches 199; Conservative 0; Mismatches 1; Indels
                                                                                                                                                                                                                            , NAME/KEY: misc_feature
; MAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030166903A1 989010.5
US-10-133-013-211
FILE REFERENCE: PA-0049 US
CURRENT APPLICATION NUMBER: US/10/133,013
CURRENT FILING DATE: 2002-04-25
PRIOR APPLICATION NUMBER: 60/287,067
PRIOR FILING DATE: 2001-04-27
NUMBER OF SEQ ID NOS: 271
SOFTWARE: PERL Program
SOFTWARE: PERL Program
SEQ ID NO 211
LENGTH: 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.5
Matches 199; Conservative
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61 AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 120
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Pred. No. 1.1e-31;
0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO ACO05549.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN BETAL SIGNAL = 2.6
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR APPLICATION NUMBER: GB 60/236,359
PRIOR PILING DATE: 2000-10-04
PRIOR PILING DATE: 2000-09-27
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
PRIOR FILING DATE: 2001-01-30
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PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR PILING DATE: 2001-01-30
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US-10-775-169-294
; Sequence 294, Application US/10775169
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Best Local Similarity 99.0
Matches 198; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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Sequence 5454, Application US/09864761

Fatent No. US20020048763A1

GENERAL INFORMATION:

FAPPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

TITLE OF INVENTION: HUMBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

FILE REFERENCE: Aconica-X-1

CURRENT APPLICATION NUMBER: US 60/180,312

FRIOR APPLICATION NUMBER: US 60/180,312

FRIOR PELLING DATE: 2000-02-04

FRIOR FILING DATE: 2000-05-26

FRIOR FULING DATE: US 00/632,366
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/10685705
Sequence 4, Application US/10685705
Publication No. US20040177387A1
GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: JAXAKRISHNA, Ambati
TITLE OF INVENTION: Degeneration
FILE REFERENCE: 050229-0415
CURRENT APPLICATION NUMBER: US/10/685,705
CURRENT PILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60422,096
PRIOR FILING DATE: 2002-10-30
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   287 AATTTTGTTGTTGAAACATTATGCCTTAAGTAATGTTAATTCTTATTTAAGTTA 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 198.4; DB 19;
Pred. No. 1.3e-31;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9279 AATTGCTTTTCCTCTTGAAC 9298
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SOFTWARE: PatentIn version 3.2
SEQ ID NO L
LENGTH: 11793
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Best Local Similarity 99.5%;
Matches 199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
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-09-864-761-5454/C
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US-10-875-094-72
US-10-875-094-72
Sequence 72, Application US/10875094
Sequence 72, Application US/10875094
Sequence 72, Application Wo. US20050130179A1
SUBJICATION: US. USZ0050130179A1
SPELICANT: INFORMATION:
APPLICANT: INFORMATION: Takova, Taetska
APPLICANT: Prudent, James R.
APPLICANT: Prudent, James R.
APPLICANT: Hall, Jeff G.
APPLICANT: Hall, Jeff G.
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        TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCCAGACACCTTGTTTTATTTTATAATG
                                                                                                                <u>AATTTTGTTTGTTGATGTGAAACATTATGCCTTAAGTAATGTTAATTTCTTATTTAAGTTA</u>
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98.4%; Score 196.8; DB 22; Length 647;
Best Local Similarity 54.0%; Pred. No. 1.3e-31;
Matches 108; Conservative 90; Mismatches 2; Indels 0;
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Sequence 66, Application US/10210120; Publication No. US20030175736A1; GENERAL INFORMATION: APPLICANT: Chinnalyan, Arul M. APPLICANT: Rubin, Mark A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        181 AATTGCTTTTCCTCTTGTAC 200
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506 AAUUGCUUUUCCUCUUGAAC 525
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                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-875-094-72
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US-09-777-430A-72
US-09-777-430A-72
Sequence 72, Application US/09777430A
Sequence 72, Application US/09777430A
Sequence 72, Application US/09777430A
Septent No. US20020128465A1
GENERAL INFORMATION:
APPLICANT: Lyamichev, Vietor
APPLICANT: Skrzypczynski, Zbigniew
APPLICANT: Mayland, Sarah R.
APPLICANT: Mayland, Sarah R.
APPLICANT: Mayland, Sarah R.
APPLICANT: Mayland, Sarah R.
APPLICANT: Neir, Bruce P.
ITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules
FILE REFERENCE: PSRS-04912
CURRENT FILING DATE: 2001-02-06
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
SEQ ID NO 72
LENGTH: 647
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LOCATION: (33)..(199)
OTHER INFORMATION: Bach "n" represents a nucleotide selected from a, t, g or C,
OTHER INFORMATION: contains no nucleotide.
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APPLICANT: Burczynski, Michael
APPLICANT: Twine, Natalie
APPLICANT: Twine, Natalie
APPLICANT: Trepicchio, William
TITLE OF INVENTION: Wethod for Monitoring Drug Activities In Vivo
FILE REPRENCE: AMO1080 (031896-013000)
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT APPLICATION NUMBER: US/10/775,169
CURRENT FILING DATE: 2004-02-11
NUMBER OF SEQ ID NOS: 5278
SEQ ID NO 294
LENDETH: 508
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98.4%; Score 196.8; DB 19; Length 508;
Best Local Similarity 99.0%; Pred. No. 1.2e-31;
Matches 198; Conservative 0; Mismatches 2; Indels 0;
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98.4%; Score 196.8; DB 9;
Best Local Similarity 54.0%; Pred. No. 1.3e-31;
Matches 108; Conservative 90; Mismatches 2;
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ORGANISM: Artificial Sequence
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OTHER INFORMATION: Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Homo sapiens
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US-10-775-169-294
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181 AATTGCTTTTCCTCTTGTAC 200
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                                         SEQUENCE CHARACTERISTICS:
LENGTH: 725 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
          TELEFAX: (650) 845-416
INFORMATION FOR SEQ ID NO: 1344:
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Best Local Similarity 99.0%;
Matches 198; Conservative
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Best Local Similarity 99.0
Matches 198; Conservative
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Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Sugan G. Stuart
Jeffrey J. Sellhamer
TILLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                       Score 196.8; DB 16; Length 725;
Pred. No. 1.3e-31;
0; Mismatches 2; Indels 0;
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MEDIUM TYPE: Ploppy disk
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSIFICATION: CURKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                     1 TGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGACACCTTGTTTATT
TITLE OF INVENTION: Expression Profile of Prostate Cancer PILB REPERBENCE: UM-07221
CURRENT APPLICATION WUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION WUMBER: US 60/309,581
PRIOR FILING DATE: 2001-08-02
PRIOR FILING DATE: 2001-11-15
NUMBER OF SEQ ID NOS: 123
SOFTWARE: PatentIn version 3.2
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REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS:
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Best Local Similarity 99.0%;
Matches 198; Conservative
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                                                                                                                                                                                                                                                           ; ORGANISM: Homo sapiens
US-10-210-120-66
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                                                                                                                                                                                                   SEQ ID NO 66
LENGTH: 725
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439 AATTTTGTTTGTTGATGTGAACATTATGCCTTAAGTAATGTTAATTCTTATTTTAAGTTA 498
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Sequence 58, Application US/10283975A

Publication No. US20040110792A1

GENERAL INFORMATION:

TITLE OF INVENTION:

FILE REFERENCE: CDS 293 PCT

CURRENT APPLICATION NUMBER: US/10/283,975A

CURRENT APPLICATION NUMBER: 60/340,938

PRIOR APPLICATION NUMBER: 60/340,938

PRIOR APPLICATION NUMBER: 60/340,938

PRIOR FILING DATE: 2001-10-30

PRIOR PILING DATE: 2001-10-30

PRIOR PILING DATE: 2001-10-30

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PRIOR PILING DATE: 2001-10-30

PRIOR PILING DATE: 2001-10-30

PRIOR PILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 900

SOFTWARE: Patentin Version 3.1

SEQ ID NO 58
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                                                                                                                             Score 196.8; DB 18; Length
Pred. No. 1.3e-31;
0; Mismatches 2; Indels
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Pred. No. 1.3e-31;
0; Mismatches 2; Indels
CLONE: 934513
; SEQUENCE DESCRIPTION: SEQ ID NO: 1344
US-10-641-643-1344
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; TYPE: DNA; ORGANISM: Homo sapiens
US-10-445-790-3
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; ORGANISM: Homo sapiens
US-10-852-335A-46
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APPLICANT: Xu, Haiyan
APPLICANT: Chen, Hong
APPLICANT: Chen, Hong
APPLICANT: Barnes, Glenn
ITILE OF INVENTION: METHODS AND COMPOSITIONS FOR USE OF
ITILE OF INVENTION: METABOLIC DISORDERS
ITILE OF INVENTION: METABOLIC DISORDERS
ITILE OF INVENTION: METABOLIC DISORDERS
ITILE OF INVENTION: METABOLIC DISORDERS
CURRENT APPLICATION NUMBER: US/10/764,649
CURRENT FILING DATE: 2004-01-26
REIOR FILING DATE: 2003-02-07
NUMBER OF SEQ ID NOS: 20
SOFTWARE: FASELSEQ for Windows Version 4.0
ISOFTWARE: FASELSEQ for Windows Version 4.0
ILENGTH: 725
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Sequence 3, Application US/10445790

Publication No. US20040197305A1

GENERAL INFORMATION:

APPLICANT: DeVico, Anthony L.

APPLICANT: Devico, Anthony L.

APPLICANT: Garatano, Alfedo

TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination

FILE REFERENCE: 4115-109 CIP DIV

CURRENT FILING DATE: 2003-05-27

PRIOR APPLICATION NUMBER: PCT/US98/26291

PRIOR APPLICATION NUMBER: US 09/591,992

PRIOR FILING DATE: 2000-12-06

PRIOR FILING DATE: US 000-12-06

PRIOR PLILNG DATE: UNMBER: US 60/186,416
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                   TIGATGITITAAGITITATCITICATGGTACTAGTGTTTTTTAGATACAGAGACTTGGGGA 558
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Pred. No. 1.3e-31;
0; Mismatches 2;
                                                                                                                                                                                                    Sequence 17, Application US/10764649
Publication No. US20040157253A1
GENERAL INFORMATION:
                                                                        181 AATTGCTTTTCCTCTTGTAC 200
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Best Local Similarity 99.0%;
Matches 198; Conservative (
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; LOCATION: (54)...(353)
US-10-764-649-17
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ORGANISM: human
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US-10-852-335A-46

i Sequence 46, Application US/10852335A

i Publication No. US20050112129A1

i GENERAL INFORMATION:
    APPLICANT: HEIDI S. PHILLIPS

TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
    TITLE OF INVENTION: Treatment of Tumors of Glial Origin

TITLE OF INVENTION: Treatment of Tumors of Glial Origin

CURRENT APPLICATION NUMBER: US/10/852,335A

CURRENT APPLICATION NUMBER: US 60/548,299

PRIOR PILLING DATE: 2004-02-24

PRIOR PILLING DATE: 2004-02-3

PRIOR FILLING DATE: 2004-02-3

NUMBER OF SEQ ID NOS: 190

SEQ ID NOS: 190
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99.0%; Pred. No. 1.3e-31;
tive 0; Mismatches 2; Indels
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Pred. No. 1.3e-31;
0; Mismatches 2; I
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PRIOR FILING DATE: 2000-03-02
PRIOR PELLANG NUMBER: US 60/069,281
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
SEQ ID NO 3
LENGTH: 725
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Matches 198; Conservative
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Best Local Similarity 99.0
Matches 198; Conservative
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AY046055 Homo sapi
AC009488 Homo sapi
AC141828 Apis mell
AC086970 Homo sapi
AC086990 Homo sapi
AC17556 Mus muscu
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AC132816 Homo sapi
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AL928956 Mouse DNA
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 Oryza sat
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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AC104383 H
AC145968 E
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AC074214 H
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Matches 150; Conservative 0; Mismatches 0; Indels
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 3 from Patent EP1170372.
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Homo sapiens
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Source
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AC134230 Oryza sat
AP000776 Homo sapi
AC073756 Mus muscu
BT003528 Drosophil
AC147691 Pongo pyg
AC132388 Mus muscu
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12833 Homo sapien
AC021520 Homo sapi
AC005549 Homo sapi
M37719 Human monoc
X6001 H sapiens g
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AX346555 Sequence
L32659 Bovine mono
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                GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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AX346554
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ACO73756
BT003528
ACI32388
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	AF519531 LOCUS AF519531 LOCUS AF519531 DEFINITION Homo sapiens small inducible cytokine A2 (monocyte chemotactic protein 1) (SCYA2) gene, complete cds.	ACCESSION AF519531 VERSION AF519531.1 GI:21435976 KFYWARDIS	HOH HOM	REFERENCE 1 (bases 1 to 9174) AUTHORS Rieder, W.J., Armel, T.Z., Carrington, D.P., Ozuna, M., Kuldanek, S.A., AUTHORS Rieder, M. M., Porth E. T. Vi.O. and Nickerson, D.A.		1705 NE Pacific, Seattle, m. SeattleSNPs. NHLBI HL66682 Program COMMENT To cite this work please use: SeattleSNPs. NHLBI HL66682 Program for Genomic Applications, UW FHCRC, Seattle, WA (URL:	FERTURES 1. 19174 "Transpare"				variation 305 /Frequency="0.15" /replace="t"	variation 334 /frequency="0.01"	replace= 9 / replace= 9 / requency="0.16" / frequency="0.16" / frequency="0.16"	/replace='c." variation 609 /frequency="0.02" /frequency="0.02"	repeat_region 614 /rpt_family="MIR" /rpt_type=dispersed					variation 1.20 /frequency="0.23" /replace="a" //replace="a"	/frequency="0.15" /replace="g" 1548		variation 1564 /frequency="0.04" /replace="9"	variation 1707 /frequency="0.02"

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PRI 18-OCT-2000
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                                                                                                                                                                                                                        Finzer, P., Soto, U., Delius, H., Patzelt, A., Coy, J.F., Poustka, A., zur Hausen, H. and Rosl, F.
Differential transcriptional regulation of the monocyte-chemoatractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HPV 18 positive cells: the role of the chromatin structure and AP-1 composition
00ncogene 19 (29), 3235-3244 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKFZ
(German Cancer Research Institute), Im Neuenheimer Feld 506, 69120
Heidelberg, FRG
                                                                                                                                                                           Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens (human)
Homo sapiens
                                                   HSY18933 11793 bp DNA 13
Homo sapiens MCP-1 gene and enhancer region.
Y18933
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All repeats were identified using RepeatMasker:

All repeats were identified using RepeatMasker:

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Attributed Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research
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98.9%; Score 148.4;

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Birren, B. Fasman, K. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Backerly, R., Banderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangello, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Gage, D., Gardyna, S., Geraigery, K., Grant, G., Forreit, C., Furke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Mardonald, P., Mardonald, P., Mardonald, P., Molla, M., Morris, W., McGurk, A., McGurk, M., McGurk, M., McGurk, M., McGurk, M., McGurk, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Pavilin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Roy, A., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, Y., Wyman, D., Ye, W. J., Zhao, J. and Zody, M.
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Burren, B., Fasman, K., Lintcon, L., Nusbaum, C., Lander, B., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Domear, K., Donean, L., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Gersigery, K., Grant, G., Hagos, B., Haedrod, A., Herena, L., Horton, L., Howland, J. C., Jacotot, L., Jones, C., Kann, L., Kartas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Maylor, J., Niloff, M., O'Connorl, T., O'Donnell, P., Pavlin, B., Peterson, K., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella Miller, I., Vasuliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Schauster, Subraman, Stone, C., Subramission
                                                                                                                                                                                        57870
                                                                                                                                                                                                                                                                 AC005549 147416 bp DNA linear PRI 22-SEP-1998
Homo sapiens chromosome 17, clone hRPR.215_E_13, complete sequence.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 17, clone hRPK.215_E_13
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40112. .40151 /rpt_family="AT_rich" complement (40152. .40442) /rpt_family="Aludo" complement (40810. .40898) /rpt family="Alusx"
complement(33593. .39359)
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Schwarz, E., Fan, E., Kallin, B., Sorrentino, V. and Bloom, B.
The IFN-gamma inducible cDNA gamma. 1 is an incompletely spliced JE
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Submitted (16-MAY-1991) E. Schwarz, Albert Einstein College of
Medicine, Dept of Microbiology & Immunology, Forchheimer Bldg Room
411, 1300 Morris Park Avenue, Bronx NY 10461, USA
Location/Qualifiers
                                                                                                                                                                                                  1304 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
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     1975. .>2080
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/gene="gamma 1,hje"
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Schwarz, E.
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                                                                                                                            /protein_id="AAA18102.1"
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| VQRLASYRRIISSKCPKEAVIFKTIVAKEICADPKQKWVQDSMDHLDKQTQTPKT"
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                                                                1 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
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/175. .2080
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/db_xref="taxon:9606"
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            CAAAGATCACATTCTAAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
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/mol type="unassigned DNA"

/db Zref="teaxon:32630"

/note="chemically treated genomic DNA (Homo sapiens)"
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1 CAAAGAICACAITCIAGCICIGAGGIAIAGGCAGAAGCACIGGGAITTAAIGAGCICTIT
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Diagnosis of diseases associated with the immune system
Diagnosis of diseases associated with the immune system
Diagnosis of diseases associated with the immune system
Diagnosis of diseases associated with the immune system
Epigenomics AG (DE)
Location/Qualifiers
1. .5926
/organism="synthetic construct"
/mol_type="unassigned DNA"
                                                                                                                                                                                                                                                                                                  Olek,A., Piepenbrock,C. and Berlin,K.
Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1626 03-JAN-2002;
Epigenomics AG (DE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 5926;
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Pred. No. 8.1e-21;
0; Mismatches 24;
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AX346554.1 GI:18494440
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Best Local Similarity 84.0%;
Matches 126; Conservative
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synthetic construct
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AX34655/c
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AX346554
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/product = "monocyte chemoattractant protein-1"
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/protein_id="AAA60956.1"
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MQRLMNYRRYISSKCPKEAVIFKTILGKELCADPRQKWVQDSINYLNKKNQTPKF"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOVMCPIX 3405 bp DNA linear MAM 17-JAN-1995 Bovine monocyte chemoattractant protein-1 (MCP-1) gene exons 1-3, complete cds.
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Wempe,F., Kuhlmann,J.K. and Scheit,K.H.
Characterization of the bovine monocyte chemoattractant protein-1
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                   2 AAAGAICACAITCIAAGCICIGAAGGIAIAAGGCAAGAACACIGGGAITTAATGAAGCICITIC
/db_xref="taxon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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/gene="MCP-1"

join(1403. .1478,2227. .2344,2695. .2800)

/gene="MCP-1"

/codon_start=1
                                                                                          Length 5926;
                                                                                      Score 92; DB 6; Length 592
Pred. No. 2.4e-15;
0; Mismatches 35; Indels
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Location/Qualifiers
1. .3405
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monocyte chemoattractant protein-1.
Bos taurus (cow)
Bos taurus
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/mol type="genomic DNA"
/db_xref="taxon:9913"
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1310._1315
| gene="MCP-1"
| /note="putative"
| 1342._1478
| /gene="MCP-1"
| /number=1
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/gene="MCP-1"
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/gene="MCP-1"
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/gene="MCP-1"
                                                                                               Query Match 61.3%;
Best Local Similarity 76.4%;
Matches 113; Conservative
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McCombie, W.R.
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Best Local Similarity
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Loud (19-70M-2002) Lita Annenberg Hazen Genome Sequencing Center. Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA

On Jun 29, 2002 this sequence version replaced gi:16973721.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest.

RP23-155E23 is a partial sequence. The remainder of RP23-155E23 is covered by an overlap with clone RP23-110F14 (AC096863).

Approximately 2kb of the overlap is included in this submission for reference. The overlap is as follows: base 14 to base 2777 on RP23-155E23 matches from base 131225 to base 134001 on RP23-110F14.
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Submitted (11-SEP-2001) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA
(bases 1 to 109929)
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MCCombie, W.R., de la Bastide, M., Spiegel, L., Preston, R., Kitchoff, K., Kuit, K., Mascimento, L., Zutavern, T., Balija, V., Bell, M., Baker, J., Miller, B., Katzenberger, F., Muller, S., King, L., Sullivan, P., Yang, C., Dike, S., Palmer, L., O'Shaughnessy, A. and
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clone RP23-155E23, from
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Genomic sequence for Mus musculus,
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Unpublished
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AC093922.5 GI:21629259
                            2695. .3227
/gene="MCP-1"
/number=3
3202. .3207
/gene="MCP-1"
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Submitted (16-JUL-2002) Lita Annenberg Hazen Genome Sequencing Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring Harbor, NY 11724, USA
Harbor, NY 11724, USA
On Jul 26, 2002 this sequence version replaced gi:16117547.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction diggest.

RP23-239M9 overlaps clone RP23-155E23 (AC093922) from base 1 to base 56914. The overlap is from base 53016 to base 109929 on
                                                                                                                                  /clone_hes_Rect_23"
/clone_lbs=Rect_23"
61234._.61266
/note="We believe the assembly to be correct. The sequence is covered by a single high quality subclone sequenced with dye terminator chemistry. The assembly is consistent with restriction digest information."
90140...90343
/note="We believe the assembly to be correct. The sequence is a dinucleotide (T) (Cn) repeat in which the exact number of repeat copies is unknown. Two subclones span the repeat into unique sequence on both sides."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              90164 GAGGGAGAGGGAGAGGGAGGGAGTTATTGATCTTTTTCCTTGGACCCATCCAGCTATT 90105
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Submitted (11-SEP-2001) Lita Annenberg Hazen Genome Sequencing
Center, Cold Spring Harbor Laboratory, 1 Bungtown Road, Cold Spring
Harbor, NY 11724, USA
3 (bases 1 to 166277)
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McCombie,W.R., Spiegel,L., de la Bastide,M., Preston,R., Nascimento,L., Zutavern,T., Balija,V., Bell,M., Miller,B., Katzenberger,F., Muller,S., Sullivan,P., Yang,C., Dike,S., Palmer,L., O'Shaughnessy,A. and Dedhia,N. Genomic sequence for Mus musculus, clone RP23-239M9, from
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Pred. No. 2.5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Mismatches
/mol_type="genomic DNA
/db_xref="taxon:10090"
                                                                                                               /clone="RP23-155E23"
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Mus musculus
                                                                              chromosome="17"
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60.2%;
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Arizona, 303 Forbes, Tucson, AZ 85721, USA
On Mar 11, 2003 this sequence version replaced gi:23306132.
This sequence was finished as follows unless otherwise noted: all This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate regions were either double-stranded or sequenced with an alternate of the more than one plasmid subclone; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by more than one plasmid subclone; and the assembly was confirmed by more than one plasmid subclone; and the assembly was confirmed by estriction digest. The nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto and Arizona Genomics generated by combining date There is only Syngenta reads from base 123135-123143 there is an A run where the 55503-57821. From base 123135-123143 there is an A run where is a run of about 15 °C's from base 13951-139618 there are A pop up in a couple of reads.From base 13951-139618 there are are 31-30 TA tandem repeats. There are Bacterial Transposons at the
                                                                                                                                                                                                                                                                                                                                                                                                                                AC134230 159270 bp DNA linear PLN 11-MAR-2003 Oryza sativa (japonica cultivar-group) chromosome 3 clone OSJNBA0005J15, complete sequence.
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Oryza sativa (japonica cultivar-group)
Oryza sativa (japonica cultivar-group)
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Fracheophyta;
Espermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryzae.
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                            1. 166277

| Organism=Whus musculus" |
| Amol_Vype="genomic DNA" |
| Ab_xref="lexon:10090" |
| Chromosome="17" |
| Clone="RP21-23999" |
| Clone="We believe the assembly to be correct. The |
| Amol_Voluse="We believe the assembly to be correct or the sequence is covered by a single high quality subclone sequence is covered by a single high quality.
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Direct Submission
Submitted (24-SBE-2002) Arizona Genomics Institute, University Arizona, 303 Forbes, Tucson, AZ 85721, USA
                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                           24.9%; Score 37.4; DB 10; Length 166277; illarity 60.2%; Pred. No. 2.3; Conservative 0; Mismatches 41; Indels 0;
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RP23-155E23.
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154360 CTTGCATTAAATAAAAAAGGGTTTCTGCAATTTACTTCAGTCTTTTTCTTCAAATGCC 154301
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Tel:81-45-503-9111, Fax:81-45-503-9170)
On Jun 13, 2003 this sequence version replaced gi:13359358.
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Homo sapiens genomic DNA, chromosome 11 clone:RP11-748H22, complete
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2. (bases 1 to 191270)
Hattori, M., Yada, T., Toyoda, A., Taylor, T.D., Hong-Seog, P., Fujiyama, A., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y. Direct Submission
                                                                                                                                            Location/Qualifiers

1. .159270

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following locations: 78322-81796, 80866-84661, 66433-70443, 65711-69368, 50113-55386, 25635-28807 and 35843-39327. The assembly overlaps from base 157727-159271with OSJNBa0042L15 (accession #AC119748). The overlap is from bases 1-1545 on
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24.3$; Score 36.4; DB 9; Length 191270;
Best Local Similarity 54.5$; Pred. No. 4.3;
Matches 73; Conservative 0; Mismatches 61; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                 24.4%; Score 36.6; DB 8; Length 159270; 60.6%; Pred. No. 3.9; Live 0; Mismatches 39; Indels 0;
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/db_xref="taxon:9606"
/chromosome="11"
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Best Local Similarity 60.69
Matches 60; Conservative
                                                                                                                                            OSJNBa0042L15
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contig of 4568 bp in length
gap of unknown length
contig of 4613 bp in length
contig of 1101 bp in length
contig of 1101 bp in length
gap of unknown length
contig of 20985 bp in length
gap of unknown length
contig of 4757 bp in length
contig of 4757 bp in length
contig of 17540 bp in length
gap of unknown length
contig of 6771 bp in length
gap of unknown length
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/clone_lib="RPCI mouse BAC library 23"

    .198211
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/mol_type="genomic DNA"
/db_xref="taxon:10090"

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105415:
106516:
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Job time : 608.915 secs
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DOB Joint Genome Institute.

DOB Joint Genome Institute.

Sequencing of Mouse

1 (Dabasa I to 198211)

DOB Joint Genome Institute.

Direct Submission

Submitted (29-JUN-2000) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA On Jul 18, 2000 this sequence version replaced gi:8810373.

Center: Joint Genome Institute

Center: Joint Genome Institute
154300 ACCTAGCATCTTTCTCAGGGCTCTTTTGTGAATATAATATCAATGTAATAGATTTT 154241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Consensus quality: 181038 bases at least Q40
Consensus quality: 192296 bases at least Q30
Consensus quality: 192296 bases at least Q30
Consensus quality: 194577 bases at least Q30
Consensus quality: 194577 bases at least Q30
Estimated insert size: 194000; agarose-fp estimation
Estimated insert size: 194000; agarose-fp estimation
Quality coverage: 6.22 in Q20 bases; sum-of-contigs estimation

* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. Gaps between the contigs
* are represented as runs of N. The order of the places
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* This sequence will be preserved.
* 19139 19238 gap of unknown length
* 19239 28743: contig of 19138 bp in length
* 28744 30952: contig of 2109 bp in length
* 28944 30952: contig of 2105 bp in length
* 52409 52508 gap of unknown length
* 52509 57315: contig of 4807 bp in length
* 52509 57315: contig of 4807 bp in length
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Mus musculus clone RP23-336A14, WORKING DRAFT SEQUENCE, 24 ordered
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC073756.2 GI:9256783
HTG: HTGS PHASE2; HTGS DRAFT.
MUS musculus (house mouse)
MUS musculus
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TITLE
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156512 AGAAGCAGGGTGATCCCTTGAGCCACTTTTCAGCAACAGGCTGTTTCCTTGTGACATCCC 156453
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     Length 198211;
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                                                       46; Indels
Query Match 24.3%; Score 36.4; DB 2; Best Local Similarity 58.2%; Pred. No. 4.2; Matches 64; Conservative 0; Mismatches 46;
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The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein acid of the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 3; 30pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Roesl F, Soto U, Coy
Zur Hausen H, Patzelt
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Adq18538 Human sof
Continuation (4 of
Aai64628 MOUSE MIT
Aai64621 Mouse MIT
Aai64627 Mouse MIT
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Aas83745 DNA encod
Adg83497 Human tum
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Abx63839 Human CDN
Adx03803 Human Ccl
Acfe4399 Human McP
Abk47979 Human mma
Abl33653 Human imm
Abl33652 Human imm
Abk47980 Human mma
                                                                                August 3, 2005, 15:09:47; Search time 99.413 Seconds (without alignments) 8932.047 Million cell updates/sec
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GenCore version 5.1.6
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	; human;	monocy	te-chem	batt	ds; human; monocyte-chemoattractant-protein-1; MCP-1;	1, cytostatic;
KW an	antiarteriosclerotic; gene cervical carcinoma.	carcinoma	tic; gel la.	ne t	therapy; atherosclerosis	; cancer;
	Homo sapiens	. 80				
	3					
	EP1170372-A1	41 .				
60	-JAN-2002	~:				
PF 06	06-JUL-2000;		2000EP-00114560	4560		
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				9	761.001	
PA (D	(DEKR-) DEUT		SFURSCH	SPCS	KREBSFORSCHUNGSZENTRUM.	

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identify a molecule or compound that specifically binds a cDNA of the invention. A protein encoded by the CDNA may be used to screen several molecules or compounds to identify a ligand that specifically binds to the protein, or to produce or purify an antibody to the protein that can the protein, or to protein in a sample or purify a natural or combinant protein from a sample. The nucleotides may be useful for recombinant protein from a sample. The nucleotides may be useful for disease, hypertension, diabetes, pre-eclampsia, ischaemia- reperfusion of a vascular disease, e.g. atherosclerosis, cancer, coronary artery consists, restensis, or stroke. The cDNAs can also be used for large-scale injury, restensis, or stroke. The cDNAs can also be used for large-scale injury, restensis, or stroke. The cDNAs can also be used for large-scale concerts or gene expression analysis of several new nucleic acid genetic or gene expression analysis of several new nucleic acid concerts. Antibodies to the proteins encoded by the cDNAs are useful for molecules. Antibodies to the proteins encoded by the cDNAs are useful for associated with abnormalities in the expression, amount or distribution confirmed protein. The present sequence represents a cDNA of the invention confirmed that is differentially expressed in activated vascular tissue. Note: The sequence data for this patent did not form part of the specification, but the confirmed in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Testing candidate drug for treating age-related macular degeneration, by administering drug to Cc12-deficient, Ccr2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         368 CICTTCICCTGCCTGTTTTGCTTTTTCCTCAIGACTCTTTTCTGCTCTTAAGATCAGA 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTCTTCTCCTGCCTGCCTTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 CAAAGAICACATICTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen; lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Length 724;
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 724 BP; 184 A; 180 C; 154 G; 204 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                           http.segdata.uspto.gov/sequence.html?DocID=20020137081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human Cc12 gene and enhancer region DNA SeqID 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 150; DB 8; 100.0%; Pred. No. 4.4e-34;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВЪ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2003; 2003WO-US032933.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD003803 standard; DNA; 11793
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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Best Local Similarity 100.
Matches 150; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant; hypotensive; antidiabetic; gynaecological; vasctropic; cerebroprotective; gene therapy; vascular disease; cancer; coronary; artery disease; hypertension; diabetes; pre-eclampsia; restenosis; ischaemia-reperfusion injury; stroke.
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                                                                                                                                                                                                                                                                                                                    CTCTTCTCCTGCCTGCCTTTTTGCTTCATGACTCTTTTCTGCTCTTAAGATCAGA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Combination for diagnosing, staging, treating, or monitoring the progression of treatment of a vascular disease, e.g. atherosclerosis, comprises several cDNAs that are differentially expressed in activated
                          pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human cDNA #839 differentially expressed in activated vascular tissue.
                                                                                                                                                                                                                                         CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                         ö
                                                                                                                                                                      Length 150;
                                                                                                                                                                                                         Indels
                                                                                                                              Sequence 150 BP; 34 A; 37 C; 23 G; 56 T; 0 U; 0 Other;
                                                                                                                                                                      ; DB 6;
2.9e-34;
                                                                                                                                                                    ; Score 150; DB
; Pred. No. 2.9e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                          121 ATAATCCAGTTCATCCTAAAATGCTTTTTC 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-JUL-2000; 2000US-0222469P.
08-JAN-2001; 2001US-0260483P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-JAN-2002; 2002US-00044090
                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX63839 standard; cDNA; 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2003-110597/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BAND/) BANDMAN O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vascular tissue.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-SEP-2002.
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comprising: (a) a sequence comprising at least 15 contiguous nucleotides of a sequence comprising variant sequences (A) from Table 4 given in the specification; or (b) a sequence that is complementary to (A). Also described: (1) an array of (PN)s comprising two or more of the isolated (PN)s; (2) detecting a (PN) in an individual; (3) a computer-readable storage medium, where each record has a field identifying a base occupying a (PN) site and a location of the polymorphic site; and (4) a signal carrying data for access by a application program having executed on a data processing system. The (PN) can be used for detecting loci associated with multiple sclerosis. ACF64025 to ACF6424 represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               217 STCTTCTCCTGCCTGCCTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGA 276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New genetic variants having polymorphisms in the small inducible cytokine Al (SCYA2 ) gene, useful for studying the function of SCYA2 , and for treating disorders affected by expression or function of the SCYA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                   157 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGACACTGGGATTTAATGAGCTCTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CTCTTCTCCTGCCTGCCTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                           1 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
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haplotyping; atherosclerosis; antiarteriosclerotic; gene therapy;
single nucleotide polymorphism; genotyping; drug screening;
                                                                                                                                                                                                                                     sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                            Score 149.6; DB 8; Length 750;
Pred. No. 5.8e-34;
1; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                   Sequence 750 BP; 186 A; 199 C; 144 G; 219 T; 0 U; 2 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human small inducible cytokine A2 (SCYA2) genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277 ATAATCCAGTTCATCCTAAAATGCTTTTTC 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ATAATCCAGTTCATCCTAAAATGCTTTTTC 150
                                                                                                                                                                                                                                                                                                                                                                             1; Mismatches
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598. .2080
/*tag= a
/product= "Human SCYA2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK47979 standard; DNA; 2775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-AUG-2001; 2001WO-US026899.
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                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 99.3%;
Matches 149; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome 17q11.2-q21.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2002-339655/37.
P-PSDB; AAU77179.
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ABK47979
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                                                                                    This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated mecular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular CC12-deficient, CCr2-deficient and/ or a Cc12-deficient/CCr2-deficient dual knockout mouse. The present invention describes analyshing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordinally, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polynucleotide sequence is the human Cc12 gene and enchancer region DNA of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; detection; computer-readable storage medium; polymorphic site; signal carrying data; data processing system; multiple sclerosis; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polynucleotide, useful for detecting loci associated with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGGATTTAATGAGCTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 11793;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Natsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 150; DB 12; Best Local Similarity 100.0%; Pred. No. 8.8e-34; Matches 150; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rienhoff HY, Jin W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8419 ATAATCCAGTTCATCCTAAAATGCTTTTTC 8448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human MCP1 nucleotide sequence >MCP1_02.
                                                Disclosure; SEQ ID NO 4; 64pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-2001; 2001US-0310741P.
24-SEP-2001; 2001US-0324790P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-OCT-2003 (first entry)
  accumulation in eye.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DNAS-) DNA SCI INC
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ABL33652;
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                                                                                                                                                                                                                                                                                                                                 Query Match
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                            The invention relates to single nucleotide polymorphisms in the gene encoding human small inducible cytokine A2 (SCYA2) polymeptide. A method encoding human small inducible cytokine A2 (SCYA2) polymeptide. A method conformation of the SCYA2 gene in a individual comprises identifying the for haplotyping at one of the SCYA2 haplotypes given of the copies of the gene is defined by one of the SCYA2 haplotypes given of the specification or whether both copies are defined by a haplotype pair. This method is useful in genotyping, whereby all possible haplotype copair. This method is useful in genotypes. An association between a pair and a haplotype or haplotype pair of the SCYA2 gene can be trait and a haplotype or haplotype pair of the haplotype or haplotype pair in a reference population, where a higher haplotype or h
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CICTICICCIGCCIGCCITITITICCCICATGACTCTITICIGCTCTTAAGATCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAAGATCACATTCTAGCTCTGAGGTATAAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
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                                                                                                                                                                                                                                                                                                                                                       Sequence 2775 BP; 699 A; 723 C; 565 G; 778 T; 0 U; 10 Other;
                                                                                                                                                                                                                                                                                                                                                                                        Length 2775;
                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human immune system associated gene SEQ ID NO: 1626.
                                                                                                                                                                                                                                                                                                                                                                            Score 146; DB 6; Le
Pred. No. 9.1e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                              1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1424 ATAATCCAGTTCATCCTAAAATGCTTTT 1451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berlin K;
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01-SEP-2000; 2000DE-01043826.
          Claim 1; Fig 1; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABL33653 standard; DNA; 5926
                                                                                                                                                                                                                                                                                                                                                                                              97.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 146; Conservative
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                                                                                                                                                                                                                                                                                                                                 human SCYA2 polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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ABL33653/
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                                    fragment of chemically modified gene, useful f
of diseases associated with abnormal cytosine
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                                                                                                                                                         Claim 1; SEQ ID NO 1626; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human immune system associated gene SEQ ID NO: 1625.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 111.6; DB 6
Pred. No. 1.4e-22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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01-SEP-2000; 2000DE-01043826.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74.4%;
84.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best_Local Similarity 84.0
Matches 126; Conservative
                                                         Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS
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WPI; 2002-130909/17
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                                                                                                                  methylation.
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5817
                                                                                           The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, Alzheilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                            genetic variants having polymorphisms in the small inducible cytokine (SCYA2) gene, useful for studying the function of SCYA2, and for ating disorders affected by expression or function of the SCYA2
                                                                                                                                                                                                                                                                                                                                                                                                          121
                                                                                                                                                                                                                                                                                                                                          61
 fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                        2 AAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTTC
                                                                                                                                                                                                                                                                                                                                                                                                          TCTTCTCCTGCCTGCCTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGAA
                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human, small inducible cytokine A2, SCYA2; gene; ds. haplotype pair, haplotyping, atherosclerosis, antiarteriosclerotic, gene therapy, single nucleotide polymorphism; genotyping, drug screening;
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                                                                                                                                                                                                                                          Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                                Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                        35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human small inducible cytokine A2 (SCYA2) modified DNA.
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                                                                                                                                                                                                                                                                        Score 92; DB 6; I
Pred. No. 7.7e-17;
0; Mismatches 35;
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                                                                                                                                                                                                                                                                        61.3%;
ilarity 76.4%;
Conservative
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 Nucleic acid comprising diagnosis and treatment
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                                                                                                                                                                                                                                                                                         Local Similarity
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Nucleic acid
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                                 methylation
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concoding human small inducible cytokine A2 (SCYA2) polypeptide. A method for haplotyping the SCYA2 gene in an individual comprises identifying the nucleotide at one or more polymorphic sites and determining whether one of the copies of the gene is defined by one of the SCYA2 haplotypes given for the copies of the gene is defined by one of the SCYA2 haplotypes given in the specification or whether both copies are defined by a haplotype cypeles. This method is useful in genotyphing, whereby all possible haplotype pairs can be assigned to specific genotypes. An association between a trait and a haplotype or haplotype pair of the SCYA2 gene can be considentified by comparing the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype or haplotype pair in a reference population, where a higher haplotype con haplotype pair. SCYA2 and its corresponding DNA are used for studying the expression and function of SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2, and in screening for satherosclerosis. This sequence represents human SCYA2 modified DNA that shows the polymorphic sites in a uniform format to facilitate electronic searching of the SCYA2 haplotypes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining whether an individual is predisposed to susceptibility to low bone mineral density (BMD) and/or bone damage, involves identifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           low bone mineral density; BMD; bone damage; polymorphism; osteoporosis; single nucleotide polymorphism; SNP; gene; ds; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a method of determining whether an individual is predisposed to susceptibility to low bone mineral density (BMD) and/or bone damage comprising identifying whether the individual has at least one polymorphism in a polymoclectide encoding a protein, where the polymuclectide is one of 81 200-500 nuclectide sequences (S1, see ADC98235 to ADC98215). An agent identified in an method from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  361 CAGAAGCACTGGGATTTAATGAGCTCTTTSTCTTCTCCTGCCTGCCTTTTGTTTTTTCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 58; DB 6; Length 840; Pred. No. 4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 840 BP; 88 A; 115 C; 72 G; 138 T; 0 U; 427 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polymorphisms in associated genes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 225; 246pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                38.7%;
96.7%;
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ID ADC98306 standard; DNA; 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                58; Conservative
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Mckay I, Schafer A;
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Best Local Similarity
Matches 58; Conserv
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The invention relates to detecting (MI) granulocyte (GC) activation (GCA), by detecting the level of expression of gene(s) (GS) identified by (GCA), by detecting the level of expression of gene(s) (GS) identified by DNA chip analysis as given in the specification, and comparing the expression level to an expression level in an unactivated GC, where differential expression of Gs is indicative of GCA. Also included are modulating (M2) GA by contacting GC with an agent that alters the modulating GCA or an inflammation (especially chronic) in a capable of modulating GCA or an inflammation (especially chronic) in a tissue, an allergic response in a subject, exposure of a subject to a profile; (3) detecting (M4) an inflammation (especially chronic) in a profile; (3) detecting (M4) an inflammation (especially chronic) in a pathogen or sterile inflammatory disease, by detecting the level of pathogen or sterile inflammatory disease, by detecting the level expression in a sample of the tissue of gene(s) from GS, where the level
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detecting granulocyte activation by detecting differential expression of genes associated with granulocyte activation, which serves as diagnostic markers that is useful for monitoring disease states and drug toxicity.
present invention which can be used for the prevention or treatment of a disease resulting in susceptibility to low BMD and/or bone damage is useful in the manufacture of a medicament for use in medulating the susceptibility to low BMD and/or bone damage. The disease associated with low BMD and/or bone damage is osteoporosis. The present sequence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                149
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                                                                                                                                                                                                                                                                                      TCITITICIGCICITAAGAICAGAATAAICCAGTICAICCTAAAAIGCITITIC
                                                                                                                                                                                                                                                                                                                cDNA differentially expressed in granulocytic cells #68
                                                                                                                                                                                                   Length 201;
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                                                                                                                                                          Sequence 201 BP; 59 A; 39 C; 46 G; 56 T; 0 U; 1 Other;
                                                                                                                                                                                                      DB 10; L
9.1e-06;
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                                                                                                                                                                                                      Query Match
Best Local Similarity 100.0%; Pred. No. 9.1
Matches 53; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK83497 standard; cDNA; 227968 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 10
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of expression of the gene is indicative of inflammation; (4) treating composed in a subject, exposure, an atlergic response in a subject, exposure of a subject to a pathogen or sterile inflammatory disease, by contacting a tissue having inflammation with an eagent that modulates the expression of gene(s) from Gs in the tissue. MI agent that modulates the expression of gene(s) from Gs in the tissue. MI composite the capable of modulating GA, M3 is useful for screening an agent capable of modulating GCA preferably in an composition of a tissue, M4 is useful for detecting an inflammation inflammation in a tissue, M5 suseful for modulating GA, M3 is useful composure of a subject to a pathogen or sterile inflammatory disease (e.g. exposure of a subject to a pathogen or sterile inflammatory disease (e.g. cardiac reperfusion injury, renal reperfusion injury, ARDS, adult cardiac reperfusion injury, renal reperfusion injury, ARDS, adult cardiac reperfusion injury, renal reperfusion injury, ARDS, adult cardiac reperfusion injury, renal reperfusion injury, ARDS, adult cardiac reperfusion, parasitic infection, protozoal infection, infection, parasitic infection, protozoal infection, conditions. The present sequence represents a gene differentially conditions. The present sequence represents a gene differentially conditions and M5 is useful for treating one of the above conditions and m5 is useful for treating one of the above conditions and m5 is useful for treating one of the above conditions and m5 is useful for treating one of the above conditions and m5 is useful for treating one of the above conditions and m5 is useful for treating one of the above conditions and m5 is useful for treating one of the above conditions. The present sequence agene differentially
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    soft tissue sarcoma; cytostatic; gene therapy; vaccine; screening; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barly detection of soft tissue sarcoma comprises determining expression of a gene in a first soft tissue sample and a normal soft tissue sample and comparing the gene expression, also useful in treating soft tissue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 227968 BP; 53185 A; 60440 C; 61985 G; 52358 T; 0 U; 0 Other;
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57.9%; Pred. No. 10;
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1997 ITCCTCCTCCTCCTTCTTCTATCATCATCATCATCTTCTTTGTTTTCTTCTT 1938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Polypeptides that control MITF and MITF gene in mast cells for use in
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          Mouse MITF-origin protein isoform encoding cDNA SEQ ID
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                                         Mouse; MITF; origin; c-kit; mast cell; microphtalmia-associated transcription factor;
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                                                                                                                    Location/Qualifiers
122. .1534
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54.9%;
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Best Local Similarity 54.99
Warches 67; Conservative
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                                                                                        Mus musculus.
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The invention relates to a novel method for detecting soft tissue sarcome which comprises obtaining a first soft tissue sample from an individual data and a normal soft tissue sample from the same or different individual, determining the expression of some in both soft tissue samples and comparing the expression of the gene in both soft tissue samples and comparing the expression in the first soft tissue sample indicates the presence of soft tissue samples. The indicates the presence of soft tissue sarcoma. The method of the invention has cytostatic applications and may be useful for detecting soft tissue sarcoma, possibly via gene therapy or vaccine production. The nucleic acid sequences may be useful in diagnostic and screening applications. The current sequence is that of a human soft tissue sarcoma-upregulated DNA of the invention. The current sequence is not shown within the specification per se but was submitted in CD format by the inventor.
                                                                                                                                                                                                                                                                                                                                                                        44522 GACTICCIGGATIGATCCICCAAACCIGTTICCTTTTTTTTCT
                                                                                                                                                                                                                                                                                                                                        44 GATTTAATGAGCTCTTTCTCTTCTCCTGCCTGCCTTTTTGCTTTTTCCTCATGACTCTTTT
                                                                                                                                                                                                                                       Sequence 227968 BP; 53185 A; 60440 C; 61985 G; 52358 T; 0 U; 0 Other;
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Pred. No. 11;
0; Mismatches
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fragments
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Continuation (4 of 17) on WP Sequence split into 17 WP Fragment Name WP AAV21209 01 WP AAV21209 02 WP AAV21209 03 WP AAV21209 04 WP AAV21209 06 WP AAV21209 06 WP AAV21209 09 WP AAV21209 09 WP AAV21209 11 WP AAV21209 11 WP AAV21209 12 WP AAV21209 11 WP AAV21209 13 WP AAV21209 14 WP AAV21209 14 WP AAV21209 14 WP AAV21209 14 WP AAV21209 15 WP AAV21209 14 WP AAV21209 15 WP AAV21209 15
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Matches 61; Conserv
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Gaps

08-MAR-2000; 2000JP-00063959

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22.7%; Score 34; DB 4; Length 2125;
Best Local Similarity 54.9%; Pred. No. 6.2;
Matches 67; Conservative 0; Mismatches 55; Indels
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59. .1663
/*tag= a
/product= "MITF"
                                                                                                                                                                                                                    Claim 5; Page 57-59; 65pp; Japanese
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                                                          07-MAR-2001; 2001WO-JP001752
                                                                                 08-MAR-2000; 2000JP-00063959
                                                                                                                                 Naito K;
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                                                                                                                                                                                              related medical area
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                                                                                                                                                                                                                                                                                                                                          98
                                                                                                 Polypeptides that control MITF and MITF gene in mast cells for use in a related medical area.
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Pred. No. 6.3;
0; Mismatches
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                                              Naito
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                                            Asakura E,
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Best Local Similarity
Matches 52; Conserv
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JOURNAL
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AUTHORS
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  BU3589171 603283157
BH355897 CH230-199
AZ117778 RPCI -23-4
AZ094475 RPCI -23-4
CE406656 tigr-g88-
CC474603 tigr-g88-
CC26712 WG0218.B
CC977097 t093121ba
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BU422000 604131767
BX269592 BX269592
BU448827 PPMZ-9K0
CC140850 EST836216
CC141545 EST836216
CC141545 EST836216
CC141545 BU42390
BU401493 604442980
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                                             August 4, 2005, 04:04:35 ; Search time 707.976 Seconds
      GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                - nucleic search, using sw model
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gb_htc::
gb_est2::
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

E. (bases 1 to 750)

NIH-MGC http://mgc.nci.nih.gov/.

L. Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tisaue Procurement: ATCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

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CDNA Library Preparation: Life Technologies, Inc.

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

Clone distribution: MGC Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

High quality sequence stop: 671.
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/mol type="mxNA"
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/note="Organ: bone; Vector: pCMV-SPORT6; Site 1: NotI;
Site=2: Sall; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies.
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602280491F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4367999 5',
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12 I (Beer K., J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Shetty, J., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D., Rigges, F., de Jong, P. and Fraser, C.M. CHORI-230 EcoRI segment Rat BAC End Sequences from Library CHORI-230 EcoRI segment Unpublished (1999)

Ochec GSss. CH230-199118.TV

Contact: Shaying Zhao

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

The Institute for Genomic Research

Far: 301 838 0208

Fax: 301 838 0208
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Email: szhao@tigr.org

Email: szhao@tigr.org

Clones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.bkm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

Plate: 199 row: I column: 18

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Class: BAC ends.
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                                                                                                                                                    660 bp DNA linear GSS 03-DEC-2001
CH230-199118,TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-199118, genomic survey sequence.
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/cell type="Brain"
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/clone lib="CHOR1-230 Segment 1"
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/note="Vector: pTARBAC2.1; Site 1: EcoR1; Produced by Pieter de Jong"
TCATGACTOTTTTCTGCTCTTAAGATCAGAATAATCCAGTTCATCCTAAAATGCTTTTTC 150
                                          Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                55 CICTICICITCICCIGCCIGCCTITIGCTTITICCTCALGACTCTTTTCTGCTCTTAAG
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RPCI-23-478J14.TJ RPCI-23 Mus musculus genomic clone
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/mol_type="genomic DNA"
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/clone="CH230-199118"
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/tiseuale_uype="not cerebrum or cerebellum"
/dev stage="adult"
/lab_host="adult"
/lab_host="adult"
/cloof_lib="CSEQCHN73"
/cloof_lib="CSEQCHN73"
/cloof="Grgan: brain; Vector: pBluescript II KS(+); Site_1:
/note="Grgan: brain; Vector: pBluescript II KS(+); Site_1:
/note="Grgan: brain; Vector: pBluescript II KS(+); Site_1:
/note="Grgan: brain; Vector: pBluescript II KS(+); Site_1:
/note="Grgan: brain; Vector: ndillion independent clones. CDNA
constructed_from I million independent clones. CDNA
synthesis was initiated using an oligo(dT) primer, using
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded cDNA
was blunted, ligated to NotI adapters, digested with
RcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
pBluescript (KS+) vector. The library was normalized in 2
pBluescript (KS+) vector. The library was normalized in 2
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research (1996): 791. except that a significantly longer
reannealing hybridization was used."
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (chicken)
Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianinae; Gallus
Phasianinae; Gallus
1 (bases 1 to 750)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
Romprehensive Collection of Chicken cDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
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                                                                                                                                                                                                                                                                                                        BU369171
603568157F1 CSEQCHN73 Gallus gallus CDNA clone ChEST524a16 5', mRNA
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                                  CIGGGAITTAATGAGCTCTTTCTCTTCTGCCTGCCTTTTTGCTTTTTCCTCATGACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ..
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/organism="Gallus gallus"
/mol_type="mRNA"
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/db_xref="teaxon:9031"
/clone="ChEST524a16"
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PO Box 88, Manchester, M60 1QD, UK
PI 101612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
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BU369171/c
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Mus musculus (house mouse)
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Bukmalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 564)
Libases 1 to 564)
Libases 1 to 564)
Akinret, B., Levine, M., Mcgann, T., Malek, J., Shatsman, S.,
Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Opubblished (1999)
Other_GSSS: RPCI-23-270M5.TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850, USA
71: 301 838 0208
Fax: 301 838 0208
       GI:7069572
       AQ994475.1
GSS.
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/#Strain="C57BL/G1"
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Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
E. (Dases I to 522)
E. (Dases I to 522)
Akinret, B., Levins, M., Peldblyum, T., Malek, J., Shatsman, S., Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other GSSs: RPCI-23-478J14.TV
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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Seq primer: SP6
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26;
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RPCI-23-478J14, genomic survey sequence.
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53.6%; Pred. No. 26;
iive 0; Mismatches
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Mus musculus
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                                                                       AZ117778.1 · GI:7781248
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Matches 75; Conserv
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tigr-gss-dog-17000335613614 Dog Library Canis familiaris genomic, genomic survey sequence.
CR406656.1 GI:36659452
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           selected DNA was cloned into the pBACe3.6 vector at the ECORI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /lab_host="DH10B"
/clone_lib="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
EcoRI, Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
Email: stabookigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC

Clones are derived from the mouse BAC library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)

or from Resea ch Genetics (info@resgen.com). BAC end page:

Plate: 270 row: M column: 5

Seq primer: SP6

Class: BAC ends.
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AQ994475

564 bp DNA linear GSS 24-FEB-2000
RPCI-23-270M5.TJ RPCI-23 Mus musculus genomic clone RPCI-23-270M5,
genomic survey sequence.

AQ994475/c DEFINITION

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Populus balsamifera subsp. trichocarpa x Populus nigra Populus balsamifera subsp. trichocarpa x Populus nigra Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Streptophyta; Embryophyta; Tracheophyta; Streptophyta; Streptophyta; Streptophyta; Streptophyta; Streptophyta; Streptophyta; Malpighiales; Salicacae; Saliceae; Populus. 1 (bases 1 to 643)
11 (bases 1 to 643)
12 (Apply S., Cooper, D., Kolsova, N., Oddy, C., Butterfield, Y., Rirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Kirkpatrick, R., Liu, J., Palmquist, D., Stott, J., Barber, S., Yang, G., Rirkpatrick, R., Enom-John, M., Chand, S., Featherstone, R., Masson, A., Mayo, M., Morah, J., Olson, T., Wong, D., Ritland, C.B., Siddigul, A., Holt, R., Jones, S., Marra, M., Ellis, B.E., Douglas, C., Ritland, K. and Bohlmann, J.
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Genome BC forest genomics program
Genome BC forest genomics program
University of British Columbia
University of British Columbia,
Vancouver, British Columbia, Canada, V6T 123
Tel: 1-604-822-0282
Tel: 1-604-822-6997
Bmail: bohlmanndanterchange.ubc.ca
Plate: WS02018 row: K column: 16
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                                                                                                                                                               /organism="Canis familiaris"
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24.0%; Score 36; DB 9; Length 706;
Best Local Similarity 54.5%; Pred. No. 27;
Matches 72; Conservative 0; Mismatches 60; Indels
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Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
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The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
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I. (bases 1 to 706)
Xirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.
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The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
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                 Canis familiaris (dog)

Canis familiaris

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi,

Bammalia, Eutheria, Carnivora, Fissipedia, Canidae,

Ti (bases I to 706)

Kirkness, E. F., Bafna, V., Halpern, A.L., Levy, S., Remington, R.,

Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and

Venter, J.C.
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/strain="Standard Poodle"
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/note="Site_1" BstXI; Libraries were prepared from peripheral blood"
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24.0%; Score 36; DB 9; Length 706;
Best Local Similarity 55.6%; Pred. No. 27;
Matches 69; Conservative 0; Mismatches 55; Indel8
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CE774603
                                                                                                               ORGANISM
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JOURNAL
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                                                                                                                                                                                                                                                                      AUTHORS
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ORIGIN

8 요 ð 셤 δ

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/cell_type="Blood"
/clone_lib="TAWBT"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; TAMBT Bovine BAC library (Male) produced by Texas
A&M University, Department of Animal Science."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 23.7%;
Best Local Similarity 53.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (human)
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                                                                                                                                                                                   Query Match
Best Local S:
Matches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
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TITLE
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BU854111
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                                      /lab host="E. coli DH10B T1 phage resistant cells"
/lab host="E. coli DH10B T1 phage resistant cells"
/clone_lib="PTXN-IB-N-A-11"
/clone_lib="PTXN-IB-N-A-11"
/note="Vector: pBluescript II SK (+) XR; Site 1: EccRI (5'
end of cDNA); Site 2: XhoI (3' end of cDNA); Sapling trees
two metres in height and grown under greenhouse conditions
were exposed to continuous feeding by Cryptorhynchus
lapathi (poplar and willow borer) adults caged on the
sapling using mesh bags. Bark (with phloem and cambium
attached) from within the caged region was harvested 2
hours, 6 hours and 48 hours after the onset of treatment.
mRNA was isolated from each tissue source independently
and equal quantities of mRNA from each tissue were then
pooled. cDNA was prepared from 5 micrograms of mRNA and
directionally ligated into the pBluescript II SK (+) XR
vector using the pBluescript II XR cDNA Library
Construction Kit according to manufacturer's instructions
with modifications (Stratagene). Plasmid DNA was then
transformed by electroporation into DH10B cells
(Invitrogen) for propagation. Normalization was applied
according to published methods [Bonaldo M.F. et al. (1996)
Genome Research 6(9):791] in order to reduce the abundance
of highly expressed transcripts."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC927097 740 bp DNA linear GSS 08-AUG-2003 t093j2lba.fl TAMBT Bos taurus genomic clone t093j2lba, genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 TCATGACTCTTTTCTGCTCTTAAGATCAGAATAATCCAGTTCATCCTAAAATGCTTTTT 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bos taurus
Sukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rcgirrririricicrcriarirrcargerrarrcracagcricrcrriraaragcrarir 35
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Lin, S., Najar, F.Z., Adelson, D., Gill, C.A. and Roe, B.A.

Lin, S., Najar, F.Z., Adelson, D., Gill, C.A. and Roe, B.A.

Bovine BAC End Sequences from Library TAMBT

Contact: Bruce A. Roe

Advanced Center for Genome Technology

Miversity of Oklahoma Department of Chemistry and Biochemistry

620 Parrington Oval, Room 208, Norman, OK 73019, USA

Tel: 405 325 7762

Email: broe@ou.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
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/db_xref="taxon:9913"
/clone="t093j21ba"
/eax="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 7; Length 643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
23.9%; Score 35.8; DE
Best Local Similarity 56.3%; Pred. No. 31;
Matches 67; Conservative 0; Mismatches
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Location/Qualifiers
1. .740
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clone="WS02018 K16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Burvey sequence.
CC927097
CC927097.1 GI:33562436
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AGENCOURT_10402929 NIH_MGC_82 Homo sapiens cDNA clone IMAGE:6621266
5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                       258 ATGGTCAGTTTCCCTTCTCATGCCTGCACTTCGTTCTTTCCTAAAGCTTCTGGAGGAGTG 199
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 749)
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Email: Ggapbs-r@mail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://amage.llnl.gov
Plate: LLCM2872 row: 1 column: 02
High quality sequence stop: 585.
                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NIN-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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     Length 740;
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Score 35.6; DB 9; Length 74
Pred. No. 35;
0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                           110 TTAAGATCAGAATAATCCAGTTCATCCTAAAATGCTTT 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     198 TTTGCATCAGGGAAATCCAGAGGAGCAGAGGCTGCTAT 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35.6; DB 5;
Pred. No. 36;
0; Mismatches 64;
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/organism="Homo sapiens"
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ch 23.7%;
1 Similarity 60.2%;
59; Conservative
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Unpublished (2004)
Contact: Christina M. Clover
Contact: Christina M. Clover
Growth Biology Laboratory
Animal and Natural Resources Institute
Animal and Natural Resources
Bldg. 200 Rm215 BARC-East, Beltsville, MD 20705, USA
Bldg. 200 Rm215 BARC-East, Beltsville, MD 20705, USA
Tel: 3015048623
Fax: 3015048623
Fax: 3015048623
Email: chrisc@anri.barc.usda.gov
Email: chrisc@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
Single pass sequencing. Trim alt '' -trim fastaVector identified by
Cross match using options -trim alt '' -trim fastaVector identified by
Cross match using options -minmatch 12 -minscore 12
Plate: 27 row: P column: 09
Plate: 27 row: P column: 09
Seq primer: CCCAGTCACGACGTTCAAAACG
High quality sequence stop: 491.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .491

/organism="Gallus gallus"

/mol type="makh"

/mol type="makh"

/strain="Leghorn and broiler"

/db xref="acht_27P09"

/clone="acht_27P09"

/lab host="acht_27P09"

/lab host="acht_2P00"

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/note="Vector: pBluescript, SK+, Stratagene; Site_1: NotI;

/note="Vector: pBluescript, SK+, Stratagene; Site_1: NotI;

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/note="Vector: pBluescript, SK+, Stratagene; Site_1: NotI;

/notI;

/notI;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gallus gallus (chicken)
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Galliformes; Phasianidae;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
1 (bases 1 to 546)
Min. W., Lillehoj, H.S., Ashwell, C.M., Matukumalli, L.K., van
Min. W., Lillehoj, H.S., Ashwell, C.M., Gatukumalli, L.K., van
Chicken intestinal lymphocyte EST database as a resource for the analysis of mucosal immune function
Unpublished (2003)
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianines; Gallus.
[basianines | fallus.]
[closes | to 491)
[svock-Clover,C.M., Ashwell,C.M., McMurtry,J.P., Lillehoj,H.S., Matukumalli,L.K. and Van Tassell,C.P.
[characterization of expressed sequence tags generated from multiple
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31 gchaphacacraggarrrandagcrererreggrerecrecergecrarrace
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Animal Parasite Diseases Laboratory
Animal and Natural Resources Institute, USDA
Animal and Natural Resources Institute, TSDA
Endg.1043, BARC-East, Beltsville, MD 20705, U
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1 Similarity 56.4%; Pred. No. 38;
66; Conservative 0; Mismatches
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Gallus gallus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sterky, F., Bhalerao, R.R., Unneberg, P., Segerman, B., Nilsson, P., Sterky, F., Bhalerao, R.R., Jonsson-Lindvall, J., Tandre, K., Strauss, S.H., Sundberg, B., Gustafsson, P., Uhlen, M., Bhalerao, R.P., Nilsson, O., Sandberg, B., Karlsson, J., Lundeberg, J. and Jansson, S. A. Populus EST resource for functional genomics Unpublished (2003)
Other ESTS: 1014P80P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98 rdrrdracaaaaaaarregaaddaaraaraacagcrcrrrcrrrcrrccrccrdcrracrdr 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                CK094148 Linear EST 01-DEC-2003 1014P80.3PR Populus senescing leaves cDNA library Populus tremula CDNA clone 1014P80 3', mRNA sequence.
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae; Streptophyta; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
1 (bases 1 to 434)
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                                                                                                                70 TGCCTGCCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGAATAATCCAG 129
                                                                                                                                                                    328 CTCAGITCTITAACHGITTCTIAGITCCTCTTTTGGACAIAAICTGGGGTTTTTAGIA 387
                                                   268 CATIGAAGAIGGGAGAGAGTAGCCIGAGAACTGACCTITICIGITCIGAGTCIGAGCTIC 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 nganggranangcananangnantraangkangtangtangtangtangcangtangtang
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/db_xref="taxon:113636"
/dl_one="104P80"
/tiseue_type="Senescing leaves"
/clone_lib="Populus senescing leaves cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Umea Plant Science Center, Department of Plant Physiology Umea University
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/organism="Populus tremula"
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Location/Qualifiers
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                                                                                                                                                                                                                                                        130 TICATCCIAAAATGCTIT 147
                                                                                                                                                                                                                                                                                               CK094148.1 GI:38578473
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Tel: +46 90 786 5279
Fax: +46 90 786 6676
Email: bo.segerman@pla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Populus tremula
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CK094148/c
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/ gax="Male and female"
/ dev stage="adult"
/ lab_host="Ublob"
/ lab_host="Ublob"
/ clone lib="CSEQRBN37"
/ clone lib="CSEQRBN37"
/ note="Organ: pancreas; Vector: pBluescript II KS(+);
Site=1: BcoRi; Site=2: Not!; This normalized library was
constructed from | million independent clones. cDNA
synthesis was initiated using an oligo(dT) primer, using
methylated C in the first strand synthesis reaction.
Following this first strand reaction, double-stranded
was blunted, ligated to NotI adapters, digested with
ECOMI, size-selected, and cloned into the NotI and ECORI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Editaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianiae; Phasianiae; Gallus.

1 (Dases 1 to 638)

1 (Dases 1 to 638)

2 Herault,F., Le Meuth-Metzinger,V., Desert,C., Retout,E., Piumi,F., Klopp.C. and Douaire,M.

Construction and primary characterization of chicken normalized multi-tissue cDNA libraries

Unpublished (2003)

On Feb 27, 2003 this sequence version replaced gi:28592193.

Confect: Douaire M.

INRA, UMR INRA-ENSAR Genetique Animale
65, rue de Saint-Brieuc, RENNES cedex, 35042, FRANCE
Tel: +33 (0) 2.23.48.54.70

Email: Madeleine.Douaire@roazhon.inra.fr
Sequence cleaned of vector, adaptator and repetitions. Contact us at sigenasupport@jouy.inra.fr to obtain the chromatogram of this
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BX269592 AGENAE Gallus gallus multi-tissues normalized library (gcag) Gallus gallus clone gcag0019c.1.12 3prim, mRNA
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/tissue_type="multi-tissues"
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1 Similarity 56.4%; Pred. No. 39;
66; Conservative 0; Mismatches
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|organism="Gallus gallus"
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|db_xref="taxon:9031"
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clone="ChEST959f18"
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Best Local Similarity
Matches 66; Conserv
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Gallus gallus
Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus
1 (bases 1 to 612)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E., Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken cDNAs
Curr Biol. 12 (22), 1965-1969 (2002)
           Email: hilleho@anri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
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by cross_match using options -minmatch 12 -minscore 12
Plate: 7 row: D column: 16
Seq primer: ATTAGGTGACACTATAG
High quality sequence stop: 546.
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University of Manchester Institute of Science and Technology
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23.6%; Score 35.4; DB 6; Length 546;
Best Local Similarity 56.4%; Pred. No. 39;
Matches 66; Conservative 0; Mismatches 51; Indels (
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BU492000
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Fax: 01612360409
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Gaps

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/dev stage="from embryos to adults"

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                                                     OM nucleic - nucleic search, using sw model
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Sequence 1, Application US/08916421B
Patent No. 6503729
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FACENT NO. 6503729
TILLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanocompatent No. 6503729
TILLE OF INVENTION: januaschii
FILE REFERENCE: PARTS
CURRENT APPLICATION NUMBER: US/08/916,421B
CURRENT PILIOR DATE: 1997-08-22
FRIOR REPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
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ORGANISM: Methanococcus jannaschii
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US-08-916-421B-1/C
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71119 98567 100567

46 ITTAATGAGCTCTTTCTCTCTGCCTGCCTTTTGCTTTTTCCTCATGACTCTTTTCT 105 Gaps Query Match

23.1%; Score 34.6; DB 4; Length 1664976;
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Matches 61; Conservative 0; Mismatches 44; Indels 0; 397084 ATCATCATRATCATAATCATCGCAATRATCATAATCCTCTTC 397040 106 GCTCTTAAGATCAGAATAATCCAGTTCATCCTAAAATGCTTTTTC 150 NAME/KEY: misc feature LOCATION: (1664854)..(1664855) CTHER INFORMATION: n equals a, t, c, or g US-08-916-421B-1 b מ ρ מ b ρ מ ρ ρ ы מ ρ g b or οr or or c, or or or or or or ö or or or or ö ö ů ú ú ญั ΰ ϋ ΰ ΰ ບັ ပဲ ϋ RESULT 2 US-09-622-570-1/c i sequence 1, Application US/09692570 ; Patent No. 6797466 NAME/KEY: misc_feature LOCATION: (1637998)..(1637998) OTHER INFORMATION: n equals a, t, ú ú ú NAME/KEY: misc feature
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (1130881)..(1130881) OTHER INFORMATION: n equals a, t, NAME/KEY: misc_feature LOCATION: (1310988)..(1310988) OTHER INFORMATION: n equals a, t, OTHER INFORMATION: n equals a, NAME/KEY: misc feature roration: (1603734)...(1603734) LOCATION: (1470091,...LOCATION: (1470091,...OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
TOCATION: (1569020)...(1569020) LOCATION: (1569020)..(1569020) OTHER INFORMATION: n equals a, NAME/KEY: misc_feature INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1313224)..(1313224) OTHER INFORMATION: n equals a, NAME/KEY: misc feature LOCATION: (1470091)..(1470091) misc_feature (1602912)..(1602912) 엄 ò

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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a, t, c, or (
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LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t,
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LOCATION: (234220) ..(234220)
OTHER INFORMATION: n equals a, t,
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LOCATION: (600992)..(600992)
OTHER INFORMATION: n equals a, t,
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a, t,
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LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t,
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LOCATION: (309418)...(309418)
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a,
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LOCATION: (312837)..(312837)
OTHER INFORMATION: n equals a,
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LOCATION: (312993)..(312993)
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LOCATION: (559241)..(559241)
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
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LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a,
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LOCATION: (657203)..(657203)
DTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals
                                   NAME/KEY: misc feature
LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals
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LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals
OTHER INFORMATION: n equals
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             APPLICANT: Bult et al.

TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: Januaschii
FILE REFERENCE: P8275C1
CURRENT APPLICATION NUMBER: US/09/692,570
CURRENT FILING DATE: 2003-01-14
PRIOR PILING DATE: 1996-08-22
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 20
SOFTWARE: Patentin version 3.1
SEQ ID NO 1.
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a, t, c,
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ORGANISM: Methanococcus jannaschii
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a, t,
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LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (148948). (148948)
OTHER INFORMATION: n equals a,
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LOCATION: (163385)..(163385)
OTHER INFORMATION: n equals a,
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LOCATION: (28222)
OTHER INFORMATION: n equals a,
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a,
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a,
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals a,
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LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (191989)..(191989)
GENERAL INFORMATION:
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RESULT 4

US-09-949-016-152710

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JEDICATION APPLICATION US/09949016

JEDICATI VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

APPLICANTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FASTSEQ for Windows Version 4.0

LENGTH: 601
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WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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                               FILE OF ANY DEATH AND THE TEREBRICE: CLOOL 307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRESESEQ for Windows Version 4.0
SEQ ID NO 15630
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NAME/KEY: misc_feature
LOCATION: (1)...(112705)
CTHER INFORMATION: n = A,T,C or G
US-09-949-016-15630
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Query Match
Best Local Similarity 58.63
Matches 58; Conservative
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Best Local Similarity 60.2
Matches 56; Conservative
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US-09-949-016-152710
                        TITLE OF INVENTION:
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ORGANISM: Human
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OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (1084830) .. (1084830)
OTHER INFORMATION: n equals a, t, c,
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OTHER INFORMATION: n equals a, t,
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LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t,
                                                                      NAME/KEY: misc feature
LOCATION: (713552)..(713652)
OTHER INFORMATION: n equals a, t,
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LOCATION: (741684)...(741684)
OTHER INFORMATION: n equals a, t,
FEATURE:
NAME/KEY: misc feature
LOCATION: (779455)...(779455)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a,
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US-09-949-016-15630
US-09-949-016-15630, Application US/09949016
Sequence 15630, Application US/09949016
Patent No. 6812339
Patent No. More Application:
GRANGRAL INFORMATION:
TRILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES

RESULT 3

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US-09-949-016-13725/c
; Sequence 13725, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; PAPLICANT: VERYER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REPERENCE: CL001307
; CURRENT FILING DATE: 2000-04-14
; PRIOR PELICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR APPLICATION NUMBER: 60/241,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-10-03
; PRIOR PLING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE PAREOED FOR Windows Version 4.0
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                                              41 TGGGATTTAATGAGCTCTTTCTCTTCTCTGCCTGCCTTTTGCTTTTTCCTCATGACTCT 100
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  Gaps
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  23; Indels
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; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
    APPLICANT: DORNER, F.
    APPLICANT: SCHEIFLINGER, F.
    APPLICANT: RALKNER, F. G.
    TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
    CORRESPONDENCES: 52
    CORRESPONDENCE ADDRESS:
    ADDRESSEB: Foley & Lardner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4;
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  Mismatches
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Pred. No. 4;
0; Mismatches
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13725
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22.1%;
Best Local Similarity 67.1%;
Matches 47; Conservative
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47; Conservative
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
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  Matches
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                                                                                                      APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 05/024,1755

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREESEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.3%; Score 33.4; DB 4; Length 155019; 58.6%; Pred. No. 4.1;
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Pred. No. 4;
                                  Sequence 16029, Application US/09949016
Patent No. 6812339
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Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; LOCATION: (1)._.(155019)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-16029
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US-09-949-016-12511
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67.1%;
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Matches 58; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature
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Best Local Similarity
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 16029
LENGTH: 155019
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LENGTH: 100463
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  Indels
    63;
    0; Mismatches
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                                                                                                                                                                                                       121 ATAATCCAGTTCA 133
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Best Local Similarity 58.9
Matches 73; Conservative
        70; Conservative
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US-09-949-016-16994
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          Matches
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Sequence 16423, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR PILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012

SOFUTANE: FASESEQ for Windows Version 4.0

LENGTH: 167708
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21.5%; Score 32.2; DB 1; Length 7218;
Best Local Similarity 13.1%; Pred. No. 2.9;
Matches 19; Conservative 74; Mismatches 52; Indels 0
            OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                              FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REFERENCE/DOCKET NUMBER: 39,768
RECISTRATION NUMBER: 29,768
RECISTRATION NUMBER: 39,768
TELEPHONE: (703) 836-9300
TELEPHONE: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32.2; |
Pred. No. 10;
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52.6%;
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US-08-232-463-14
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Best Local Similarity
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; ORGANISM: Human
US-09-949-016-16423
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Sequence 16994, Application US/09949016
; Sequence 16994, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLOOL307
; CURRENT APPLICATION NUMBER: 00/241,755
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR PLING DATE: 2000-10-20
; PRIOR PLING DATE: 2000-10-09-08
; PRIOR PLING DATE: 2000-10-09-08
; PRIOR PLING DATE: 2000-10-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 16994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/09328925

Sequence 4, Application US/09328925

Sequence 4, Application US/09328925

GENERAL INFORMATION:

APPLICANT: Kurachi, Kotoku

APPLICANT: Kurachi, Sumiko

TITLE OF INVENTION: Use Thereof

TITLE OF INVENTION: Use Thereof

FILE REFREENCE: UM-03603

CURRENT APPLICATION NUMBER: US/09/328,925

CURRENT FILING DATE: 1999-06-09

NUMBER OF SEQ ID NOS: 84

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 4

LENGTH: 38059
                                                                                                                                                                                               68906 GCCAİCİCCIATCİĞTTCİİCTĞİAİTİTÜCİĞTAĞCTİCCİİİĞİTĞAAĞCTÂCÖATI 68965
                                                            68846 črárgairrichritokárririrágagrakéragágrirriccargraacriggericari 68905
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                                                                                                                                   61 CTCTTCTCCTGCCTGTTTTGCTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGA
1 CAAAGAICACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELICATION NUMBER: 60/241,755
PRIOR PLICATION NUMBER: 60/241,756
PRIOR PLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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PRIOR FILING DATE: 2000-10-03
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Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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0; Mismatches
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CURRENT PILING DATE: 2000-04-14
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PELING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: RestSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 21.2%; Score 31.8; Best Local Similarity 64.0%; Pred. No. 15 Matches 48; Conservative 0; Mismatche
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Pred. No. 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (1)...(194537)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ION: (1)...(201529)
INFORMATION: n = A,T,C or G
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64.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
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Best Local Similarity
Matches 48; Conserv
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US-09-949-016-12740
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-949-016-12928
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LENGTH: 194537
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Sequence 16308, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CL001307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,756

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: Fast SEQ ID NOS: 207012

SEQ ID NO 16308

LENGTH: 48691
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                                                                                                                 DB 4; Length 38059;
                                                                                                                                                                     50; Indels
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                                                                                                           Query Match 21.3%; Score 32; DB 4
Best Local Similarity 58.9%; Pred. No. 6.6;
Matches 73; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
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Patent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCATION: (1)... (48691)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 51.0
Matches 75; Conservative
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-328-925-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-949-016-12928
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123 AATCCAGTTCATCCT 137

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RESULT 15

US-09-949-016-4716

Sequence 4716, Application US/09949016

Sequence 4716, Application US/09949016

Sequence 4716, Application US/09949016

Sequence 4716, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINDER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

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LENGTH: 4745
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21.1%; Score 31.6; DB 4; Length 4745;
Best Local Similarity 55.5%; Pred. No. 3.9;
Matches 61; Conservative 0; Mismatches 49; Indels 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3955 TIGITAATGCTTTTAAAACAAATGAGTTTTTTATATAAATAAAGTTTTT 4004
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Job time : 39.9109 secs
                TYPE: DNA
ORGANISM: Human
US-09-949-016-4716
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Listing first 45 summaries
                                                                                                                                                       OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli Sequence 839, App Sequence 4, Appli Sequence 2, Appli Sequence 1626, Ap Sequence 1626, Ap Sequence 1625, Ap
SUMMARIES ID	9 US-09-899-276-3 13 US-10-044-090-839 19 US-10-865-705-4 22 US-10-833-655-2 15 US-10-311-455-1626 15 US-10-311-455-1625 20 US-10-311-455-1625
DB	9 13 15 15 20
% Query Match Length DB	100.0 150 100.0 724 100.0 11793 97.6 2776 774 5926 61.3 5926
& Query Match	100.0 100.0 100.0 97.6 74.4 61.3
Score	150 150 150 146.4 111.6

Result No.

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equence 673,	equence 10589	equence 10589	equence 10589	equence 10589	10589	1058	1918	equence 1918	m	equence 1918	equence 1918	equence 1918	equence 926,	equence 8798	equence 1331	equence 11,	equence 2248	2248	2347	equence 2347	e 2347	23476	m	e 37294	37295,		10579	10579	10579	equence 10579	equence 10579	18618,	-	18620,	equence 18618,	equence 18619,	18620,
-10-322-281-673	-10-02/-632-10589/	-10-027-632-105898	-10-027-632-105899	-10-027-632-105897	7-632-105898	-105899	-10-027-632-19185	-10-027-632-19186	-632-19187	-10-027-632-19185	-10-027-632-19186	-19187	1-926	-10-425-115-8798	-09-918-995-13313	-263-11	-10-027-632-224845	-632-224845	-234763	-632-234764	2-234763	8-10-027-632-234764	-09-880-107-3095 S	10-972-079-37294	-10-972-079-37295	-10-027-632-105792	-10-027-632-105793	-10-027-632-105794	-10-027-632-105792	-10-027-632-105793	-632-10579	-632-18618	-632-18619		-632 - 1	US-10-027-632-18619 S	7-632-1862
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ALIGNMENTS

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APPLICANT: Scot, Ubaldo
APPLICANT: Scot, Ubaldo
APPLICANT: Scot, Ubaldo
APPLICANT: Cov, Johannes
APPLICANT: Cov, Johannes
APPLICANT: Delius, Hajo
APPLICANT: Poustka, Annemarie
APPLICANT: Perzelt, Annemarie
APPLICANT: Parzelt, Andrea
APPLICANT: Parzelt, Andrea
APPLICANT: PAFRENCES
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APPLICANT: DOI 104 999,276
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: EP 00 114 560.6
PRIOR APPLICATION NUMBER: EP 00 114 560.6
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.0%; Score 150; DB 9; 3
Best Local Similarity 100.0%; Pred. No. 3.4e-37;
Matches 150; Conservative 0; Mismatches 0;
                   Sequence 3, Application US/09899276
Patent No. US20020106355A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 150
US-09-899-276-3
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Gaps

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Indels

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FEATURE:
NAME/KEY: misc feature
LOCATION: (2583) .. (2583)
OTHER INFORMATION: n = c, a
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NAME/KEY: misc_feature
LOCATION: (2582)..(2582)
OTHER INFORMATION: n = c,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-685-705-4
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; Sequence 4, Application US/10685705
; Publication No. US20040177387A1
; GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Ambati
TITLE OF INVENTION: Degeneration
FILE REFERENCE: 050229-0415
CURRENT APPLICATION NUMBER: US/10/685,705
CURRENT FILING DATE: 2003-10-16
PRIOR APPLICATION NUMBER: 60/422,096
PRIOR APPLICATION NUMBER: 60/422,096
PRIOR PLING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 11793
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                                                                     CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
                  CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc feature
CTHER INFORMATION: Incyte ID No. US20020137081A1 1075405.1
NAME/KEY: unsure
LOCATION: 677, 710
CTHER INFORMATION: a, t, c, g, or other
US-10-044-090-839
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Best Local Similarity 100.C
Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
ORGANISM: Homo sapiens
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US-10-044-090-839
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1364 CTCTTCTCCTGCCTGTTTTTTTTTTTTCCTCATGACTCTTTTCTGCTCTTAAGATCAGA 1423
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                                                                                                                                                                     CICTICICCIGCCIGCCTTTIGCTTTTICCTCATGACTTTTCTGCTGTTAAGATCAGA 120
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APPLICANT: Wandi, Roman
APPLICANT: Doods, Henri
APPLICANT: Lenter, Martin
APPLICANT: Lenter, Martin
APPLICANT: Lenter, Martin
APPLICANT: Lenter, Martin
APPLICANT: Lenter, Martin
APPLICANT: Construction of an N-terminally modified
TITLE OF INVENTION: Chemotactic factor
FILIG REPRENCE: Case 1/140/833,656
CURRENT APPLICATION NUMBER: US/10/833,656
CURRENT FILING DATE: 2004-04-28
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 2776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CAAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTT
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                                                                                     1 CAAAGATCACATTCTAGGTCTGAGGTATAGGCAGAAAGCACTGGGATTTAATGAGGTCTTT
                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 97.6%; Score 146.4; DB 22; Length 2776; Best Local Similarity 99.3%; Pred. No. 1.4e-35; Matches 147; Conservative 0; Mismatches 1; Indels 0;
Length 11793;
                                              Indels
    Score 150; DB 19;
Pred. No. 1.7e-36;
Mismatches 0;
                                                                                                                                                                                                                                                                                                       8419 ATAATCCAGTTCATCCTAAAATGCTTTTTC 8448
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    Query Match
100.0%; Score 150; D)
Best Local Similarity 100.0%; Pred. No. 1.74
Matches 150; Conservative 0; Mismatches
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LOCATION: (2585)..(2585)
OTHER INFORMATION: n = c, a, t or g
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Sequence 1357, Application US/10723860
; Publication No. US20040253606A1
; SERREAL INFORMATION:
    APPLICANT: Aziz, Natasha
; APPLICANT: Glinsburg, Wendy M.
    APPLICANT: Zlotnik, Albert
; TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions & TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators; FILE REFRENCE: 05882.0193.NPUS01
; CURRENT FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,739
; PRIOR APPLICATION NUMBER: 60/429,739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ô
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                                                                                                     2 AAAGATCACATTCTAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTTC
                                                  Gaps
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DB 15; Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: David W. Morris
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: NOVel Compositions and Methods in Cancer
FILE REFERENCE: 52945200100
CURRENT APPLICATION NUMBER: US/10/322,281
CURRENT FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 673
LENGTH: 81684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Indels
Score 92; DB 15; Length 59
Pred. No. 2.5e-18;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 23.3%; Score 35; DB 3
Best Local Similarity 57.9%; Pred. No. 8.7;
Matches 62; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 8393
SOFTWARE: Patentin version 3.2
SEQ ID NO 1357
LENGTH: 227968
Query Match 61.3%;
Best Local Similarity 76.4%;
Matches 113; Conservative
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LOCATION: (1)...(81684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
US-10-723-860-1357
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; Bequence 1625, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
    APPLICANT: DIEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Oylosine methylation
; TITLE OF INVENTION: Oylosine methylation
; TITLE OF INVENTION: Oylosine methylation
; TITLE OF INVENTION: Oylosine methylation
; FILE REPERBNCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455
; CURRENT FILING DATE: 2002-02-12-16
; PRIOR APPLICATION NUMBER: PCY/EP01/07537
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR PILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; RIOR FILING DATE: 2000-06-30
; RIOR FILING DATE: 2000-06-30
; RUDBER OF SEQ ID NOS: 2424
; SEQ ID NO 1625
                                                                                                                    APPLICANT: OLEK, Alexander

APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Cytosine methylation
FILE REFERBNCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: DE7/BP01/07537
FRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1626
LENGTH: 5926
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74.4%; Score 111.6; DB 15; Length 5926;
Best Local Similarity 84.0%; Pred. No. 1.7e-24;
Matches 126; Conservative 0; Mismatches 24; Indels 0;
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CRGANISM: Artificial Sequence
FRATURE:
CTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
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                                             Sequence 1626, Application US/10311455
Publication No. US20030143606A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Seguence
                         -10-311-455-1626/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-10-311-455-1626
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US-10-311-455-1625
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46 TITAARGAGGICITITCICITICCCIGCCTGCCTTTTGCTTTTTCCTCATGACTCTTTTCT 105
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58.6%;
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Best Local Similarity 58.6
Matches 58; Conservative
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US-10-027-632-105898
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Sequence 105897, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

Publication No. US20020198371A1

GENERAL INFORMATION:

TITLE OF INVENTION: Dealymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

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TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REPERRING: 1088271

PRIOR FILING DATE: 2000-07-29

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-09-28

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PRIOR PILING DATE: 1999-09-38

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GENERAL INCOMATION

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108027-1129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30
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                                                                                                        Length 81684;
                                                                                                                                                                                                                                      15 TAGCTCTGAGGTATAGGCAGAAGCACTGGGATTTAATGAGCTCTTTCTCT
                                                                                                                                                                     Indels
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                                                                                                        DB 19;
                                                                                                        22.4%; Score 33.6; DB 19;
59.4%; Pred. No. 16;
tive 0; Mismatches 39;
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; Sequence 105898, Application US/10027632
; Publication No. US20020198371A1
; OTHER INFORMATION: n = A,T,C or G
US-10-322-281-673
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Best Local Similarity 58.6
Matches 58; Conservative
                                                                                                                   Query Match 22.4°
Best Local Similarity 59.4°
Matches 57; Conservative
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US-10-027-632-105897
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46 TITAATGAGCTCTTTCTCTTCTCTGCCTGCCTTTTGCTTTTTCCTCATGACTCTTTTCT 105
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Sequence 105899, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION: US20020198371A1

GENERAL INFORMATION: Jearld G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-12

PRIOR FILING DATE: 2000-04-12

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-09-28

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Pred. No. 3.1;
0; Mismatches 41;
PRIOR APPLICATION NUMBER: US 60/218,000
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 2000-02-24
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PILING DATE: 1999-11-23
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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219 TTCAACTAGTTTTGTTTCTCTCCTCCCTTCCACTCCCTTTTCCTTTTTT 160
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Publication No. US200302040759

Publication No. US200302040759

Publication No. US200302040759

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: PolyMorphisms in the Human Genome

FILE REPERENCE: 108027, 129

CURRENT PILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/219,006

PRIOR PELING DATE: 2000-00-12

PRIOR PELING DATE: 2000-00-12

PRIOR PELING DATE: 2000-00-12

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR APPLICATION NUMBER: US 60/185,318

PRIOR PILING DATE: 1999-01-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/166,358

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PILING DATE: 1999-09-09

NUMBER OF SEQ ID NOS: 325720

SOFTWARE: PSESEE FORESEQ FOR WINDOWS VERSION 4.0

SEQ ID NO 105897
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Publication No. US20030204075A9;
Fublication No. US20030204075A9;
Fublication No. US20030204075A9;
Fublication No. US20030204075A9;
Fublication No. US20030204075A9;
FILE REFERENCE: 108827.129
FURRENT APPLICATION NUMBER: US 40/10/27,632;
CURRENT PILING DATE: 2002-04-30;
FRIOR PILING DATE: 2002-04-30;
FRIOR PILING DATE: 2000-04-12;
FRIOR PILING DATE: 2000-04-20;
FRIOR PILING DATE: 2000-04-20;
FRIOR PILING DATE: 2000-04-20;
FRIOR FILING DATE: 2000-03-29;
FRIOR FILING DATE: 2000-03-29;
FRIOR FILING DATE: 2000-03-29;
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                                                                                 106 GCTCTTAAGATCAGAATAATCCAGTTCATCCTAAAATGC 144
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58.6%;
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Best Local Similarity 58.64
Matches 58; Conservative
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US-10-027-632-105897/c
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US-10-027-632-105897
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Sequence 105899, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Delymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT PELING DATE: 2002-04.30

PRIOR FILING DATE: 2000-04.20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 2000-02-24

PRIOR FILING DATE: 1999-11-23

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Pred. No. 3.1;
0; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33.4; DE Pred. No. 3.1; 0; Mismatches
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 325720
SEQUENCE: PSECSEQ FOR Windows Version 4.0
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58.6%;
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RESULT 15

US-10-072-632-19185/C

US-10-072-632-19185, Application US/10027632

Sequence 19185, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: David G.

TITLE OF INVENTION: David G.

TITLE OF INVENTION: DAVE: 2002-04-30

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR PAPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-07-12

PRIOR PALING DATE: 2000-03-29

PRIOR PLIING DATE: 2000-03-29

PRIOR PLIING DATE: 2000-03-29

PRIOR PLIING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 19185

LENGTH: 754

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22.3%; Score 33.4; DB 13; Length 754;
Best Local Similarity 58.6%; Pred. No. 3.4;
Matches 58; Conservative 0; Mismatches 41; Indels 0
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AC133423 Rattus no
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AC13063 MUB MUBCU
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AC05210 HOMO SADI
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db_xref="taxon:9606"
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Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Original source text: Human lung fibroblast W138 cell line, DNA, clones hJE-34 and lambda-hJE-7.

(lones hJE-34 and lambda-hJE-7.

(l) sites for [Unpublished (1989) Dana-Farber Cancer Inst., Boston, Ma., 02115].

Draft entry and computer readable sequence for [Unpublished (1989) Dana-Farber Cancer Inst., Boston, Ma., 02115] kindly provided by Dana-Farber Cancer Inst., Boston, Ma., 02115] kindly provided by Dana-Farber Cancer Inst., Boston, Ma., 02115] kindly provided by Localins 17-JUL-1989.

B.J. closu-lype="genomic DNA" | Localine Lype="genomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="fenomic DNA" | Localine Lype="f
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Human JE gene encoding a monocyte secretory protein, exon 1.

M28223 M26035

M28223.1 G1:338003

Secretory protein.

1 of 3

Homo sapiens (human)

Homo sapiens
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Rollins, B.J., Stier, P., Ernst, T. and Wong, G.G.
The human homolog of the JE gene encodes a monocyte secretory protein.
40 AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAAATGGATTTAATGCATTGTAT
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Best Local Similarity 100.0%; Pred. No. 9.3e-70;
Matches 250; Conservative 0; Mismarches 0;
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Original source text: Human WI-38 embryo lung fibroblast DNA, clone
hJB-34, passage 14.
Location/Qualifiers
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1 (bases 1 to 681)

Rollins, B.J., Stier, P., Ernst, T. and Wong, G.G.
The human homolog of the JE gene encodes a monocyte secretory
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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         linear
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Methods for assessing and treating leukemia
Methods (NO 03038129-A 95 08-MAY-2003;
Patent: WO 03038129-A 95 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Ortho-Clocation/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 9.3e-70;
Matches 250; Conservative 0; Mismatches 0;
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     AX774779 681 bp
Sequence 95 from Patent W003038129.
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Cytokine; secretory protein.
1 of 3
Homo sapiens (human)
                                                                  AX774779.1 GI:32486295
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Homo sapiens
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                              /product="MCP1"
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2807. ..2882
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/protecf="G1:34559720"
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MCP-1; monocyte chemoattractant protein-1.
Homo sapiens (human)
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                                    /replace="t"
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SM Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 3221)

S Nyquiet; P.A. and Degraba, T.J.

Two New Single Nucleotide Polymorphisms (SNPS) in the MCP-1

Promoter in Patients with Carotid Atherosclerosis: Transcriptional

Induction and New Protein Binding Sites

Induction and Degraba, T.J.

Nyquist; P.A. and Degraba, T.J.

Nyquist; P.A. and Degraba, T.J.

Direct Submission

Direct Submission

Submitted (31-JUJ-2003) Medicine, Inova Fairfax, 3300 Gallows Road, Palls Church, VA 22402-3300, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AY357296 3221 bp DNA linear PRI 15-SEP-2003 Homo sapiens MCP1 (MCP1) gene, promoter region and partial cds. AY357296
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Best Local Similarity 100.0%; Score 250; DB 9; Length 681;
Best Local Similarity 100.0%; Pred. No. 9.3e-70;
Matches 250; Conservative 0; Mismatches 0; Indels (
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/db_xref="taxon:9606"
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/gene="MCPl"
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225
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/replace="c"
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                                                                                                         PRI 18-OCT-2000
                                                                                                                                                                                                                                                                          Finzer, P., Soto, U., Delius, H., Patzelt, A., Coy, J.F., Poustka, A., zur Hausen, H. and Rosl, F.
Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HPV 18 positive cells: the role of the chromatin structure and AP-1 composition Oncogene 19 (29), 3235-3244 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roesl, F. Submission DKPZ Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKPZ Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKPZ German Cancer Research Institute), Im Neuenheimer Feld 506, 69120 Heidelberg, FRG
                                                                                                                                                                                                                             Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                    11793 bp DNA 1:
Homo sapiens MCP-1 gene and enhancer region.
Y18933
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3 (base 1 to 3227)
Ueda, A., Okuda, K., Ohno, S., Shirai, A., Igarashi, T., Matsunaga, K.,
Fukushima, J., Kawamoto, S., Ishigatsubo, Y. and Okubo, T.
Fukushima , J., Kawamoto, S., Ishigatsubo, Y. and Okubo, T.
Fr. Rappa B and Spl regulate transcription of the human monocyte chemoattractant protein-1 gene
J. Immunol. 153 (5), 2052-2063 (1994)
                                                                                                                                                                                                                                                                     Direct Submission
Submitted (06-DEC-1993) Atsuhisa Ueda, Yokohama City University School of Medicine, First Department of Internal Medicine; 3-9 Fukuura, Kanazawa-ku, Yokohama 236, Japan (Tel:045-787-2630, Pax:045-786-344)
Submitted (06-Dec-1993) to DDBJ by:
Atsuhisa Ueda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GGGAGCCGGCCAAAGCTTGAGAGCTCCTTGGCTGGGAGGCCCCTTGGAATGTGGCCT
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   Shyy, Y.J., Li, Y.S. and Kolattukudy, P.E. Structure of human monocyte chemotactic protein gene and its
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                     regulation by TPA
Biochem. Biophys. Res. Commun. 169 (2), 346-351 (1990)
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Yokohama City University School of Medicine
3-9 Fukuura, Kanazawa-ku
Yokohama 236
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100.0%; Pred. No. 1.1e-69;
ative 0; Mismatches 0;
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join(4118. .4193,4990. .5107,5490. .5595)
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/codon_start=1
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/rpt_type=dispersed
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578
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1537
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Rieder,M.J., Armel,T.Z., Carrington,D.P., Ozuna,M., Kuldanek,S.A., Rajkumar,N., Toth,E.J., Yi,Q. and Nickerson,D.A.
                                                                                                                                                                                                                                                    61 GGGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCT
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                                            Query Match
100.0%; Score 250; DB 9; Length 11793;
Best Local Similarity 100.0%; Pred. No. 1.2e-69;
Matches 250; Conservative 0; Mismatches 0; Indels 0;
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614. .720
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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

(CE 1 (Dases lto 147416)

Birren, B., Linton, L., Nusbaum, C. and Lander, B.

Homo sapiens

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Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
AC005549
HTG.
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complement (40810. .40899)
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Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collimore, A., Cooke, P., Corliss, D., Depayre, B., Devon, K., Dewar, K., Donelan, L., Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagos, B., Heaford, A., Herena, L., Horton, L., Howland, J.C., Jacotot, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Maldrim, J., Molla, M., Morris, W., Morrow, J., Mychaleckyj, J., Nahf, R., Naylor, J., Niloff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Rilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Ye, W.J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Direct, Submission
                                                                                                                                                                                                                                                                                                                                Submitted (12-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 4 (bases 1 to 147416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 13, 1998 this sequence version replaced gi:3581743. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Only the first 147416 bases of this clone are being submitted. Bases 145417-155040 overlap accession number AC004147 (WICGR project L228). The first 2Kb of the overlapping region are submitted to confirm overlap.

Location/Qualifiers
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family="MIR"

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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1626 03-JAN-2002;
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1590. .1974
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                                                                                                                                                                                                   674. .1471
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Pred. No. 1.3e-65;
0; Mismatches 1;
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other sequences; artificial sequences.
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1 (bases 1 to 2776)
Shyy Y.J., Li,Y.S. and Kolattukudy, P.E. Structure of human monocyte chemotactic protein gene and its regulation by TPA
Biochem. Biophys. Res. Commun. 169 (2), 346-351 (1990)
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99.4%; Score 248.4; DB 9;
Best Local Similarity 99.6%; Pred. No. 5.1e-69;
Matches 249; Conservative 0; Mismatches 1;
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Location/Qualifiers
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monocyte chemotactic protein.
Homo sapiens (human)
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BOVMCPIX 3405 bp DNA linear MAM 17-JAN-1995
Bovine monocyte chemoattractant protein-1 (MCP-1) gene exons 1-3,
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MQRLMNYRRVTSSKCPKEAVIFKTILGKELCADPKQKWVQDSINYLNKKNQTPKP"
1479. .2226
/gene="MCP-1"
                      4674 TITGIAGITITGGITITAGAGAAAGTAGAATITITAAAAATAATITITITAGITITATATT 4733
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 181 TCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC 240
                                                                                                                                                                                                                                                                                                                                                                                                               Wempe, F., Kuhlmann, J.K. and Scheit, K.H.
Characterization of the bovine monocyte chemoattractant protein-1
                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'codom_start=1
'product="monocyte chemoattractant protein-1"
'protein id="AAA60956.1"
'db_xref="GI:624394"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 3405;
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gene="MCP-1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oin(1403. 1478,2227. .2344,2695.
|gene="MCP-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Original source text: Bos taurus male DNA Location/Qualifiers
                                                                                                                                                                                                                                                                   L32659.1 GI:624393
monocyte chemcattractant protein-1.
Bos taurus (cow)
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic DNA"
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2227. .2344
/gene="MCP-1"
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|gene="MCP-1"
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/gene="MCP-1"
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/gene="MCP-1"
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/gene="MCP-1"
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                                                                                             4734 TGTGGTTAGT 4743
                                                                        241 TGTGGTCAGT 250
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                                                                                                                                                                                                                                                                                                                                                                          124 GGTAAGCTGGCAGCGAGCCTGACATGCTTTCATCTAGTTTCCTCGCTTCCTTTCT 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 GAAGGTAAGCTGGCAGCGAGCCTGACATGCTTTCATCTAGTTTCCTCGCTTCCTTTT 180
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                                                                                                                                                                                                                                 4 CTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCAGGG
           Location (Valifiers
1. .5926
| /organism="synthetic construct" | /mol type="unassigned DNA" | /db_xref="taxon:32630" | /note="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 5926
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="teaxon:32630"
/noTe="chemically treated genomic DNA (Homo sapiens)"
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1625 03-JAN-2002;
Epigenomics AG (DE)
Location/Qualifiers
                                                                                                                                                            Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 64.2%; Score 160.4; DB 6; Length 5926; Best Local Similarity 77.6%; Pred. No. 1.4e-40; Matches 194; Conservative 0; Mismatches 56; Indels 0;
                                                                                                                                                                                                Indels
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                                                                                                                                                       64.9%; Score 162.2; DB 6;
larity 78.5%; Pred. No. 3.6e-41;
Conservative 0; Mismatches 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other sequences; artificial sequences.
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synthetic construct
Epigenomics AG (DE)
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                                                                                                                                                         Query Match
Best Local Similarity
Matches 194; Conserv.
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              PEATURES
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(bases 1 to 279170)
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1 (bases 1 to 2791/0)

Namer, D. Marie, Metrker M. Lee., Abramson, S., Adams, C., Alder, J., Allan, Metrker, M. Halbrocke, S., Amin, A., Anguisho, D., Allan, C., Allan, M., Anguisho, M., Benalbmed, F., Balden, H., Anguisho, P., Barder, M., Berantsead, M., Benalbmed, F., Balden, D., Bandsernal Balden, D., Barder, M., Barnstead, M., Benalbmed, F., Balden, D., Bandstranal Balden, D., Barder, M., Barnstead, M., Benalbmed, F., Bayalo, K., Buhay, C., Burch, P., Chen, C., Conken, S., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, Z., Chen, J., Davila, M., L., Davis, C., Cavas, C., Coyle, M. Care, M., Pargen, C., Beran, C., Chen, Y., Din, H., Dugar, Rocha, S., Dunn, A., Durchi, K., Din, T., Faser, C., Chen, Y., Chen, C., Caras, C., Para
                                                                                                                                                                                                                                                                                                        ALL/1645
Rattus norvegicus clone CH230-230H10, *** SEQUENCING IN PROGRESS
A.*, 2 unordered pieces.
                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
         AGGCTICTATGAIGCTACTATTCTGCAITTGAATGAGAATGGATTTAATGCATTGTCA 60
                                                                                                                                  61 gega-ecceanacrigaeacricerrecrigecressagecerring 110
                                                                                                                                                                                         744 deserectrectalastricasatretetetetretraderetetades 794
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HTG; HTGS_PHARE1; HTGS_DRAFT; F
Rattus norvegicus (Norway rat)
Rattus norvegicus
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TITLE

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AL Submitted (08-007-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Baylor Plaza, Houston, TX 77030, USA
Daylor Plaza, Houston, TX 77030, USA
On Sep 19, 2002 this sequence version replaced gi:21953804.
On Sep 19, 2002 this sequence expension of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contigs accontigs are ordered and oriented, and separated individual sequence contigs are ordered and there may be sequence by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contigs will be indicated in the feature shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
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NOTE: This is a 'working draft' sequence. It currently consists of 2 contigs. The true order of the places is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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                                        Submitted (18-JUL-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center project name: GRM10
Center project name: GRM10-230H10
Center clone name: CH230-230H10
Assembly program: Phrap; version 0.990329
Consensus quality: 146772 bases at least Q40
Consensus quality: 148340 bases at least Q20
Consensus quality: 149405 bases at least Q20
Estimated insert size: 164568; sum-of-contigs estimation Quality coverage: 3x in Q20 bases; sum-of-contigs estimation
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58.0%; Pred. No. 0.52;
tive 0; Mismatches 50; Indels
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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1. 279170
/organism="Rattus norvegicus"
/mol type="genomic DNA"
/db_xref="taxon:10116"
/clone="GR30-230H10"
                                                                                                                                                                                               Rat Genome Sequencing Consortium.
Direct Submission
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240512. .241705
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/note="wgs_contig"
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Best Local Similarity 58.01
Matches 69; Conservative
Worley, K.C.
Direct Submission
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102688 TACTTTTTTTTGGATGTGTTGCTTATACTTATTTGTCGTTTGATGTTCTGAAATA 102747
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48507 TGAAATGGATCCCAAATTGAGCCTGACAGACTTTCCTTTAGTCTCTTCTCTATTTTTGTC 48566
                                                                                                                                                                                       AC008692 145807 bp DNA linear PRI 18-DEC-2001
Homo sapiens chromosome 5 clone CTB-65N22, complete seguence.
AC008692
                                                                                48567 TTGTAGTTTTTTTAGATTTGAACAATTCTGGATCAGAAATTTTGACTCTGTTGGTTAACA 48625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 145807)
DOB Joint Genome Institute.
DOB Joint Genome Institute.
Direct Submission
Submitsed (03-4006-1999) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 145807)
DOB Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submission
Submission
Submission
Dorse, Wallow Creek, CA 94598, USA
On Dec 18, 2001 this sequence version replaced gi:9256030.
Draft Sequence Produced by DOB Joint Genome Institute
Www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
Www-spg.stanford.edu
Quality: Phrap Quality >=40 100% of Sequence;
Estimated Total Number of Errors is 0.

1. .145807
                                          180 TTCTGCAGTTTTCGCTTCACAGAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACA 238
                                                                                                                                                                                                                                                                                                                                                                  Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo. 1 (bases 1 to 145807) DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   88 TTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 IGCTITCATCIAGTITCCICGCTICCTITCTICTGCAGTITTCGCTTCACAGAAGCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 53.4%; Pred. No. 1.4;
Matches 79; Conservative 0; Mismatches 69; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             102748 TCTTCCCAAAGATTAACCCTCTTATTTC 102775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/mol_type="genomic DNA"
/mb_xref="taxon:9606"
/chromosome="5"
/clone="CTB-65N2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     208 GAATCCTTAAAAATAACCCTCTTAGTTC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: August 4, 2005, 11:16:50 Job time : 1009.86 secs
                                                                                                                                                                                                                                                                          AC008692.6 GI:17921192
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Homo sapiens
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                                                                                                                                                                                                                        DEFINITION
ACCESSION
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AUTHORS
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AC008692
LOCUS
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GenCore version 5.1.6

Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 3, 2005, 15:09:47; Search time 165.688 Seconds (without alignments)

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Rost-processing table: 1 aggcttctatgatgctacta.....agttcacatctgtggtcagt 250

Scoring table: 1 aggcttctatgatgctacta.....agttcacatctgtggtcagt 250

Gapop 10.0, Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum Match 00*

Maximum Match 00*

Maximum Match 100*

Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

genesegn2003as:*
genesegn2003bs:*
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Database

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		d			SUMMARIES	
Result No.	Score	Query Match	l Query Match Length DB	DB	ID	Description
-1	250	100.0	250	9	ADH13941	Adh13941 Human mon
7	250	100.0	681	10	ADE84876	Ade84876 Farnesyl
٣	250	100.0	3221	12	ADN12120	Adn12120 MCP1 gene
4	250	100.0	3221	12	AD003802	Ado03802 Human Cc1
5	250	100.0	11793	12	AD003803	Ado03803 Human Cc1
9	237.4	95.0	2775	9	ABK47979	Abk47979 Human sma
C 7	162.2	64.9	5926	9	ABL33653	Abl33653 Human imm
80	160.4	64.2	5926	9	ABL33652	Abl33652 Human imm
0	91.4	36.6	800	80	ACF64398	Acf64398 Human MCP
c 10	36.4	14.6	80275	12	ADQ97310	Adq97310 Mouse can
c 11	36.4	14.6	109559	13	ABD33157	Abd33157 Murine ca
c 12	35.8	14.3	165	9	ABL86846	Abl86846 Human ova
13	34	13.6	1500	2	AAS88382	Aas88382 DNA encod
c 14	33.8	13.5	31051	4	AAK73223	Aak73223 Human imm
15	33.6	13.4	673	9	ABK35434	Abk35434 Human cDN
16	33.2	13.3	227968	9	ABK83497	Abk83497 Human cDN
17	33.2	13.3	227968	12	ADQ18538	Adq18538 Human sof
18	33	13.2	141586	11	ABD20695	Abd20695 Human pul
19	32.8	13.1	23406	11	ACN44442	Acn44442 Human gen
20	32.8	13.1	260160	17	ADQ20017	Adq20017 Human sof

Abk81833 DNA repre	Abn86540 N. tabacu	Acn47169 Cotton pr	Aak64539 Human imm	Adq52904 Novel can	Abv24663 Human pro	Ada72185 Rice gene	Aad48709 Rat metab	Adj75271 Marker ge	Adj75181 Marker ge	Adr24834 Breast ca	Adj75182 Marker ge	Abx76394 Lung canc	Abx76140 Lung canc	Adn39009 Cancer/an	Abx76393 Lung canc	Abx76141 Lung canc	Adn39007 Cancer/an	Aak57161 Human imm	Aak65201 Human imm	Aak65200 Human imm	Acn45162 Human gen	Abl27938 Drosophil	Aca30151 Prokaryot	Acd05595 cDNA enco
ABK81833	ABN86540	ACN47169	AAK64539	ADQ52904	ABV24663	ADA72185	AAD48709	ADJ75271	ADJ75181		ADJ75182	ABX76394	ABX76140	ADN39009	ABX76393	ABX76141	ADN39007	AAK57161	AAK65201	AAK65200	ACN45162	ABL27938	ACA30151	ACD05595
9	4	13	4	13	Ŋ	œ	œ	12	12	13	12	ω	œ	11	σ,	æ	11	4	4	4	1	4	œ	œ
2092	2943	469	463	495	1118	2000	3417	5879	5879	5879	5920	6921	6921	6921	7043	7043	7043	662	2118	2118	51615	2285	4491	1074
3.0	3.0	8.	12.7	12.7	12.6	9.8	9.2	9.2	5.6	9.2	9.2	9.2	9.2	9.7	5.6	9.2	9.	5.51	2.5	2.5	5.5	12.3	2.3	2.5
H	H	ä	ä	ä	ä	H	H	H	H	H	H	ä	H	H	ä	H	H	ä	H	H	H	H	H	ä
32.6	32.4	32	31.8	31.8	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.6	31.2	31.2	31.2	31.2	30.8	30.8	30.6
21	22	23	24	25	56	27	28	53	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45
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ALIGNMENTS

ADH13941 standard; DNA; 250 BP.

RESULT 1 ADH13941

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer. ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:4. Poustka A; Finzer P, Delius H, Disclosure; SEQ ID NO 4; 30pp; English. (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM. 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. 11-MAR-2004 (first entry) Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A; WPI; 2002-165895/22. Homo sapiens. EP1170372-A1. 09-JAN-2002. ADH13941;

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17-JUN-2004
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ID ADN1
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                                                                                                                                                                                                                   TCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC 240
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                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
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pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                <u> AGGCTTCTATGCTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCA</u>
                                                                                                                                          GGGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCT
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                                                                                                                                                                               GAAGGTAAGCTGGCAGCGAGCCTGACATGCTTTCATCTAGTTTCCTCGGTTCCTTCTTTT
                                                                                                      AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCA
                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                               ss; cytostatic; farnesyl transferase inhibitor; gene expression; quinolinone; leukemia; cancer.
                                                                                     ..
                                                                                                                                                                                                                                                                                                                                                                               Farnesyl transferase inhibitor modulated leukemia associated
                                                                    250;
                                                                                     Indels
                                                                    Length
                                                 76 T; 0 U; 0 Other;
                                                                   Score 250; DB 6;
Pred. No. 7.9e-73;
                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; SEQ ID NO 95; 346pp; English.
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                                                  Sequence 250 BP; 56 A; 60 C; 58 G;
                                                                                                                                                                                                                                                                                                                            BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-OCT-2002; 2002WO-US034784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-OCT-2001; 2001US-0338997P.
30-OCT-2001; 2001US-0340081P.
30-OCT-2001; 2001US-0340938P.
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                                                                    Query Match
Best Local Similarity 100.0%;
Matches 250; Conservative 0
                                                                                                                                                                                                                                                                                                                           ADE84876 standard; DNA; 681
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presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chloropheny])(1-methyl-1H-imidazol-5-yl)amethyl]-4-(3-chlorophenyl)-1-methyl-2-(1H)quinolinone, montroring the therapy of a patient, treating a patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be
                                                                                                                                                                                                                                                                                                                                                                                           120
                                                                                                                                                                                                                                                                                                                                                                                                                                     159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          major histocompatibility class I; MHC-I; MHC-II; Cytostatic; EBV-associated cancer; Hodgkin's lymphoma; nasopharyngeal carcinoma; gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma; parotid carcinoma; breast carcinoma; lelomyosarcoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New human cell line modified to comprise and express genes encoding immunomodulators and an antigen of Epstein-Barr virus (EBV), useful for inducing or stimulating an immune response in a human to EBV-associated
                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                                                                                                                     TCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCA
                                                                                                                                                                                                                                                                                                                                                                                           GGGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                160 GAAGGTAAGCTGGCAGCCTGACATGCTTTCATCTAGTTTCCTCCGCTTCCTTT
                                                                                                                                                                                                                                                                                                       1 AGGCTTCTATGATGCTACTATTCTGCATTTGAATGGAATTGGATTTAATGCATTGTCA
                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                         681;
                                                                                                                                                                           Sequence 681 BP; 153 A; 205 C; 140 G; 183 T; 0 U; 0 Other;
                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                         Score 250; DB 10;
Pred. No. 1.2e-72;
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                                                                                                                                                                                                                                                                  0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Borrello IM,
                                                                                                                                    modulated in the presence of FTI
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                                                                                                                                                                                                                             100.08;
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Matches 250; Conserv
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The present invention relates to a human cell line, which lacks major histocompatibility class I(MHC-I) and MHC-II antigens and which has been modified to comprise and express a gene encoding an immunomodulator and a gene encoding an antigen of Epstein-Barr virus (EBV). The human cell line, compositions and methods are useful for inducing or stimulating an immune response in a human to an EBV-associated cancer, where the human immune are insk for Hodgkin's lymphoma, nasopharyngeal carcinoma, gastric carcinoma, Burkit's lymphoma, T-cell lymphoma, B-cell lymphoma, parotid carcinoma, bareast carcinoma, and leiomyosarcoma. The present sequence represents a nucleotide sequence associated with the cell line
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen; lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy; promoter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human Cc12 promoter region used for gene knockout animal models SeqID
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Matches 250; Conservative
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                                                                     This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drugs to gene knockout mice, in particular Ccl2-deficient, Ccr2-deficient and/ or a Ccl2-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polynucleotide sequence is the human Ccl2 promoter region DNA of the invention.
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lipofuscin accumulation, Bruch's membrane, retinal degeneration,
choroidal neovascularisation, ophthalmological, gene therapy.
                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 250; DB 12; Length 3221; 100.0%; Pred. No. 2.5e-72; ive 0; Mismatches 0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         animal model; age-related macular degeneration; AMD;
                                                                                                                                                                                                                                                                                                                   Sequence 3221 BP; 859 A; 793 C; 727 G; 842 T; 0 U; 0 Other;
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                                    Disclosure; SEQ ID NO 3; 64pp; English.
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Matches 250, Conservative
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accumulation in eye.
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ABL33653 standard; DNA; 5926
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Matches 249; Conservative
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P-PSDB; AAU77179.
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                                                                                                                                    This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular Collectiont, Corleficient and/ or a Colledicient/Corleficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and accumulation and ensed for gene therapy purposes. This polymucleotide sequence is the human Coll gene and enchancer region DNA of the invention.
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                                 Testing candidate drug for treating age-related macular degeneration, by administering drug to Cc12-deficient, Ccr2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; small inducible cytokine A2; SCYA2; gene; ds; haplotype pair; haplotyping; atherosclerosis; antiarteriosclerotic; gene therapy; single nucleotide polymorphism; genotyping; drug screening; chromosome 17q11.2-q21.1.
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                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 250; DB 12;
100.0%; Pred. No. 4.5e-72;
trive 0; Mismatches 0;
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598. .2080
/*tag= a
/product= "Human SCYA2"
                                                                                                                  Disclosure; SEQ ID NO 4; 64pp; English.
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Matches 250; Conservative
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                WPI; 2004-400512/37.
                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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The invention relates to single nucleotide polymorphisms in the gene concoling human small inducible cytckine A2 (SCYA2) polypeptide. A method conclude human small inducible cytckine A2 (SCYA2) polypeptide. A method for haplotyping the SCYA2 gene in an individual comprises identifying the coff the copies of the small specification or whether both copies are defined by a haplotype pair. This method is useful in genotyphing, whereby all possible haplotype pair. This method is useful in genotyphing, whereby all possible haplotype comparing the frequency of the haplotype or haplotype or haplotype or haplotype pair of the frequency of the haplotype or haplotype pair in a reference population, where a higher haplotype cor haplotype pair in a reference population, where a higher haplotype cor haplotype pair is corresponding by comparing the trait with the frequency of the haplotype cor haplotype pair. SCYA2 and its corresponding by comparing the expression and function of SCYA2, and in screening for for studying the expression and function of SCYA2, and in screening for candidate drugs to treat diseases related to SCYA2 and in screening for the haplotype screening sequence represents genomic DNA which encodes the human grava or human grav
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                                                                                                                                                                                                                                                                                                                                                                                                                                     New genetic variants having polymorphisms in the small inducible cytokine Al (SCYA2) gene, useful for studying the function of SCYA2, and for treating disorders affected by expression or function of the SCYA2
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Pred. No. 3.7e-68;
0; Mismatches 1; Indels 1;
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                                                                                                                                                                                                                                                             Koshy
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                                                                                                                                                                       (GENA-) GENAISSANCE PHARM INC.
                                                                                 28-AUG-2000; 2000US-0228496P.
28-AUG-2001; 2001WO-US026899.
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120 154 180 214

9 94 274

BP.

Human immune system associated gene SEQ ID NO: 1625

(first entry)

26-MAR-2002

ABL33652;

BP.

ABL33652 standard; DNA; 5926

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid reluxaemia, Alzhaimer's disease, Alzhailepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              184 GCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATCTGT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
                                                         antiarteriosclerotic, antianaemic, cytostatic, nootropic, neuroprotective; anti-HIV; anticonvulsant, ophthalmological, antirhematic, antiartitic, antidabetic, antipsoriatic, antirhematicy, accer; eye disease; arteriosclerosis, anaemia, acute myeloid leukaemia, Alzheimer's disease, AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AACCGACCAAAACTTAAAAACTCCTTCCTAACTAAAAAAACCCCTTAAAATATAAACCTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                              antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5926 BP; 1554 A; 55 C; 1492 G; 2825 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 1626; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                Human immune system associated gene SEQ ID NO: 1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      64.9%; Score 162.2; DB 6; 78.5%; Pred. No. 6.1e-43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                 ĸ
                                                                                                                                                                                                                                                                                                                                                                                                   Berlin
                                                                                                                                                                                                                                                                                    02-JUL-2001; 2001WO-EP007537
                                                                                                                                                                                                                                                                                                                    30-JUN-2000; 2000DE-01032529 01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                  (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                       WO200200928-A2
                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 194;
                                                                                                                                                                                                                                                      03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1430
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                                                                                                                                                                                                                                                                                                                                                                                                 Olek A,
셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              셤
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RESULT 8 ABL33652

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGCAGTTTTCGCTTCACAGAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC 240
                                                                                                                                      antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, ansemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid comprising fragment of chemically modified gene, useful f diagnosis and treatment of diseases associated with abnormal cytosine methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4494 AGGITITIAIGAIGTIAITAITATITIGIAITAGAAIGAGIAAAAIGGAITITAAIGIAITAATIGIIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGAGCCGCCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64.2%; Score 160.4; DB 6; Length 5926; 77.6%; Pred. No. 2.4e-42; ive 0; Mismatches 56; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        77.6%; Pre-
                                                                                                                                                                                                                                                                                                                                                                 02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000DE-01032529
                                                                                                                                                                                                                                                                                                                                                                                                                 01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 77.6
Matches 194; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGGTCAGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                               (EPIG-) EPIGENOMICS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                     WO200200928-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              olek A,
                                                                                                                                                                                                                                                                     Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
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4734 TGTGGTTAGT 4743

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comprising: (a) a sequence comprising at least 15 contiguous nucleotides of a sequence comprising at least 15 contiguous nucleotides of a sequence comprising at least 15 contiguous nucleotides of a sequence comprising variant sequences (A) from Table 4 given in the specification; or (b) a sequence that is complementary to (A). Also described: (1) an array of (PN) is comprising two or more of the isolated described: (1) an array of (PN) in an individual; (3) a computer-readable storage medium, where each record has a field identifying a base occupying a (PN) site and a location of the polymorphic site; and (4) a occupying a (PN) site and a location of the polymorphic site; and (4) a signal carrying adra for access by an application program having executed associated with multiple sclerosis. ACF64025 to ACF64424 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 INGTITICTICGETICCTICTTITITICTGCAGTTTCGCTTCAGAGAAAGCAGAATCCTTAA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       158 TAGTTTCCTCGCTTCCTTTCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAA
                                                                                                                                         detection; computer-readable storage medium; polymorphic site; carrying data; data processing system; multiple sclerosis; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New polynucleotide, useful for detecting loci associated with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes an isolated polynucleotide (PN)
                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                                                 Natsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 800 BP; 185 A; 250 C; 165 G; 200 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, Indels
                                                                                                                                                                                                                                                                                                                                                                                                                  Jin W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 91.4; DB 8;
Pred. No. 9.8e-20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         218 AAATAACCCTCTTAGTTCACATCTGTGGTCAGT 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAATAACCCTCTTAGTTCACATCTGTGGTCAGT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                  Rienhoff HY,
                                                                                                                   Human MCP1 nucleotide sequence >MCP1_01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 74; 93pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADQ97310 standard; DNA; 80275 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36.6%;
nilarity 98.9%;
Conservative 0
                       ACF64398 standard; DNA; 800 BP.
                                                                                                                                                                                                                                                                                                                                        07-AUG-2001; 2001US-0310741P.
24-SEP-2001; 2001US-0324790P.
                                                                                                                                                                                                                                                                                                         07-AUG-2002; 2002WO-US025268.
                                                                                                                                                                                                                                                                                                                                                                                                                      Jones HB, Xu H, White R,
                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2003-268196/26.
                                                                                                                                                                                                                                                                                                                                                                                           (DNAS-) DNA SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                      signal carrying
                                                                                                                                                                                                                                                   WO2003014319-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92;
                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                 20-FEB-2003
                                                                                          13-OCT-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADQ97310;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                               ACF64398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Loc
Matches
                                                                                                                                                            Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADQ97310/
                  ACF64398
RESULT
                                                셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer-associated protein; CAP; cancer-associated gene; CA; gene;
                                                                                                                                                                                                                                                                          New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                      The present invention relates to cancer associated sequences (ADO97025-9098004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 TGAAGGTAAGCTGGCAGCCTGACATGCTTTCATCTAGTTTCCTCGCTTCCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 80275 BP; 21152 A; 19490 C; 18637 G; 20855 T; 0 U; 141 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              60 AGGGAGCCGGCCAAAGGTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 80275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 TICTGCAGTITTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACC 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                Mouse cancer associated sequence MD08-030, SEQ ID 287.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%; Score 36.4; DB 12;
ilarity 51.2%; Pred. No. 1.7;
Conservative 0; Mismatches 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Murine cancer-associated (CA) gene MD07-021.
                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 287; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABD33157 standard; DNA; 109559
                                                                                                                                                                               27-DEC-2002; 2002US-00330773.
                                                                                                                                                                                                       (SAGR-) SAGRES DISCOVERY INC.
                                                                                                                                                     22-DEC-2003; 2003WO-US041389.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ds; cancer; cytostatic
                                                                                                                                                                                                                                    Malandro MS;
                                                                                                                                                                                                                                                           WPI; 2004-543781/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
Les 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO2004058146-A2
                                                                                                     WO2004060304-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JUL-2004
                                                                             Mus musculus.
07-OCT-2004
                                                                                                                                22-JUL-2004.
                                                                                                                                                                                                                                      Morris DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABD33157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mouse;
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The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour colypeptide encoded by a polyputoleocide (III) having a cDNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell population of (II), cor antigen presenting cells that express (II). (I) has cytostatic cativity. An oligonucleotide (IV) that hybridises to (S1) can be used for activity. An oligonucleotide (IV) that hybridises to (S1) can be used for cativity. An oligonucleotide (IV), detecting the amount of polypucleotide (NY), detecting to (S1) can be biological sample from a patient with (IV), detecting to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the camount of polypucleotide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the computating and/or expanding T cells specific for an ovarian cutour protein comprising contacting T cells with (III) and/or (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proceins in tumour cells; and contacting the expression of the tumour polypeptides and proceins in tumour cells; and the contacting the contacting receins in tumour cells; and the contacting the contacting receins in tumour cells; and the contacting the contacting receins in tumour cells; and the contacting the contacting captures and contacting contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures and contacting captures captures captures captures captures captures captures captur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87 CTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGAC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 AJGCTTTCATCTAGTTTCCTCGCTTCCTTTCTTGCAGTTTTCGCTTCACAGAAGC 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 145 CTGCCTGCAGGTGTGGCCCCTTGGCCTGAACTGGGGCCTGAATTGTGGGAAGGGTGGT
                                                                                                                                                                                 Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, chromosome mapping, gene mapping, gene therapy; forensic; food supplement, medical imaging, diagnostic, genetic disorder, ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 165 BP; 67 A; 37 C; 38 G; 22 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding novel human diagnostic protein #24186.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35.8;
                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 9824; 489pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    library using well known techniques
                                                                          Jones R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAS88382 standard; cDNA; 1500 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAATCCTTAAAAATA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.3%;
53.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-MAR-2001; 2001WO-US008631.
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                                                                          Harlocker SL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAATTAATAACNCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 53.7
Matches 73; Conservative
       (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200175067-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002
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                                                                          Algate PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS88382;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              106445 AGGAGCTTGCTCGCATGGTTGTGAAGGAAGGCCAGGTGTGTCCCAGGCCTGCTTCGAGGC 106386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          106385 TGGGAGGAGCCTAGGCAT-TGGGATGGAGGCAGGGTTGTAGGCTTACCTAGCTCCATTCT 106327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to cancer-associated proteins (CAP) and the cancer-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 109559 BP; 31165 A; 24061 C; 22798 G; 30464 T; 0 U; 1071 Other;
                                                                                                                                                                                                                                                                                                                                  Novel human cancer associated protein encoded within open reading frame of cancer associated gene, useful as targets for diagnosing cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14.6%; Score 36.4; DB 13; Length 109559; 55.6%; Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; ovarian cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTAGTTTCCTCGCTTCCTTCTTTTCTGCAGTTTTCGCTTC 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human ovarian cancer related cDNA clone SEQ ID NO:9824.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; SEQ ID NO 137; 182pp; English.
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15-DEC-2003; 2003WO-US040081.
                                                               17-DEC-2002; 2002US-00322281.
                                                                                                                                   (SAGR-) SAGRES DISCOVERY INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 55.00
Best Local 90; Conservative
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                                                                                                                                                                                               Malandro MS;
                                                                                                                                                                                                                                                                  WPI; 2004-499109/47.
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Gaps

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05-SEP-2000; 2000US-0229509P.
06-SEP-2000; 2000US-0229513P.
06-SEP-2000; 2000US-0230437P.
06-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231243P.
08-SEP-2000; 2000US-0231244P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0231413P.
08-SEP-2000; 2000US-0232080P.
12-SEP-2000; 2000US-0232080P.
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14-SEP-2000; 2000US-0232400P.
14-SEP-2000; 2000US-0232401P.
14-SEP-2000; 2000US-0233063P.
14-SEP-2000; 2000US-0233064P.
14-SEP-2000; 2000US-0233065P.
21-SEP-2000; 2000US-0233055P.
21-SEP-2000; 2000US-0234223P.
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2000US-022526P.
2000US-022526P.
2000US-022526P.
2000US-022570P.
2000US-022547P.
2000US-022547P.
2000US-022575P.
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2000US-0214886P.
2000US-0215135P.
2000US-0216647P.
2000US-0216880P.
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2000US-0217496P.
2000US-0218290P.
2000US-0220963P.
200US-0229518P.
2000US-0224518P.
2000US-0225213P.
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2000US-0180628P.
2000US-0184664P.
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2000US-0226681P.
2000US-0226868P.
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                                                                      17-JAN-2001; 2001WO-US001354
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14-SEP-2000;
14-SEP-2000;
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27-SEP-2000;
              WO200157182-A2
                                                                                                                                                                                                                                            28-JUN-2000;
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14-AUG-2000;
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14-AUG-2000;
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22-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-AUG-2000;
                                          09-AUG-2001
The invention relates to isolated polymucleotide (I) and polypeptide (II) cadences. (I) is useful as hybridiation probes, polymerase chain cadences. (I) is useful as hybridiation probes, polymerase chain. Consequences (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polymicleotides are also used in disponsition as expressed sequence tags for identifying expressed consequily in general production of (II) is useful in gene therapy techniques to restore normal consequily for generating attibodies against it, detecting or quantitating a cuseful for generating antibodies against it, detecting or quantitating a polyment. (II) and its binding partners are useful for treating disorders of sites expressing (II). (I) and (II) are useful for treating disorders of supplement. (II) and its binding partners are useful for treating of supplement. (II) and its binding partners are useful for treating disorders of involving aberrant protein expression or biological activity. The polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications in polypeptide and polymucleotide sequences have applications of mutations diagnostic formations while and products dependent on DNA and conding sequences. Abs64197-Abs94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at the conding application of the printed specification, but was obtained in the printed specification, but was obtained in the printed specification, but we be applied in the printed sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1362 ccTTGCCCAGCTCGAAAAAGGGGAGAGGGTCTGCGGGCAAGTCGACCGCCGCCGCCTACTA 1421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1302 échcgiachiatchgchagcechagccgrocchochagachgradharaitroicha 1361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          97 GGGAGGCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGACATGCTTTCAT 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human immune/haematopoietic antigen genomic sequence SEQ ID NO:28035.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                   New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 13.6%; Score 34; DB 5; Length 1500; Local Similarity 50.6%; Pred. No. 1.8; es 82; Conservative 0; Mismatches 80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1500 BP; 292 A; 380 C; 440 G; 388 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             157 CTAGTITCCTCGCTTCCTTTTCTGCAGTTTTCGCTTCA 198
                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 24186; 103pp; English.
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                                                                                                   Tang YT;
                        31-MAR-2000; 2000US-00540217.
23-AUG-2000; 2000US-00649167.
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                                                                                                                                WPI; 2001-639362/73.
P-PSDB; ABG24195.
                                                                                                      Liu C,
                                                                       (HYSE-) HYSEQ INC.
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Amountain a cid sequences given in AAMB1921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) to proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) collynucleotides may be used to produce the secreted (I), by inserting the molieic acids into a host cell and culturing the cell to express the colloning and polynucleotides may be used to produce the secreted (I), by inserting the protein. (I) proteins and polynucleotides may be used to prevent, cancers and cancer metastases of haematopoietic-related diseases, especially concern metastases of haematopoietic antigen genomic to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54950 and AAM83169 represent sequences used in the exemplification of the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27616 reacraegeaaarrecriaacreccriarcrercaaregeceaarriraagesrrecri 27557
                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; gene; ss; nutritional supplement; haemophilia; viral infection; bacterial infection; fungal infection; diabetes; asthma; autoimmune disorder; rheumatoid arthritis; multiple sclerosis; tumour; autoimmune thyroiditis; allergic reaction; neurodegenerative disease; Alzheimer's disease; Parkinson's disease; liver fibrosis; cancer; ulcer; coagulation disorder; inflammatory disorder; Crohn's disease; incision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83
                                                                                                                                                                                                    AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 31051 BP; 6999 A; 8773 C; 8261 G; 7018 T; 0 U; 0 Other;
                                                                                                                                                            Disclosure; SEQ ID NO 28035; 3071pp + Sequence Listing; English.
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56.9%;
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Matches 62; Conservative
Barash SC,
                                            WPI; 2001-483426/52.
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    Rosen CA,
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06-APR-2000; 2000US-0195582P. 29-MAR-2001; 2001WO-US010224

(GEMY) GENETICS INST INC.

Resnick RJ;

Howes SH,

Agostino MJ,

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Five hundred and ninety two polynucleotides derived from a variety of human tissue sources which encode secreted proteins, useful for treating immune deficiencies and disorders such as autoimmune disorders.
Wong GG, Clark HF, Fechtel K,
Gulukota K, Graham JR;
                       WPI; 2002-179321/23
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The invention relates to 592 polynucleotides which have been derived from a variety of human tissue sources and which encode novel secreted a variety of human tissue sources and which encode novel secreted a variety of human tissues can be used as probes for the identification and isolation of full length cDNA and genomic DNA. The identification and isolation of full length cDNA and genomic DNA. The comparison of polynucleotides and proteins can also be used as nutritional supplements. The proteins are useful in the treatment of various immune deficiencies of and disorders such as viral infections, bacterial infections, fungal confections, autoimmune disorders (e.g. rheumatoid arthritis, multiple infections, autoimmune thyroiditis and diabetes) and allergic reactions sclerosis, autoimmune thyroiditis and diabetes) and allergic reactions concursodesmerative diseases (e.g. Alzheimer's disease, Parkinson's disease), liver fibrosis, coagulation disorders (e.g. haemophilia), disease), liver fibrosis, coagulation disorders (e.g. cromn's disease) and tumours. They are also useful for regulating burns, incisions and ulcers. The proteins are also useful for regulating commune, incisions and ulcers. The proteins are also useful for regulating commune, incisions and ulcers. The proteins are also useful for regulating commune, incisions and for treating myeloid or lymphoid cell deficiencies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 673 BP; 117 A; 226 C; 168 G; 162 T; 0 U; 0 Other;
Claim 1; Page 365; 372pp; English.
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Search completed: August 4, 2005, 08:31:14 Job time : 169.688 secs 652 AGAATTAATAACACTA 667

207 AGAATCCTTAAAAATA 222

206

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0; Gaps

87 CTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGAC 146

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Query Match
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                                                                                                                           August 4, 2005, 04:04:35; Search time 1179.96 Seconds (without alignments) 8064.741 Million cell updates/sec
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68.8%; Score 172; DB 8; Length 707; 100.0%; Pred. No. 8.9e-42;

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Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eutheria; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 768)

S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Haalth, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: Capabs-r@mail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Preparation: Life Genomica, Inc.

cDNA Library Preparation: MGC clone distribution information can be found through the I.M.A.G.B. Consortium/LINL at:

http://image.llnl.gov

Location/Qualifiers

High quality Sequence Stop: 690.
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                                                    79 GAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAACG 138
                                                                                                                                                                  139 AGCCTGACATGCTTTCATCTAGTTTCCTTCCTTCCTTTTCTGCAGTTTTCGCTTCA 198
                                                                                                                                                                                                    61 ACCTGACATGCTTTCATCTAGTTTCCTCGCTTCCTTTTTTTCTGCAGTTTTCGCTTCA 120
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   ö
         0; Indels
         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BG121617.1 GI:12615126
            Matches 172; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       390 TGA 392
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TITLE
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Contact: Robert Strausberg, Ph.D.

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui,

Tissue Procurement: W. Marston Linehan, Ph.D.

M.D., Michael Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.

CDNA Library Arrayed by: Genome Systems

Clone distribution: NCI-CGAP Clone distribution information can be

found through the I.M.A.G.E. Consortium/LINL at:

www-bio.llnl.gov/bbrp/image/image.html

Seg primer: -40m13 fwd. ET from Amersham

High quality sequence stop: 394.

High quality sequence stop: 394.

Location/Qualifiers

L. -437.

L. -437.
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/dev stage="DH10B"
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/lab_host="DH10B"
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AA568299 437 bp mRNA linear BST 22-AUG-1997 nf15a05.s1 NCI_CGAP_Pr1 Homo sapiens cDNA clone IMAGE:913808, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo. 1 (Bases 1 to 437)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
14.8%; Score 37; DB 1;
Best Local Similarity 100.0%; Pred. No. 3.4;
Matches 37; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:913808"
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A1962277
A1962277.1 GI:5754990
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Homo sapiens
                                                                                                                                                                                                                                                       AA568299.1 GI:2341353
                                                                                                                                                                                                                                                                                                                                                               sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tumor Gene Index
Unpublished (1997)
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Homo sapiens
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Laboratory Mouse DNR Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligomucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil | 4732114 | gb| | 123072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AZ536871 481 bp DNA linear GSS 06-NOV-2000 Gm_ISb001_082_J15_R ISU Soybean BAC Library (pBeloBAC11 HindIII) Glycine max genomic clone Gm_ISb001_082_J15, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="E. coli strain XLIO-Gold, T1-resistant, F-" /clone lib="Mouse 10kb plasmid UUGC2M library" /note="Vector: PWAGAVY; Purified genomic DNA from M. musculus GS7BL/6J (female) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chemically-competent E. coli XLIO-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69 GCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAA 128
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      whole genome scaffolding with paired end reads from 10kb
                            plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 380, Biomedical Polymers Research Bldg., 20 S. 2030 184112, USA
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                                                                                                                                                                                                                                 Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Brror: 0.00
Plate: 0284 row: F column: 07
Seq primer: CGTGTAAAACGACGACCAGT
Class: plasmid ends
High quality sequence stop: 371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
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AZ536871.1
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AZ536871/c
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue type="pooled germ cell tumors"
/lab_host="norl cape germ cell tumors"
/lab_host="DH10B"
/clone llb="morI cGAP GC (Pharmacia) with a modified
/note="Vector: pT717D-Pac (Pharmacia) with a modified
/note="Vector: pT717D-Pac (Pharmacia) with a modified
/note="Vector: pT717D-Pac (Pharmacia) with a modified
polylinker; Site 1: Not I; Site 2: Eco RI; Plasmid DNA
from the normalized library NCI CGAP GC4 was prepared, and
ss circles were made in vitro. Following HAP purification,
this DNA was used as tracer in a subtractive hybridization
reaction. The driver was PCR-amplified cDNAs from a pool
of 5,000 clones made from the same library (cloneIDs
1257096-1258631, l469064-1470983, and 1475592-1476743).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
                                                                                                                                                                                                                              Email: cgapbs-r@mail.nib.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima
Bonaldo, Ph.D
cDNA Library Arrayed by: Greg Lennon, Ph.D.
cDNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 161)
NCI-GAP http://www.ncbi.nlm.nih.gov/ncicgap.
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Sciurognathi; Muridae; Murinae; Mus.
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Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
181am,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D.,Weiss,R.
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14.7%; Score 36.8; DB 1; Length 161;
Best Local Similarity 54.4%; Pred. No. 2.9;
Matches 74; Conservative 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="mRNA"
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                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Rodentia;
1 (bases 1 to 371)
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                                                                                                                                                      Tumor Gene Index
Unpublished (1997)
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AZ997556
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셤 ò 68

Gaps

ORGANISM

SOURCE

AUTHORS TITLE JOURNAL COMMENT

REFERENCE

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AL LORDES & LO. 4.D.).

NOT-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Thuror Gene Index

Tumor Gene Index

Thuror Gene Index

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.

Emmert-Buck, M.D., Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Greg Lennon, Ph.D.

CNA Library Arrayed by: Greg Lennon, Ph.D.

CONA Library Arrayed by: Greg Lennon, Ph.D.

NA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NOT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiML at:

www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 2791 Std Error: 0.00

Seq primer: -40UP from Gibco

High quality Sequence stop: 127.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /wol_type="mRNM"
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Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          391 bp DNA linear GSS 22-JUL-200: Lotus corniculatus var. japonicus DNA, clone:LjT60c08_not, genomic survey sequence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 165)
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Pred. No. 6;
0; Mismatches
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1 Similarity 53.7%;
73; Conservative 0
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/dev stage="cotyledon stage"
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/clone_lib="ISU Soybean BAC Library (pBeloBAC11 HindIII)"
/note="Vector: pBeloBAC11; The ISU BAC library (Marek and Shoemaker, Genome 40.420, 1997) was constructed using the HindIII site in pBeloBAC11. The library consists of approximately 40,000 clones with an average insert size of approximately 40,000 clones with an average insert size of che library is done by PCR amplification of DNA pools.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         http://genome.cornell.edu/cgi-bin/webAce/webace?db=soybase.
Please see as an authority for the mapping/naming: Cregan P.B., T.
Jarvik, A.L. Bush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya,
T.T. VanToai, D.G. Lohnes, J. Chung, and J.E.Specht. 1999a. An
integrated genetic linkage map of the soybean genome. Crop Sci.
39: (In press)
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                                                                            Eukaryota, viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; Eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                             Marek, L.F., Paz, M., Darnielle, L., Hanson, N. and Shoemaker, R.C. BAC End sequences from a soybean genomic library (ISU) Unpublished (2000)
Contact: Shoemaker Randy C
Agronomy Department
                                                                                                                                                                                                                                                                                                                                                                                                                          Iowa State University
Ames, IA 50011-1010, USA
Tel: 515 294 1205
Fax: 515 294 2229
Email: reshoediastate.edu
This BAC identified by SSR Satt129. For more information, see
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AI280614
AI280614.1 GI:3918847
EST.
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Class: BAC ends.
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                         Glycine max (soybean)
Glycine max
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Matches 69; Conserv
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                                                                                                                                                                                                           Glycine.
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FEATURES

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Email: cgapbs-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. cDNA Library Preparation: Life
Technologies, Inc. cDNA Library Arrayed by: Christa Prange, The
T.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image.html
Insert Length, 440 Std Error: 0.00
  /lab_host="DH10B"
/clone_lib="0B_Ba"
/note="Vector: pAGIBAC1; Site_l: HindIII; Site_2: HindIII"
                                                                                                                                                                                                                71 CAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGC 130
                                                                                                                                                                                                                                                                                                       87 CTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGAC 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A1950785 LU28 LU28 Homo Bapiens cDNA clone IMAGE:2547531 3' similar to contains element MER22 repetitive element ;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 200)

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/tissue_type="two pooled squamous cell carcinomas"
/tlab.host="DH10B"
/clone_lib="NCI_CGAP_Lu28"
/note="Organ: lung; Vector: pCMV-SPORT6; Site 1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                         50 caaarcagaagargarcaractagcacagarccrcaggcgaagaggaggrgagc
                                                                                                                                                                                                                                                                                                                                                                                                191 TCGCTTCACAGAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC 240
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                                                                                                                   Length 571;
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14.1%; Score 35.2; DB 1; Length 200;
Best Local Similarity 53.7%; Pred. No. 9.8;
Matches 73; Conservative 0; Mismatches 63; Indels
                                                                                                                                                                   84; Indels
                                                                                                                     DB 9;
                                                                                                                   Score 35.6; DB
Pred. No. 10;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -400P con gibco
High quality sequence stop: 145.
Location/Qualifiers
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                                                                                                                   ch 14.2%;
1 Similarity 50.6%;
86; Conservative
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                                                                                                                                             Best Local Similarity
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            Sato, S.

Direct Submission

Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA ...

The First Laboratory for Plant Gene Research; 2-6-7

Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan

(E-mail:ssato@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/,

Tel:81-438-52-3935 (ex.2336), Fax:81-438-52-3934)

Location/Qualifiers

Location/Qualifiers
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Oryza brachyantha
Doryza brachyantha
Bukaryoza, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Wagnoliophyta; Liliopsida; Poales; Poaceae;
Bhrhartoideae; Oryzeae; Oryza.
I (basea I to S71)
Kim, H., Yu,Y., Stum,D., Yost,D., Rao,K., Luo,M., Jetty,R.,
Kidrna,D., Muller,C., Hatfield,J., Soderlund,C. and Wing,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       137 CGAGCCTGACATGCTTTCATCTAGTTTCCTCGCTTCCTTTTTCTGCAGTTTTCGCTT 196
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0
                                                                                                                                                                                                                                                                                                /variety="japonicus"
/db xref="taxon:34305"
/clone="lj160008_not"
/clone=lib="genomic TAC library"
/note="VECTOR:pXLTAC7-synonym: Lotus japonicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OB_Ba0037K16.r OB_Ba Oryza brachyantha genomic clone OB_Ba0037K16.r OB_Ba Oryza brachyantha genomic clone CL579550
CL579550.1 GI:48537062
GSS.79550.1 GI:48537062
                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.2%; Score 35.6; DB 9; Length 391; 60.2%; Pred. No. 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OMAP Project

Ombbished (2004)

Contact: Rod A. Wing

Arizona Genomics Institute
University of Arizona

Forbes Building Room 303, Tucson, AZ 85721-0036, USA

Tel: $20 626 9595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  197 CACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTT 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTTAAAAAGATTAATGCATAAAAGTAAAAATATTAGTT 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length: 145000 Std Brror: 0.00 Plate: 0037 row: K column: 16 Seq primer: CAC TCA TTA GGC ACC CCA

    .571
    /organism="Oryza brachyantha"

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FORWARD: TAA TAC GAC TCA CTA TAG GG
BACKWARD: CAC TCA TTA GGC ACC CCA
Innert Length: 145000 Std Brror: 0
Plate: 0037 row: K column: 16
                                                                                                                                                                                                                                                       /mol_type="genomic DNA"
/strain="Miyakojima MG-20"
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/db_xref="texon:4533"
/clone="nob_Ba0037K16"
/tissue_type="leaves"
/dev_stage="mature"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: http://genome.arizona.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 location/Qualifiers
  2 (bases 1 to 391)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59; Conservative
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                                                                                                                                                                                                                                     AI302643.1 GI:3961989
             207 AGAATCCTTAAAAATA 222
                                              30 AGAATTAATAACACTA 15
                                                                                                                                                                                                                                                                                 Homo sapiens (human)
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                                                                                                                                                                                                    mRNA sequence.
AI302643
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gex="male"
/lab host="PHIDB"
/clone lib="Soares testis NHT"
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a modified
/note="Vector: pT7T3D-Pac (Pharmacia) with a strand cDNA
/polylinker; Site_1: Nor I, Site_2: Eco RI; 1st strand cDNA
/was prepared from mRNA obtained from Clontech
Laboratories, Inc., and primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Bonardo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be

Clone distribution: NCI-CGAP clone distribution information can be

Clone distribution: NCI-CGAP clone distribution

Inscribution: NA.G.B. Consortium/LIML at:

www.bio.llnl.gov/bbrp/inage/image.html

Inscri Length: 570

Std Error: 0.00

Seq primer: 400P from Gibco

High quality sequence stop: 345.
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                                                                                                                                                                                                                                           378 bp mRNA linear EST 29-NOV-1998 gg36c09.x1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:1837264 3', mRNA sequence.
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Homo sapiens
Homo sapiens
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 378)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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                                                                               150 ciecciócacerenedeccicrindeceredacidecedecreaarrenedaaadeer
                                            147 AIGCITICATCIAGITICCICGCITCCTTTTTCTGCAGITTTCGCTTCACAGAAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
Email: ggapbs-r@mail.nih.gov
cDNA_Library Preparation: M. Bento Soares, Ph.D., M. Fatima
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Pred. No. 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
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/clone="IMAGE:1837264"
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1 Similarity 53.7%;
73; Conservative
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                                                                                                                                      207 AGAATCCTTAAAAATA 222
                                                                                                                                                                                50 AGAATTAATAACCCTA 35
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Unpublished (1997)
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Tumor Gene Index

Tumor Gene Index

Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: capabb=:remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGT-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:
www-bio.lln!gov/bbrp/image/image.html
Insert Length: 2148 Std Error: 0.00
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/mol_type="mRNA"
/mol_type="mRNA"
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/clone="IMAGE:1901458"
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/tissue_type="2 pooled tumors (clear cell type)"
/tissue_type="2 pooled tumors (clear cell type)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87 CITCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGAC 146
AI302643 396 bp mRNA linear BST 01-FBB-1999
qn48a06.xl NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1901458 3',
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1 (bases 1 to 396)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           146 cireccifecagárérgécecetrajacergalectigagecergaairgragaaldger
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High quality sequence stop: 375.
Location/Qualifiers
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us-09-899-276c-4.rst

RESULT 13

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Email: eggen@jouv.inra.fr
Clones are derived from the INRA bovine BAC library
(http://locus.jouv.inra.fr/pc/cattle_bac_map.htm). For BAC library
availability, please contact Andre Eggen (eggen@jouv.inra.fr). This
work was undertaken as part of the International Bovine BAC
Mapping Consortium (IBBMC) by INRA (Jouy-en-Josas) and Genoscope
(Evry) Plate: 95 row: A column: 11
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="INRA bovine BAC"
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INRA Bovine BAC library (Male) produced by Andre
Eggen-Genoscope sequence ID : GROAAA76AG10RM1
                                                  CR841822 641 bp DNA linear GSS 27-SEP-2004 GROAAA76AG10RM1 INRA BAC Bos taurus genomic clone INRAb_95A11, DNA sequence, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-SEP-2004) Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30 TGAATGAGCAAATGGATTTAATGCATTGTCAGGGAGCCGGCCAAAGCT---TGAGAGCTC 86
                                                                                                                                                                                                                                                                              Bovinae; Bos.

1 (bases 1 to 641)

Eggen, A., Schibler, L. and Roy, A..

Bovine BAC End Sequences from the INRA bovine BAC library Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            - LGbC

    .641
    /organism="Bos taurus"
    /mol_type="genomic DNA"
    /strain="breed: Holstein"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9913"
/clone="INRAb_95A11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Department of Animal Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       - Web : www.genoscope.cns.fr)
Contact: Andre Eggen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78350 Jouy-en-Josas, France
Tel: 33 1 34 65 24 24
Fax: 33 1 34 65 24 78
                                                                                                                                CR841822
CR841822.1 GI:52777910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 641)
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Matches 93; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                                                                                                                                                                        Bos taurus (cow)
Bos taurus
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RESULT 14
CR841822/c
LOCUS
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                                                                                                                                                                                                                                                                                                                                                      Tumor Gene Index
Inpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Distribution: Clone distribution information can be obtained
from Dr. M. Bento Soares, bento-soares@miowa.edu
The following repetitive elements were found in this CDNA
seq primer: M13 FORWARD
POLYA-Yes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1...683
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/mol_type="mRNA"
/mol_type="mRNA"
/mol_type="mRNA"
/db xxef="taxon:9606"
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/dev_stage="Adult"
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/clone lib="NCI_CGAP_DFO"
/lab_host="BulloB (Life Technologies)"
/clone lib="NCI_CGAP_DFO"
/roce="Organ: Bone; Vector: pT773-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI_CGAP_DFO is a cDNA library containing the following tissue(s): Subchondral Bone. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT773-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is GTTAAGCGTC.
                        BUG16089 683 bp mRNA linear EST 23-SEP-2002 UI-H-DF0-bex-i-14-0-UI.81 NCI CGAP DF0 Homo sapiens cDNA clone UI-H-DF0-bex-i-14-0-UI 3', mRNA sequence.
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                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 683) NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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TAG_SEQ=GTTAAGCGTC"
                                                                                                   BU616089
BU616089.1 GI:23282297
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                                                                                                                                                                        Homo sapiens (human)
Homo sapiens
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Matches 73; Conserv
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AUTHORS
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87 CTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGAC 146 260 TGAGAGAACAAATTGCATTGATGCACAGACACAGTGGTCCCCAAGGCTGTCAGTGCCTTG 201 200 TACTCTGGCAAGTAACAAGCATGGATTCTGGCCTCCGAAAGCCTTGGCTCATATCCCGGC 141 147 ATGCTTTCATCTAGTTTCCTCGCTTCCTTCCTTTTCTGCAGTTTTCGCTTC 197 140 AGCCITICIGITAGIATCIGIGACCITICCIGITICCCCAGITICCTCATC RESULT 15 BH325278

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Gaps

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is 1 (bases 1 to 661)

Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,

Shoat, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K.,

Shoat, S., Shetty, J., Gebregeorgis, E., Overton, L., Russell, D.,

Riggs, F., de Jong, P. and Fraser, C.M.

Riggs, F., de Jong, P. and Fraser, C.M.

Riggs, F., de Sequences from Library CHORI-230 EcoRI segment

Rupublished (1999)

Contact: Shaying Zhao

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0208

Fax: 301 838 0208

Fax: 101 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    111 AAIGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGACATGCTTTCATCTAGTTTCGTCGCT 170
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CH230-45J13.TJ CHORI-230 Segment 1 Rattus norvegicus genomic clone
CH230-45J13, genomic survey sequence.
BH325278
BH325278.1 GI:17255992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: szhao@tigr.org

Chones are derived from the rat BAC library CHORI-230

(http://www.chori.org/bacpac/rat230.htm). For BAC library

(http://www.chori.org/bacpac/rat230.htm). For BAC library

availability, please contact Pieter de Jong (pdejong@mail.cho.org).

Clones may be purchased from BACPAC Resources

(http://www.chori.org/bacpac/or ering_information.htm). BAC end

page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html

page: http://www.igr.org/tdb/bac_ends/rat/bac_end_intro.html

Seq primer: SP6

Class: BAC ends.
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CHORI-230 Rat (BN/SSNHsd/MCW) BĀC library produced by
Pieter de Jong"
                                                                                                                                                           Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51 IGCATIGICAGGGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGGAGGCCCCTTGG
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Best Local Similarity 52.4%; Pred. No. 16;
Matches 77; Conservative 0; Mismatches 70; Indels
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/db xref="taxon:10116"
/clone="CH230 455413"
/sex="Female"
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JOURNAL
COMMENT
                                                 DEFINITION
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AUTHORS
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12243, A
15091, A
16142, A
3, Appli
16819, A
53422, A
3, Appli
                                                                                    August 4, 2005, 07:01:49; Search time 51.5182 Seconds (without alignments) 7940.282 Million cell updates/sec
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           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-503-922-2

US-09-949-016-13499

US-09-949-016-13807

US-09-949-016-13807

US-09-949-016-13807

US-09-949-016-13877

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US-08-449-699A-3
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Listing first 45 summaries
                                                              - nucleic search, using sw model
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12.5 168971
12.4 86439
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12.3 601
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12.3 202111
12.1 3408
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11.9 12089
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Sequence 12209/C
; Sequence 12209/A
; Sequence 12209, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REPERENCE: CLOOD1307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT PILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FBSESEQ for Windows Version 4.0
; SEQ ID NO 13209
; LEMCHT: 198942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83996 TTTTCCATTTCCTCTCTGATTACCATGAGAATGTGCCCTGCTGGCCAGCTGGGGGATGAG 83938
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                                                                                  Sequence 12254, P
Sequence 11782, P
Sequence 13280, P
Sequence 16274, P
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Sequence 13922,
Sequence 13923,
Sequence 13924,
Sequence 13925,
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Sequence 14699,
Sequence 14700,
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Sequence 14702,
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                                                 Sequence 1,
Sequence 1,
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US-08-957-425-3
US-08-426-3431-1
US-09-423-8218-1
US-09-949-016-12554
US-09-949-016-12524
US-09-949-016-13280
US-09-949-016-13923
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US-09-949-016-14699
US-09-949-016-14699
US-09-949-016-14700
US-09-949-016-14700
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54.6%; Pred. No. 8.2;
7ative 0; Mismatches
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US-09-503-922-2/C
; Sequence 2, Application US/09503922
; Patent No. 6410706
; GENERAL INFORMATION:
; APPLICANT: PAI, MAU-Sook
; APPLICANT: LIU, dang-Ryol
; APPLICANT: CHO, Hye-Sun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
| LOCATION: (1)...(198942)
| OTHER INFORMATION: n = A,T,C or
US-09-949-016-13209
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Best Local Similarity 54.6
Matches 65; Conservative
                                                  17415
17415
139936
139952
238866
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                                                    RESULT 1
US-09-949-016-13209/c
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ORGANISM: Human
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TYPE: DNA
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US-09-949-016-13499
i Sequence 13499, Application US/09949016
j Patent No. 6812339
i GENERAL INFORMATION;
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WINDER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTSEQ for Windows Version 4.0
LENGTH: 54245
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: KIM, Youn-Sung
TITLE OF INVENTION: A NOVEL CHITIN-BINDING RECEPTOR KINASE AND THE GENE
TITLE OF INVENTION: THEREOF
FILE REFERENCE: seq
CURRENT APPLICATION UNBER: US/09/503,922
CURRENT FILLING DATE: 2000-02-14
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATCHILIN Ver. 2.1
                                                                                                                                                                                                                                                                                                                               88 TICCIGGCIGGGAGGCCCCTIGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCTGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4; Length 54245;
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Pred. No. 0.77;
0; Mismatches 56;
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; Pred. No. 8.6;
0; Mismatches
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Best Local Similarity 50.7%;
Matches 76; Conservative
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54.1%;
                                                                                                                                                                                         TYPE: DNA;
CRGANISM: Nicotiana tabacum
US-09-503-922-2
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Query Match
Best Local Similarity 54.1%
Matches 66; Conservative
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ORGANISM: Human
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Sequence 13807, Application US/09949016

Sequence 13807, Application US/09949016

Batent No. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINDER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 13807

LENGTH: 168971

LENGTH: 168971
     Sequence 58722, Application US/09949016

Fatent No. 681233

Patent No. 681233

Fatent No. 681233

Fatent No. 681233

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WIMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/041,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRSESEQ for Windows Version 4.0

SEQ ID NO 58722

LIBRICH: 601
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Pred. No. 0.68;
1; Mismatches 57; Indels
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Best Local Similarity 52.8%;
Matches 65; Conservative <sup>1</sup>
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Best Local Similarity
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US-09-949-016-58722
RESULT 4
US-09-949-016-58722
; Sequence 58722, A
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US-09-949-016-177614
                                                                                                     ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241, 755
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231, 498
                                                                  93014 TTTCAGGGTGTGGGGGGGCAGCACGACCCTAACAGGGGGCTCCTGCTCTATCTCAGTCAC 93073
                                                                                                                                   93074 CTACCTAAGCAGGAAGATGGCTGCCAGCTGGGCTTGCCGCCCATGCTCTTGTTCCA 93133
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                                   166 TCGCTTCCTTCCTTTTCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACC
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Pred. No. 19;
0; Mismatches 40; Indels
 Mismatches 103; Indels
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Sequence 11945, Application US/09949016
Patent No. 6812339
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ilarity 57.9%;
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Best Local Similarity
.....hes 55; Conserve
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RESULT 8

US-09-949-016-177614/c

Sequence 177614 Application US/09949016

Sequence 177614 Application US/09949016

Sequence 177614 Application US/09949016

SEQUENCE 177614 Application US/09949016

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PALING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

PRIOR FILING DATE: 2000-09-08
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Patent No. 6812339
GERERAL INFORMATION:
FILL INFORMATION:
FILL OF INVENTION:
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Best Local Similarity 57.9%; Pred. No. 19;
Matches 55; Conservative 0; Mismatches 4
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NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 16990
LENGTH: 86440
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 177614
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Best Local Similarity 56.0°
Matches 56; Conservative
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Application US/09949016
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Best Local Similarity
Matches 62; Conserv
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Best Local Similarity
Matches 65; Conserv
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ORGANISM: Human
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US-09-949-016-17188
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US-09-949-016-17188
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US-09-949-016-58723
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Sequence 14449, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
APPLICANT: VENTER, VENTE
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Best Local Similarity 57.1%; Pred. No. 37;
Matches 56; Conservative 0; Mismatches 42;
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12.2%; Score 30.6; DE
Best Local Similarity 52.8%; Pred. No. 15;
Matches 66; Conservative 0; Mismatches
                                           PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASTER OF Windows Version 4.0
SEQ ID NO 13877
LENGTH: 202111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | NAME/KEY: misc_feature
| LOCATION: (1)...(202111)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13877
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US-09-949-016-14449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Human
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RESULT 11 US-09-949-016-58723

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Sequence 17188 Application US/09949016

Sequence 17188 Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERBUCKS: CLOON-0-0-4-14

CURRENT FILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR PELING DATE: 2000-10-30

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREASEQ for Windows Version 4.0

SEQ ID NO 17188

LENGTH: 31797
y Sequence 58723, Application US/09949016
Patent No. 681239
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WIWER: US/09/949,016
CURRENT FILING DATE: 2000-04-14,755
PRIOR PELING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-09-08
PRIOR PILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRACERE OF WINDOWS VETBION 4.0
SECTION: AND ADDITIONAL APPLICATION NUMBER: PARIOR PILING DATE: 2000-010-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
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al Similarity 53.9%; Pred. No. 20;
62; Conservative 0; Mismatches
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Query Match
Best Local Similarity 61.5%;
Matches 48; Conservative
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Best Local Similarity 61.5%;
Matches 48; Conservative
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ORGANISM: Human
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELICATION NUMBER: 60/241,755
PRIOR PELICATION NUMBER: 60/241,756
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
SEQ ID NO 13444
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Patent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
FILE REFERENCE: CL001307
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-09-08
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189 TITCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATCTGT
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Pred. No. 56;
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SOFTWARE: PSECSEQ for Windows Version 4.0
SEQ ID NO 14698
LENGTH: 18895
                                                                                                                                                         Sequence 13444, Application US/09949016
Patent No. 6812339
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Best Local Similarity 52.8%;
Matches 65; Conservative
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LOCATION: (1)...(18895)
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ORGANISM: Human
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RESULT 15

US-09-949-016-12245/c

i Sequence 12245, Application US/09949016

j Patent No. 6812339

i GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

PILE REPERENCE: CL001307

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-09-08

NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 12245
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Pred. No. 51;
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Score 30; DB '
Pred. No. 17;
0; Mismatches
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12245
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Description	Sequence 4, Appli Sequence 95, Appl Sequence 3, Appli Sequence 2, Appli Sequence 2, Appli Sequence 1626, Ap
SUMMARIES ID	9 US-09-899-276-4 19 US-10-283-975A-95 19 US-10-685-705-3 19 US-10-685-705-4 22 US-10-833-656-2 15 US-10-311-455-1626 15 US-10-311-455-1625
DB	19 19 15 15 15
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APPLICANT: Soto, Ubaldo
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APPLICANT: Cov. Johannes
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                                                                        ; Sequence 4, Application US/09899276
; Patent No. US20020106355A1
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US-09-899-276-4
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                                                                                                                                                                    GAAGGTAAGCTGGCAGCCTGACATGCTTTCATCTAGTTTCCTCGCTTCCTTTT 180
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AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 95, Application US/10283975A
; Sequence 95, Application US/20040110792A1
; Publication No. US20040110792A1
; GENERAL INFORMATION:
    APPLICANT: Ortho-Clinical Diagnostice, Inc.
    APPLICANT: Ortho-Clinical Diagnostice, Inc.
    TITLE OF INVENTION: Methods For Assessing and Treating Leukemia TITLE OF INVENTION: Methods For Assessing and Treating Leukemia CURRENT PILING DATE: 2002-10-30
    CURRENT FILING DATE: 2002-10-30
    PRIOR PILING DATE: 2001-10-30
    PRIOR FILING DATE: 2001-10-30
    PRIOR FILING DATE: 2001-10-30
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Best Local Similarity 100.0%; Pred. No. 1.5e-72;
Matches 250; Conservative 0; Mismatches 0;
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241 TGTGGTCAGT 250
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US-10-283-975A-95
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US-10-283-975A-95
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Sequence 4, Application US/10685705
; Sequence 4, Application US/10685705
; Publication No. US20040177387A1
; GENERAL INFORMATION:
; APPLICANT: UNIVERSITY of Kentucky Research Foundation
APPLICANT: UNIVERSITY MADALI
; TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular
; TITLE OF INVENTION: Degeneration
FILE REFERENCE: 050229-0415
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/422,096
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Version 3.2
; SEQ ID NO 4
        Sequence 3, Application US/10685705
; Sequence 3, Application US/10685705
; Sequence 3, Application No. USZO04017387A1
; Publication No. USZO04017387A1
; GENERAL INFORMATION:
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Kentucky Research Foundation
TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related
TITLE OF INVENTION: Degeneration
FILS REFERENCE: 050229-0415
; CURRENT APPLICATION NUMBER: 60/422,096
; PRIOR APPLICATION NUMBER: 60/422,096
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NOS: 2002-10-30
; SEQ ID NOS: 2002-10-30
; SEQ ID NOS: 2002-10-30
; SEQ ID NOS: 2002-10-30
; SEQ ID NOS: 2002-10-30
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2427 TCTGCAGTTTTCGCTTCACAGAAAGAGAGAATCCTTAAAAATAACCCTCTTAGTTCACATC
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Best Local Similarity 100.0%; Pred. No. 5.1e-72;
Matches 250; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 250; DB 19;
Best Local Similarity 100.0%; Pred. No. 2.9e-72;
Matches 250; Conservative 0; Mismatches 0;
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CRGANISM: Homo sapiens
US-10-685-705-4
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CRGANISM: Homo sapiens
US-10-685-705-3
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RESULT 3
US-10-685-705-3
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Sequence 1626, Application US/10311455

Sequence 1626, Application US/10311455

Publication No. US20030143606A1

GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DIEPENBROCK, Christian
APPLICANT: DIEPENBROCK, Christian
APPLICANT: DIEPENBROCK, Christian
APPLICANT: DIEPENBROCK, Christian
APPLICANT: DIEPENBROCK, Christian
APPLICANT: DISPENBROCK, Christian
APPLICANT: DISPENBROCK, Christian
APPLICANT: DIAGNOCK, Christian
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2000-10-702
PRIOR PILING DATE: 2000-00-01
PRIOR PILING DATE: 2000-00-01
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1626
LENGTH: 5926
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215 TCCTGCAGTTTTTCGCTTCAGAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACAT 274
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ORGANISM: Artificial Sequence
                                                                                      275 CTGTGGTCAGT 285
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US-10-311-455-1626/c
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Sequence 2, Application US/10833656

Publication No. US20050148507A1

GENERAL INFORMATION:

APPLICANT: Wandl, Robert

APPLICANT: Doods, Henri

APPLICANT: Lenter, Martin

APPLICANT: Sediler, Randolph

TITLE OF INVENTION: Chemotactic factor

TITLE OF INVENTION: Chemotactic factor

TITLE OF INVENTION: Chemotactic factor

TITLE OF UNDENTION: UNDER: US/10/833,656

CURRENT FILING DATE: 2004-04-28

NUMBER OF SEQ ID NOS: 4
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                            NOSO AGGCTTCTATGATGCTACTATTCTGCATTTGAATGAGCAAATGGATTTAATGCATTGTCA
                                                                                                      7110 GGGAGCCGGCCAAAGCTTGAGAGCTCCTTCCTGGCTGGGAGGCCCCTTGGAATGTGGCCT
                                                                                                                                                           GAAGGTAAGCTGGCAGCGAGCCTGACATGCTTTCATCTAGTTTCCTCGCTTCCTTTC
                                                                                                                                                                                     TCTGCAGTTTTCGCTTCACAGAAAGCAGAATCCTTAAAAATAACCCTCTTAGTTCACATC
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95.0%; Score 237.4; DB 22; Length 2776;
Best Local Similarity 99.2%; Pred. No. 4.4e-68;
Matches 249; Conservative 0; Mismatches 1; Indels 1;
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NAME/KEY: misc_feature
LOCATION: (2585). (2585)
OTHER INFORMATION: n = c, a, t or
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SEQ ID NO 2
LENGTH: 2776
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LOCATION: (2582)..(2582)
OTHER INFORMATION: n = c, a
FEATURE:
LOCATION: (2583)..(2583)
OTHER INFORMATION: n = c, a
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TYPE: DNA
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publication No. US20020198371A1

general INFORMATION:

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Delymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT APPLICATION NUMBER: US 60/218,006

PRIOR PLING DATE: 2000-07-30

PRIOR PLING DATE: 2000-07-30

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-11-23

PRIOR PLING DATE: 1999-109-28

PRIOR PLING DATE: 1999-109-28

PRIOR PLING DATE: 1999-08-28

PRIOR PLING DATE: 1999-08-28

PRIOR PLING DATE: 1999-08-28

PRIOR PLING DATE: 1999-08-28

PRIOR PLING DATE: 1999-08-38

PRIOR PLING DATE: 1999-08-38

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64.2%; Score 160.4; DB 15; Length 5926;
Best Local Similarity 77.6%; Pred. No. 2.7e-42;
Matches 194; Conservative 0; Mismatches 56; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                    ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1625
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-06-30
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 1625
; LENGTH: 5926
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Artificial Sequence
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; ORGANISM: Human
US-10-027-632-121412
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Iclantification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR PAPLICATION NUMBER: US 60/218,006
FRIOR APPLICATION NUMBER: US 60/198,676
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR APPLICATION NUMBER: US 60/193,483
FRIOR PILING DATE: 2000-03-29
FRIOR APPLICATION NUMBER: US 60/187,363
FRIOR FILING DATE: 1999-11-23
FRIOR PILING DATE: 1999-11-23
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-28
FRIOR FILING DATE: 1999-09-09-8
FRIOR FILING DATE: 1999-09-09-8
FRIOR PILING DATE: 1999-09-09-09-9
FRIOR APPLICATION NUMBER: US 60/146,002
FRIOR PILING DATE: 1999-09-09-09-09-09-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-09-00-
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Sequence 137, Application US/1032281

Publication No. US20040126762A1

GENERAL INFORMATION:

APPLICANT: David W. Morris

APPLICANT: Marc S. Malandro

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

FILE REPERBNCE: 529452001000

CURRENT APPLICATION NUMBER: US/10/322,281

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 137

LENGTH: 109559
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      Query Match
Best Local Similarity 100.0%; Pred. No. 1.6e-05;
Matches 49; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(109559)
OTHER INFORMATION: n = A,T,C or G
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US-10-322-281-137/c
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Sequence 1357, Application US/10723860

| Publication No. US20040253606A1
| GENERAL INFORMATION:
| APPLICANT: Aziz, Natasha
| APPLICANT: Zlotnik, Albert
| TITLE OF INVENTION: Methods of Diagnosis of Soft Tissue Sarcoma, Compositions of TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators | TITLE OF INVENTION: Methods for Screening for Soft Tissue Sarcoma Modulators | CURRENT APPLICANTION NUMBER: US/10/723,860 | CURRENT PILING DATE: 2003.11-26 | PRIOR PILING DATE: 2003.11-26 | PRIOR APPLICATION NUMBER: 60/429,739 | WINDER OF COLDINATION OF COLDINA
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                                     APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
FILE REPERENCE: GIN 6403
CURRENT APPLICATION NUMBER: US/09/822,849A
CURRENT FILING DATE: 2001-09-04
PRIOR PILING DATE: 2000-04-06
NUMBER OF SEQ ID NOS: 598
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 572
LENGTH: 673
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; Pred. No. 30;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        / Match 13.4%; Score 33.6; DE Local Similarity 52.9%; Pred. No. 1.9; Nes 72; Conservative 0; Mismatches
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US-10-027-632-45154
; Sequence 45154, Application US/10027632
; Publication No. US20020198371A1
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SOFTWARE: Patentin version 3.2
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Best Local Similarity 57.00
The S9; Conservative
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US-09-822-849A-572
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US-10-723-860-1357
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TGGGAGGCCCCTTGGAATGTGGCCTGAAGGTAAGCTGGCAGCGAGCCTGACATGCTTTCA 155
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Fatent No. US20020132237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FREESEQ for Windows Version 4.0
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                                                                                                                                                                                     Indels
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                                                                                   Score 36.4; DB 19;
Pred. No. 1.9;
0; Mismatches 71;
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Sequence 572, Application US/09822849A

; Patent No. US20020045170A1

; GENERAL INFORMATION:
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APPLICANT: Clark, Hilary
APPLICANT: Fechtel, Kim
APPLICANT: Agostino, Michael J.
APPLICANT: Howes, Steven H.
APPLICANT: Reenick, Richard J.
APPLICANT: Gulukota, Kamalakar
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OTHER INFORMATION: n = A,T,C or
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ilarity 55.6%;
Conservative
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                                                                     Query Match
Best Local Similarity
Matches 90; Conserv
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-09-867-701-9824/c
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US-10-322-281-137
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LENGTH: 165
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1 Sequence 45164, Application US/10027632

2 Sequence 45164, Application US/10027632

3 Sequence 45164, Application No. US20030204075A9

3 GENERAL INFORMATION:

4 APPLICANT: Wang, David G.

7 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

7 TITLE OF INVENTION: POLYMorphisms in the Human Genome

7 TITLE OF INVENTION: 10827.129

7 CURRENT FILING DATE: 2002-04-30

7 CURRENT APPLICATION NUMBER: US 60/218,006

8 PRIOR FILING DATE: 2000-07-12

8 PRIOR PLING DATE: 2000-07-12

9 PRIOR PLING DATE: 2000-03-29

8 PRIOR PLING DATE: 2000-03-29

9 PRIOR PLING DATE: 2000-03-24

9 PRIOR PLING DATE: 2000-02-24

9 PRIOR PLING DATE: 1909-01-32

9 PRIOR PLING DATE: 1909-02-34

9 PRIOR PLING DATE: 1909-11-23

9 PRIOR PLING DATE: 1999-11-23

9 PRIOR FILING DATE: 1999-11-23

9 PRIOR FILING DATE: 1999-09-28
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR PILING DATE: 2000-03-24
PRIOR PLING DATE: 2000-02-4
PRIOR PLING DATE: 2000-02-4
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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Pred. No. 3.2;
1; Mismatches
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SGFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 45154
LENGTH: 504
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48.4%;
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                                                                                                       ; TYPE: DNA
; ORGANISM: Human
US-10-027-632-45154
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BX649242 Zebrafish CR354585 Banio ver AC106158 Rattus no AC127389 Homo sapi AC102789 Mus muscu AC07339 Homo sapi AC102789 Mus muscu AC07339 Homo sapi AC112685 Mus muscu AC156126 Necator a AJ556128 Necator a AJ556128 Necator a AJ556124 Necator a AJ556124 Necator a AJ556124 Necator a AJ556124 Necator a AJ556124 Necator a AJ556124 Necator a AJ556124 Necator a AJ556124 Necator a AJ556130 Necator a AJ56131 Mouse DNA
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BX649242 Zehrri
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Regulatory sequences of the human mcp-1 gene
Patent: EP 1170372-A 5 09-JAN-2002;
DETTSCHES KREBSFORSCHUNGSZENTRUM STIFTUNG DES OEFFENTLICHEN RECHTS (DE)
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 5 from Patent EP1170372.
AX343332
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AF515531 Homo sapi
AC005549 Homo sapi
XY357296 Homo sapi
XY3873 Homo sapien
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12055.236 Million cell updates/sec
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          GenCore version 5.1.6
(c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                      4708233 seqs, 24227607955 residues
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Listing first 45 summaries
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3. (bases 1 to 3227)
Ueda, A., Okuda, K., Ohno, S., Shirai, A., Igarashi, T., Matsunaga, K.,
Tekushima, J., Kawamoto, S., Ishigatsubo, Y. and Okubo, T.
Fukushima, J., Kawamoto, S., Ishigatsubo, Y. and Okubo, T.
Fukushima, J., Kawamoto, S., Ishigatsubo, Y. and Okubo, T.
Chemoattractant protein 1 gene
Chemoattractant protein 1 gene
J. Immunol. 153 (5), 2052-2063 (1994)
                                                                                       241 TCCCTTGGAAATTAAGAAGGAAGCCAGGAGCATAGCTGCCATAACCAGGAATGAACTTCT 300
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (gites) ....... Stier, P., Ernst, T. and Wong, G.G. The human homolog of the JE gene encodes a monocyte secretory protein.
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Homo sapiens (human)
Homo sapiens
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90097880
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

Mammalia; Eucheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 9174).

Rieder, M.J., Armel, T.Z., Carrington, D.P., Ozuna, M., Kuldanek, S.A., Rajkumar, N., Toth, B.J., Yi,Q. and Nickerson, D.A.

Direct Submission

Submission

Sciences, University of Washington, Submitted (06-JUN-2002) Genome Sciences, University of Washington, Submission

To cite this work please use: SeattleSNPS. NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: Location) Qualifiers

http://pga.gs.washington.edu).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9174 bp DNA linear PRI 09-JUL-2002 Homo sapiens small inducible cytokine A2 (monocyte chemotactic AF519531
                                                                                                                                                                                                                                                                                                                                                                                                                                       1892 AACTGAGGAATGAAGGTTACGAATTCCGGAAATACTCCTCCACTGCTTACTCATG 1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1952 TCCCTTGGAAATTAAGAAGGAAGCCAGAGCATAGCTGCCATAACCAGGGATGAACTTCT 2011
                                                                                                                                                                                                                                                                                                                                                                         1831
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                                                                                                                                                                                                              0; Indels
                                                                                                                                                                    Query Match
Best Local Similarity 100.0%; Pred. No. 4.4e-83;
Matches 300; Conservative 0; Mismatches 0;
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/replace="g"
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/replace="g"
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/gene="SCYA2" /product="small inducible cytokine A2 (monocyte chemotactic protein 1) CDS (4118, 4193,4990, .5107,5490, .5595)	<pre>/gene="SCYA2" /codon_start=1 /product="small inducible cytokine chemotactic protein 1)" /protein id="AAMS4046.1"</pre>	/db_xref="G1:2143597" /translation="MKVSAALLCLLLIAATFIPGGLAQPDAINAPVTCCYNFTNRKIS VQRLASYRRITSSKCPKBAVIFKTIVAKBICADPKQKWVQDSMDHLDKQTQTPFKT" 496 4409	repeat_region 1250. 14109 /rpt_tamily="MIR" /rpt_type=dispersed	/gene="SCXA2" /freplace=""0.26" /replace="" repeat region 47774814	~~ 4 .	/gene="SCYA2" /frequency="0.14" /replace="g" 6/10		variation 5132 /gene="C" /gene="SCYA2" /formang:/"0 01"	/rrequency="0.01" /rplace="t" variation 5660				uon.	repeat_region 6837. 6916 /rpt_family="L2" /rpt_type=dispersed	/requency="0.07" /replace="t"		Variation /614 /frequency="0.01" /replace="a" variation 7659				variation 8072 $/$ Frequency="0.01"
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Ye,W.J., Zhao,J. and Zody,M.

**Librate Submission

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**Librate Research, 320 Charles Street, Cambridge, MA 02141, USA

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Barren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Boutwall, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collymore, A., Cooke, P., Corliss, D., Depayre, E., Devon, K., Dewar, K., Donelan, L., Ferreira, P., FitzHugh, W., Forrest, C., Furke, K., Gage, D., Gardyna, S., Gerajery, K., Grant, G., Jacoto, L., Jones, C., Kann, L., Karatas, A., Lehoczky, J., Mardens, M., Morton, D., Howland, J.C., Jacoto, L., Molla, M., Morris, W., Modur, M., Morla, M., Morrow, J., Mychalecky, J., Nahle, M., Morris, W., Morrow, J., Mychalecky, J., Stange-Thomann, M., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Ye, W.J., Zhao, J., and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Ye, W.J., Zhao, J. and Zody, M., Wheeler, J., Wu, Y., Wyman, D., Direct, Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (22-SEP-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA ON Sep 13, 1998 this sequence version replaced gi:3581743. All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Only the first 147416 bases of this clone are being submitted Bases 145417-155040 overlap accession number AC004147 (WICGR project L228). The first 2Xb of the overlapping region are submitted to confirm overlap.

Location/Qualifiers
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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2. 69
/rpt_family="BUR1"
490. 695
/rpt_family="LiME2"
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Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
AC005549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2757 AAGGAGGAGCACTGGGCTAGGAGAATCGAGAGATCAGAATTTTAAACTCAGCCCAGCCA 2816
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Homo sapiens
Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 147416)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 AAGGAGGAGCAGTGGGCTAGGAGAATCGAGAGATCAGAATTTTAAACTCAGCCCAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1.4e-82;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 298.4;
Pred. No. 1.4
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8597.
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Best Local Similarity 99.7
Matches 299; Conservative
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AC005549/c
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complement(5430...5549)
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complement(5941...6051)
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6131...6250
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39362. 39344
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40112. 40151
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25613. 25758
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7393. .18306
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8315. .24307
family="MLT1I"
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(2501. 12001
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2601. .32902
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62598 AACTGAGGAATGAAGTCAGGCTTTCCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG 62539
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Homo sapiens MCP1 (MCP1) gene, promoter region and partial cds.
AY357296
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2 (bases 1 to 3221)
Nyquist, P.A. and Degraba, T.J.
Direct Submission
Submitted (31-JUL-2003) Medicine, Inova Fairfax, 3300 Gallows Road, Falls Church, VA 22402-3300, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.

(bases 1 to 3221)

Nyquist, A. and Degraba, T.J.

Two New Single Nucleotide Polymorphisms (SNPs) in the MCP-1

Promoter in Patients with Carotid Atherosclerosis: Transcriptional Induction and New Protein Binding Sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 TCCCTTGGAAATTAAGAAGGAAGCCAGGAGCATAGCTGCCATAACCAGGGATGAACTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
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Best Local Similarity 99.7%; Pred. No. 1.6e-82;
Matches 299; Conservative 0; Mismatches 1; Indels
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46184. 46296
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complement (41846. .4156)

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/rpt family="MLT11"

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complement (48165, .48209)
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DEFINITION
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KEYWORDS
SOURCE
ORGANISM
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AY357296
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Euteleostomi;

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/protein_id="CAC14049.1"
/db_xxef="G1:10933861"
/db_xxef="GA:110933861"
/db_xxef="CA:110933861"
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/translation="MKVSAALLCLILIAATPIPQGIAQPDAINAPVTCCYNFTNRKIS"
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Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HPV B positive cells: the role of the chromatin structure and AP-1 composition
Oncogene 19 (29), 3235-3244 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKFZ
(German Cancer Research Institute), Im Neuenheimer Feld 506, 69120
                                                                                                                                                                 Finzer, P., Soto, U., Delius, H., Patzelt, A., Coy, J.F., Poustka, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          join(7610. .7685,8468. .8585,8968. .9073)
/gene="MCP-1"
                  MCP-1 gene; monocyte chemoattractant protein-1.
Homo sapiens (human)
Homo sapiens
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225. >>3221
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overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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------- Project Information
Center project name: 15499
Center clone name: 329_H_16
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Location/Qualifiers other sequences; artificial sequences AX346554.1 GI:18494440 Query Match 68.0%; Best Local Similarity 80.0%; Matches 240; Conservative (94.9%; synthetic construct synthetic construct Query Match
Best Local Similarity 99.0
Matches 297; Conservative 121 181 241 121 61 50196 AX346554 LOCUS DEFINITION source ORGANISM TITLE JOURNAL ACCESSION AUTHORS KEYWORDS SOURCE REFERENCE FEATURES VERSION RESULT ORIGIN g 셤 ò 셤 ò 셤 ઠ 셤 ò 셤 à 원 ò 셤 ò ਨੇ 셤 ò à

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Alberta, J.A., Irminger, J. and Stiles, C.D.
Macrophage chemoattractant protein-1 (mcp-1) S' flanking region Unpublished
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chemokine, mcp-1, macrophage chemoattractant protein-1.
Mus musculus (house mouse)
Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 3405;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 87.6; DB 4;
Pred. No. 2.7e-16;
0; Mismatches 69;
                                                                                                                                                                 /number=1
|oin(1403. .1478,2227.
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                                                                                                        /note="putative"
1342. .1478
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                                                                                                                                                                                                                                                                                                                                                                                                                        2227. .2344
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3202. .3207
/gene="MCP-1"
                                                                     2695. .3227
/gene="MCP-1"
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/gene="MCP-1"
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29.2%;
Best Local Similarity 67.9%;
Matches 152; Conservative (
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                                                      PAT 01-FEB-2002
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Wempe, F., Kuhlmann, J.K. and Scheit, K.H.
Characterization of the bovine monocyte chemoattractant protein-1
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                            /ordanism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
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94338337
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                                                      linear
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                                        5926 bp DNA Sequence 1626 from Patent W00200928. AX346555.
                                                                                                                                          synthetic construct
synthetic construct
other sequences; artificial sequences.
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monocyte chemoattractant protein-1.
Bos taurus (cow)

    .3405
    /organism="Bos taurus"

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Mus musculus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 160869)

2 Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Harris, C.,

Dederich, D., Thomas, S., Okwuonu, G., Garlock, C., Garner, T.,

Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J.,

Buhay, C., Davis, C., Delgado, O., Ding, Y., Ougan-Rocha, S.,

Fernandez, C., Perzaguto, D., Forcum-Tansey, J., Gill, R.,

Gorrell, J. H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M.,

Hosak, H., Hou, X., Huber, J., Jackson, L., Jaz, Y., Kelly, J., Kovar, C., Liu, J., Luiu, W., Lozado, R.J., Martin, R.,

Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S.,
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), *** SEQUENCING IN PROGRESS ***, 32
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                   Rollins, B.J., Morrison, B.D. and Stiles, C.D.
Cloning and expression of JE, a gene inducible by platelet-derived
growth factor and whose product has cytokine-like properties
Proc. Natl. Acad. Sci. U.S.A. 85 (11), 3738-3742 (1988)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                       Alberta, Submission
Submitted (20-JUL-1994) John A. Alberta, Cellular and Molecular
Biology, Dana Farber Cancer Institute and Harvard Medical School,
44 Binney St., Boston, MA 02115, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AAGGAGGAGGCAGTGGGCTAGGAGAATCGAGAATCAGAATTTTAAACTCAGCCCAGCCA
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/gene="mcp-1"
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59.7%; Pred. No. 4e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="Balb/c 3T3 A31"
/cell_type="fibroblast"
2788
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/organism="Mus musculus"
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/strain="Balb/c"
/db_xref="taxon:10090"
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Mus musculus clone RP23-433D8,
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Alberta, J.A.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
Contact: hgsc-help@bcm.tmc.edu

Center project Information
Center clone name: RP23-43D8
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NOTE: This is a 'working draft' sequence. It currently consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                       Worley,K.C.
Direct Submission
Submitted (29-JAN-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
On Oct 14, 2001 this sequence version replaced gi:11079355.
Neal,D., Nelson,A., Nguyen,R., Nguyen,N., Oguh,M., Parish,B., Perez,L., Reiter,D., Say,J., Shen,H., Vasquez,L., Watlington,S. Williamson,A., Wrensford,G., Zhou,X., Bouck,J., Hodgson,A., Muzny,D.M., Rives,M., Scherer,S., Sodergren,E., Weinstock,G., Worley,K. and Gibbs,R.
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Consensus quality: 143665 bases at least Q40
Consensus quality: 160562 bases at least Q20
Consensus quality: 160562 bases at least Q20
Consensus quality: 164105 bases at least Q20
Estimated insert size: 194000; pulse field gel estimation
Estimated insert size: 17634; sum-of-contigs estimation
Quality coverage: 6.92 in Q20 bases; pulse field gel estimation

* NOTE: This is a 'working draft' sequence. It currently

* consists of 48 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* trus of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
                                                                                                                                                                                                    2 (bases 1 to 180944)

DOB Joint Genome Institute.

Direct Submission

Submitted (29-JUN-2000) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA

-----Genome Center

Center: Joint Genome Institute
      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.inae; Mus. I (bases I to 180944)
DOB Joint Genome Institute.
Sequencing of Mouse
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Center clone name: RPCI-23_92G22
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Web Bite: http://www.jgi.doe.gov
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Mus musculus clone RP23-92G22, WORKING DRAFT SEQUENCE, 48 unordered
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/clone="RP23-433D8"
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RG Birren, B. Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Blivren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhqalter, B., Brown, A., Castle, A., Calangelo, M., Collins, S., Collymore, A., Bardwin, J., Bradan, L., Doyle, M., Ferreira, P., PitzHugh, W., Porrest, C., Funke, R., Gage, D., Galdgan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kam, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kam, L., Karatas, A., Klein, J., Howland, J.C., Johnson, R., Jones, C., Kam, L., Sartos, R., Severy, P., Stange-Thoman, P., McGurk, A., Norman, C.H., O'Connor, T., O'Domell, P., Stange-Thoman, N., Stojanovic, N., Subramanian, A., Talamas, J., Tartell, A., Vasailiev, H., Vo, A., Wheeler, J., Wu, X., Wyman, D. Ye, W. J., Zimmer, A. and Zody, M.

Loudission Street, Cambridge, MA 02141, USA

Submitted (122-007-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CE Johnson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Anderson, S., Brown, N., Collins, S., Collymore, A., Cooke, N., Dakrellano, K., Dewar, K., Diaz, J.S., Dodge, S., Cook, S., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Gord, S., Goyette, M., Gage, D., Galagan, J., Gardyna, S., Rarteira, P., Eitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Horton, L., Hulme, W., Iliev, I., Johnson, R., Machems, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., Macdonald, P., Major, J., Warquis, N., Walbers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuers, S., Schuer, S., Schuer, S., Schuer, S., Schuer, S., Schuer, S., Schuer,
   130696 CTGGCACGCATGTGAGAGCGCCACTCTTTTTAT-----CAAGAGTCTGCTGAAATGAAT 130749
                                                                                                                 AC012294 222121 bp DNA linear ROD 27-MAR-2002 Mus musculus chromosome 11, clone RP23-328G11, complete sequence.
                                                                        TCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGCAC 180
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Birren, B., Linton, L., Nusbaum, C. and Lander, E. Mus musculus chromosome 11, clone RP23-328G11
                                                                                                                                                                                                                                         181 AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCC 226
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Query Match 22.7%; Score 68; DB 2; Length 180944; Best Local Similarity 59.7%; Pred. No. 4.6e-10; Matches 135; Conservative 0; Mismatches 85; Indels 6

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complement (30238, .30446)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (27-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 25, 2002 this sequence version replaced gi:19683729. All repeats were identified using Repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center: Whitehead Institute/ MIT Center for Genome Research
Research, 320 Charles Street, Cambridge, MA 02141, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
------ Project_Information
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403. 560
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6718. .6747

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complement(7561. .7875)

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Center clone name: 328 G 1
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1965. .4300
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                                     12782 gaaadcrdaatraadccadacatrccactrdactrcactcatggtcc 12737
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On Nov 30, 2001 this sequence version replaced gillfoots.

On Nov 30, 2001 this sequence version replaced gillfoots.

On Nov 30, 2001 this sequence version replaced gillfoots.

Where differences are found these are annotated as variations where differences are found these are annotated as variations where differences are found these are annotated as variations wereation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with conficient as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-etranded or sequenced with an alternate regions were either double-etranded or sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the one plasmid subclone or more than one M13 subclone; and the one plasmid subclone or more than one M13 subclone; and the sastembly was confirmed by restriction dispet. The following assembly was confirmed by restriction dispet. The following subscending are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, in the feature table with their source databases: Em:, EMBL; Sw:, http://www.sander.or.uk/Droiects/C elecans/wormper RP23-35061 is
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                                                                                                                                                                                                                                                                                                                                                  103664 ichaalgechircaanirirahcechrigancacacretricreaadaahchaaccre 103605
                                                                                                                                 AL626807 223726 bp DNA linear ROD 05-APR-2002
Mouse DNA sequence from clone RP23-350G1 on chromosome 11, complete
sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus.
                                                                                                      9
                                                                                                                                                                                                    61 TIPACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT
                                                                                                1 AAGGAGGAGGAGTGGGCTAGGAGAATCGAGGATCAGAATTTTAAACTCAGCCA
                                                        Gaps
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                                                        85; Indels
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Pred. No. 4.6e-10;
                                  Pred. No. 4.6e-10;
0; Mismatches 85
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/mol_type="genomic DNO"
/db_xref="taxon:10090"
/chromosome="l1"
/clone="RP23-350G1"
/clone_lib="RPCI-23"
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Mammalia, Eutheria, Rodentia;
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AL626807.7 GI:17221258
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                                           59.78;
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Eukaryota; Metazoa;
                                                                   Matches 135; Conservative
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                                             Best Local Similarity
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AL626807/c
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KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
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August 3, 2005, 15:09:47; Search time 198.826 Seconds (without alignments) 8932.047 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                      OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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1. genesequ1980s:*

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300
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
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Result	,	Query	•			
S S	Score	Match	Match Length DB	80	ID	Description
-	300	100.0	300	9	ADH13942	Adhi3942 Human mon
7	296.8	98.9	3221	12	ADN12120	Adn12120 MCP1 gene
e	296.8	98.9	3221	12	ADO03802	Ado03802 Human Cc1
4	296.8	98.9	11793	12	ADO03803	Ado03803 Human Cc1
S	204	68.0	5926	9	ABL33652	Abl33652 Human imm
9 0	194.4	64.8	5926	9	ABL33653	Abl33653 Human imm
C 7	36.8	12.3	204621	11	ACN44486	Acn44486 Human gen
ω υ	35.4	11.8	2122	9	ABK52382	Abk52382 DNA encod
٥ ن	35	11.7	32186	ഹ	AAS34422	Aas34422 Human DNA
c 10	35	11.7	38855	12	ADN41808	Adn41808 Novel hum
11	34.4	11.5	110000	9	ABX08336_07	Continuation (8 of
12	34.4	11.5	110000	12	ADJ25985 07	Continuation (8 of
13	34.4	11.5	110000	12	ADN97989_07	Continuation (8 of
14	34.4	11.5	110000	12	ADO50281_07	Continuation (8 of
c 15	33.8	11.3	2268	Ŋ	AAS70462	Aas70462 DNA encod
c 16	33.8	11.3	2268	Ŋ	AAS72056	Aas72056 DNA encod
c 17	33.6	11.2	693	œ	ACA30296	Aca30296 Prokaryot
18	33.2	11.1	344548	11	ACN44070	Acn44070 Human gen
19	32.8	10.9	17918	9	AAS61419	Aas61419 Human gen
c 20	32.8	10.9	36485	4	AAK74751	Aak74751 Human imm

Aak68958 Human imm	Adk72196 Antimicro	Adk72243 Antimicro	Aal04311 Human rep	Aag82848 P-selecti	Aaa34926 Human ade	Aaf21048 Human low	Abz96742 Human nuc	Abd20591 Human pul	Aas33411 DNA encod	Abg77404 Human SEL	Acn44286 Human gen	Adq97337 Human can	Adq59207 MSI-H car	Aah30439 Human col	Aak73470 Human imm	Aak73471 Human imm	Adg97473 Human can	Acn44322 Human gen	Acn45154 Human gen	Adg47889 Arabidops	Adk61209 Ovarian c	Aah32965 Human col	Abl17530 Drosophil	Aas12439 DNA encod
AAK68958	ADK72196	ADK72243	AAL04311	AAQ82848	AAA34926	AAF21048	AB296742	ABD20591	AAS33411	ABQ77404	ACN44286	ADQ97337	2 ADQ59207	AAH30439	AAK73470	AAK73471	ADQ97473	·	-		ADK61209	AAH32965	ABL17530	AAS12439
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10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.9	10.8	10.8	10.8	10.8	10.8	10.8	10.7	10.7	10.7	10.7	10.7
32.8	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.4	32.4	32.4	32.4	32.4	32.4	32.2	32	32	32	32
c 21	22	23	24			c 27		c 29	30	c 31	32	33	34		c . 36		c 38	39	40	c 41	42	c 43	44	45

ALIGNMENTS

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RESULT 3
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                                                                                                                                                   TTAACATGCCTCAAGTACTCCTATCATTTTGTAAGAGACAACAGTTCACTGAAATGAAT 120
                                                                                                                                                                     rraacardecticaagracticcraticaratrigraagagacaacagricactgaaargaar 120
                                                                                                                                                                                                                                                                                                                                                                                                                    major histocompatibility class I; MHC-I; MHC-II; Cytostatic;
EBV-associated cancer; Hodgkin's lymphoma, nasopharyngeal carcinoma;
gastric carcinoma; Burkitt's lymphoma; T-cell lymphoma; B-cell lymphoma;
parotid carcinoma; breast carcinoma; leiomyosarcoma; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human cell line modified to comprise and express genes encoding immunomodulators and an antigen of Epstein-Barr virus (EBV), useful for inducing or stimulating an immune response in a human to EBV-associated
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     the treatment
                                                                                                                                                                                                                                                                      TCCCTTCGAAATTAAGAAAGGAAGCAGGAGCATAGCTGCCATAACCAGGATGAACTTCT
                                                                                                                                                                                          TCTAAGGTCTTTGGGTTTTTATCAGTGTGCCTTCTGTAGTTTCTGAGGAAATCTAAGGCAC
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                                                                                                                                                                                                                                              1 AAGGAGGAGGCAGTGGGCTAGGAGATCGAGAGTTCAGAATTTTAAACTCAGCCCAGCCA
                                                                                                                         pharmaceutical composition of the invention is useful for the treat of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
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                                                                          Length 300;
                                                                                            0; Indels
                                                    Sequence 300 BP; 92 A; 62 C; 67 G; 79 T; 0 U; 0 Other;
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                                                                         100.0%; Score 300; DB 6;
100.0%; Pred. No. 4.6e-86;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                               BP
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                                                                                                                                                                                                                                                                                                                                              ADN12120 standard; DNA; 3221
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                                                                                                Conservative
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                                                                                      Similarity
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                                                                              Query Match
Best Local Simil
Matches 300; C
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gene encoding an antigen of Epstein-Barr virus (EBV). The human cell line, compositions and methods are useful for inducing or stimulating an immune response in a human to an EBV-associated cancer, where the human has or is at risk for Hodgkin's lymphoma, nasopharyngeal carcinoma, gastric carcinoma, Burkitt's lymphoma, T-cell lymphoma, B-cell lymphoma, parotid carcinoma, breast carcinoma, and leiomyosarcoma. The present sequence represents a nucleotide sequence associated with the cell line
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Testing candidate drug for treating age-related macular degeneration, administering drug to Cc12-deficient, Ccr2-deficient knockout mouse, a malyzing development or regression of drusen and/or lipofuscin accumulation in eye.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGCAC
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                                                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                      Length 3221;
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                                                                                                                                                                                                        Sequence 3221 BP; 859 A; 793 C; 727 G; 842 T; 0 U; 0 Other;
                                                                                                                                                                                                                                            Score 296.8; DB 12; Dred, No. 1.38-84; Dred, No. 1.38-84; Dreds
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                                                                                                                                                                                                                                                             98.9%;
llarity 99.3%;
Conservative (
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                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 298; Conserv
                                                                                                                                                                              of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1625 AACTGAGGAATGAAGTCAGGCTTTCCCAATTCCCGAAATACTCCTCCACGCTTACTACTCATG 1684
               This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular CC12-deficient, CCr2-deficient and/ or a Cc12-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polymucleotide sequence is the human Cc12 promoter region DNA of the invention.
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                                                                                                                                                                                                                                                                                                 DB 12; Length 3221;
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Pred. No. 1.3e-84;
0; Mismatches 2; Indels
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AAGGAGGAGTGGGCTAGGAGAATCGAGAGATTAAAACTCAGCCCAGCCA 6308
                                                                                                                                                                                                         This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular Ccl2-deficient, Ccr2-deficient and/ or a Ccl2-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polynucleotide sequence is the human Ccl2 gene and enchancer region DNA of the invention.
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neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
acute myeloid leukaemia; Alzaheimer's disease; AIDS; epilepsy;
neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
Cc12-deficient, Ccr2-deficient knockout mouse, and
or regression of drusen and/or lipofuscin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 11793;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
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Pred. No. 2.1e-84;
0; Mismatches 2; Indels
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                                                                                                                                            4; 64pp; English
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Best Local Similarity 99.3%;
Matches 298; Conservative
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administering drug to
analyzing development
accumulation in eye.
                                                                                                                                                Disclosure; SEQ ID NO
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                                                                                                                                                                                                                                                                                                                                                                      of human immune system associated
                                                                                                                                                                                                                                                                                                                                                                The present invention provides a number of human immune system associate genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fragment of chemically modified gene, useful of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5926 BP; 1554 A; 55 C; 1492 G; 2825 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1626; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cytostatic; carcinoma; lymphoma; cancer; human; gene;
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); Mismatches 66;
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78.0%;
                                                                                    30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                02-JUL-2001; 2001WO-EP007537.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                              Nucleic acid comprising diagnosis and treatment
                                                                                                                                                                                     Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACN44486 standard;
                                                                                                                                                 (EPIG-) EPIGENOMICS
                                                                                                                                                                                                                       WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO2003073826-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-2003
                                                                                                                                                                                                                                                                                                        methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Sim
Matches 234;
                  03-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2054
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                                                                                                                                                                                       olek A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3813 TITAAGGTTTTTTGGGTTTTTTATTAGTGTGTTTTTTTGTAGTTTTTGAGGAAATTTAAGGTAT 3872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3933 TTTTTGGAAATTAAGAAGGAAGTTAGGAGATAGTTGTTATAATTAGGGATGAATTTT 3992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAGGAGGAGGTAGTGGGTTAGGAGTTCGAGAGATTAGAATTTTAAATTTAGTTTAGTTA 3752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                  The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGCAC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; immune system disease; cytosine methylation, antiasthmatic; antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antiathritic; antidiabetic; antipsoriatic; antianatory; cancer; eye disease; arteriosclerosis; anaemia; autinflammatory; cancer; eye disease; arteriosclerosis; anaemia; autiminflammatoid leukaemia; Alzheimer's disease; AlDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                       chemically modified gene, useful for associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCCCTTGGAAATTAAGAAGGCAAGGAGCATAGCTGCCATAACCAGGGATGAACTTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAGGAGGAGGAGTGGGCTAGGAGAATCGAGAGTCAGAATTTTAAACTCAGCCCAGCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human immune system associated gene SEQ ID NO: 1626.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.0%; Score 204; DB 6;
80.0%; Pred. No. 1.2e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 1.2e
0; Mismatches
                                                                                                                                                                             Nucleic acid comprising fragment of diagnosis and treatment of diseases
                                                                                                      Berlin K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP.
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        2000DE-01032529
2000DE-01043826
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Best Local Similarity 80.0
Matches 240; Conservative
                                                                                                    ú
                                                                    (EPIG-) EPIGENOMICS AG
                                                                                                        Piepenbrock
                                                                                                                                         WPI; 2002-130909/17
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            30-JUN-2000;
01-SEP-2000;
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Gaps .; 0

Indels

Length 5926;

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1079 Aacriccaacirirgiecericerrecacecercrecierecearirraceaaacearea 1020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1019 CCGAAATTGGGAATTTCGAAGTGCCTTACCATTCCACATATACTCCTGTATCGTGTATATC 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             118 AATTCTAAGGTCTTTGGGTTTTTTATCAGTGTGCTTCTGTAGTTTTCTGAGGAAATCTAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention describes a fucose-specific lectin protein with enzymic activity useful for foodstuffs, drugs and cosmetics. This sequence encodes a fucose-specific lectin protein described in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              178 CACAACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, foetal tissue antigen, ds, antiinflammatory, neuroprotective,
immunomodulator; cardiovascular; cytostatic, nephrothropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fucose-specific lectin protein with enzymic activity useful for foodstuffs, drugs and in cosmetics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2122 BP; 575 A; 484 C; 505 G; 558 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human DNA for a novel foetal antigen, SEQ ID No 1846.
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Pred. No. 1.3;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 3-4; 14pp; Japanese.
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ID AAS34422 Btandard; DNA; 32186 BP.
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Best Local Similarity 54.1%;
Matches 72; Conservative (
                                                                                                                                                                                                 1047. .1148
/*tag= b
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/*tag= b
/number= 5
                                                                                                                                                                                                                                                           149. .1211
                                                                                                               /number= 3
993. .1046
/*tag= c
/number= 3
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/number= 4
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                                                     /number= 2
777. .992
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P-PSDB; AAU97833.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (1) for screening drug candidates; (11) for screening of bioactive agent capable of bioactive agent capable of bioactive agent capable of modulating the activity of CAP; (11) for screening of a bioactive agent capable of modulating the activity of CAP; (11) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (vi) for tasting carcinoma; (vii) for neutralizing the effect of CAP; (vii) for treating carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma are appensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CA genes are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105675 TTCACAGTCAACACAGCAATGAAAGTTTATGAATTTCTCTTTTTATGAGCTTTGAAGACATA 105616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 42 ITTAAACTCAGCCCAGCCATTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACA 101
                                                                                                                                                                                                                    Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fucose-specific lectin protein; enzyme; foodstuff; drug; cosmetic; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 204621 BP; 53683 A; 43334 C; 43489 G; 57468 T; 0 U; 6647 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105615 ATACTTATGGAGACCCAATTCAGAAGTCATGCGATTTTCAGCAGGGTGAGTC 105564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 ACAGTICACTGAAATGAATTCTAAGGICTTTTGGGTTTTTATCAGTGTGTTTTC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Match 12.3%; Score 36.8; DB 11; Length 204621; Local Similarity 58.0%; Pred. No. 2.9; es 65; Conservative 0; Mismatches 47; Indels 0; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a
/product= "fucose lectin protein"
463. .498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding fucose-specific lectin protein.
                                                                                                                                                                                                                                                                                 Claim 1; SEQ ID NO 958; Opp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABK52382 standard; DNA; 2122 BP
               28-FEB-2003; 2003WO-US006235
                                                     01-MAR-2002; 2002US-00087192
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/number= 1
499. .549
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550. .726
/*tag= b
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                                                                                            (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                       WPI; 2003-328604/31
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                                                                                                                                     Morris DW;
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Best Local Si
Matches 65
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cardiovascular, autoimmune disease; rheumatoid arthritis; hyperproliferative disorder; breast neoplasm; cancer; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; cerebral ischaemia; angiogenesis; nervous system disorder; Alzhelmer's disease; infection; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; food additive.
                                                                                                                                                                              2000US-0179065P.
2000US-0180628P.
2000US-0180638P.
2000US-018974P.
2000US-018974P.
2000US-0199133P.
2000US-0218886P.
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2000US-022944P.
2000US-02294P.
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2000US-0232401P.
2000US-0233063P.
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44-FEB-2000; 2

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PR 21-SEP-2000; 2000US-0234274P.
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antiarthritic; antirheumatic; neuroprotective; antianaemic; muscular; antiallergic; antiabethmatic; gastrointestinal; anticoagulant; thrombolytic; antiarteriosclerotic; cardiant; cytostatic; nephrotropic; cardiavatic; respiratory; gene therapy; secreted protein; ochromosome identification; hybrid mapping; gene expression control; immune system disorder; immunodeficiency; Chedlak-Higashi syndrome; autoimmune disease; systemic lupus erythematosus; rheumatoid arthritis; multiple sclerosis; haemolytic anaemia; myasthenia gravis; allergic reaction; asthma: inflammatory condition; inflammatory bowel disease; B cell stimulator; T cell activator;
                                                                                                                                                                    blood-related disorder; eosinophilia; thromboeis; thromboembolism; atherosclerosis; myocardial infarction; angina; anaemia; hyperporliferative disorder; cancer; renal disorder; chronic kidney failure; renal tubular acidosis; kidney stone; cardiovascular disorder; respiratory disorder; human; ds.
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RUBEN S M.
KYAW H.
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ZENG Z.
LAFLEUR D V
MOORE P A.
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(RUBE/
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(LIYY/
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       The invention relates to novel mucleic acids encoding novel human foetal antigens. The nucleic acids and proteins are used to prevent, treat (e.g. by gene therapy) or ameliozate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a condition. The antibodies to the antigens can also be used in alleviating symptoms associated with the disorders and in diagnostic immunosasays e.g. radioimmunosasays or enzyme linked immunosorbent assays (ELISA). Disorders which are diagnosed or treated include autoimmune considers e.g. rheumatoid arthritis, hypoproliferative disorders e.g. cardioral sames of the breast or liver, cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. cardiovascular disorders e.g. pacteria, viruses and fungi and ocular disorders e.g. corneal infection.

The polypetides can also be used to aid wound healing and epithelial coll proliferation, to prevent skin aging due to sumburn, to maintain corgans before transplantation, for supporting cell culture of primary crisques, to regenerate tissues and in chemotaxis. The polypetides can also be used as a food additive or preservative to increase or decrease corgans before transplantation, for supporting cell culture of primary crisques, to regenerate tissues and in chemotaxis. The polypetides can also be used as a food additive or preservative to increase or decrease corgans before transplantation, for supporting cell culture of primary also be used as a food additive or preservative to increase or decrease corgans are given in the specification. The present sequence is a composition of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7072 CTCTAATATACATTTAAAATTTTTCACAATAAAAATTTAAAAATTTTGCCTTGGATCTTT 7013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7012 AATTTTTTACATCACTGCCCATATATÄTTTTCTAAGAAAAATACTGTAAAATTGAATA 6953
                                                                                                                                                                                                        New polynucleotides and polypeptides for diagnosing, treating, preventing or prognosing e.g. diseases or disorders of the nervous, musculoskeletal, excretory, gastrointestinal, reproductive, and respiratory systems.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 CTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAATTCTAAGGTC 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      130 TTTGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGCACAACTGAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immunomodulator; immunosuppressive; antiinflammatory; dermatological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 5; Length 32186;
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53.2%; Pred. No. 5.3;
                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 1846; 642pp; English.
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                                                                                                                                        Ruben SM;
                 08-DEC-2000; 2000US-0251989P.
08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
   2000US-0251869P
                                                                    2001US-0259678P
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1e8 74; Conservative
                                                                                                                                        Barash SC,
                                                                                                                                                                      WPI; 2001-488782/53.
                 08-DEC-2000;
08-DEC-2000;
                                                                     05-JAN-2001;
                                                                                                                                      Rosen CA,
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of ADN97989 from base 700001 (Human phosphodiesterase 4D genomin
17 fragments LOCUS ADN97989 Accession Adn97989
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B LOCUS ADJ25985 Accession Adj25985
End
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                                                                                                                                                                                                       CTTTGGGTTTTTATCAGTGT
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                                                                                                                                                    99904 ritritakaaarraktaartrigaaaarraaaaarctrorritricakoorritraar
                                                                                                                         89 TTTGTAAGAGACAACTTCACTGAAATGAATTCTAAGGTCTTTGGGTTTTTATCAGTGT
                                                                                                                                                                                  GCTTÇTGTAGTTTCTGAGGAAATCTAAGGCACACAAGGAATGAAGTCAGGCTTTCCAA
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                                                                 DB 6; Length 110000;
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Pred. No. 13;
0; Mismatches 61;
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                                                                                                    61;
                                                                                                    0; Mismatches
                                                                    Score 34.4;
Pred. No. 13;
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   1300001
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                                                                                                         Conservative
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ADN97989 07
Continuation (8 of 17) of
Continuation split into 17
WP Sequence split into 17
WP ADN97989 00
WP ADN97989 01
WP ADN97989 02
WP ADN97989 02
WP ADN97989 03
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17
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Continuation (8 of 17) of WP Sequence split into 17 WP Sequence split into 17 WP PADJ25985 00 WP ADJ25985 02 WP ADJ25985 03 WP ADJ25985 04 WP ADJ25985 06 WP ADJ25985 06 WP ADJ25985 06 WP ADJ25985 07 WP ADJ25985 07 WP ADJ25985 07 WP ADJ25985 07 WP ADJ25985 07 WP ADJ25985 07 WP
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Matches 71; Conser
                                                                                              Similarity
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ADJ25985_09
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ADJ25985_15
ADJ25985_16
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       ABX08336_13
ABX08336_14
ABX08336_15
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                                                                                                                                                                                                      The invention describes novel human secreted proteins and the nucleotides concoding them. The polynucleotides are useful in chromosome identification, for radiation hybrid mapping, in controlling gene capression, in gene therapy or as molecular weight markers. The expression, in gene therapy or as molecular weight markers. The colynucleotides and polypeptides are useful for diagnosing, treating or preventing diseases of the immune system, immunodeficienties, e.g. preventing diseases of the immune system, immunodeficienties, e.g. crythematosus, rheumatoid arthritis, multiple sclerosis, haemolytic crythematosus, rheumatoid arthritis, multiple sclerosis, haemolytic crythematory conditions, e.g. inflammatory bowel disease. They can also inflammatory conditions, e.g. inflammatory bowel disease. They can also cryator of T cells. The polynucleotides and polypeptides are also activator of T cells. The polynucleotides and polypeptides are also cuseful for treating or preventing blood-related disorders, e.g. useful for treating or preventing blood-related disorders, e.g. cosinophila, thrombosis, thrombosmbolism, atherosclerosis, myocardial creating, preventing or diagnosing hyperproliferative disorders conforming treating, preventing or diagnosing hyperproliferative disorders can also be used for infarction, unstable angina or anemia. They can also be used for infarction, unstable angina or anemia. They can also be used for infarction, unstable angina or anemia or anemia the disorders can observe the disorders can be or respiratory acidosis or kidney stones), cardiovascular disorders or respiratory acidosis or kidney stones), cardiovascular disorders or respiratory acidosis or kidney stones), cardiovascular disorders or respiratory collaporders. The sequence represents a novel human secreted protein to polynucleotide fragment. Office at the sequence is available in electronic format from the US patent office at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13681 AAİTTITİTİRCAİCÁCTĞCCĞATATAİTİTİTİTİAAĞAAAAAATİCTĞAAAAİTİĞAATA 13622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cicnaarancarraaaarriricacaaraaaaarraaaaarrricccriccarcrir 13682
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 TTTGGGTTTTTATCAGTGTGTGTTCTGTAGTTTCTGAGGAAATCTAAGGCACAATTGAGGA 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CICAAGIACICCIAICAIAITIGIAAGACAACAGITCACIGAAAIGAAITCIAAGGIC 129
                                                                                                    New isolated nucleic acid encoding human proteins, useful for treating, preventing or diagnosing e.g. rheumatoid arthritis, multiple sclerosis, anemia, inflammatory bowel disease, atherosclerosis, cancers, chronic
                                 Ζ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 38855 BP; 11951 A; 6822 C; 6960 G; 13122 T; 0 U; 0 Other;
                                   Zeng
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                                 Soppet DR, Ruben SM, Kyaw H, Li Y,
Shi Y, Olsen H, Ebner R, Birse CE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35; DB 1
Pred. No. 5.7;
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                                                                                                                                                                                      Disclosure; SEQ ID NO 930; 372pp; English.
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1000001
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1 Similarity 53.2%;
74; Conservative (
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Sequence split into 17
                                            Rosen CA,
Moore PA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                    WPI; 2004-225733/21.
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ABX08336 00
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ABXO8336_02
ABXO8336_03
ABXO8336_05
ABXO8336_05
ABXO8336_07
ABXO8336_09
ABXO8336_09
ABXO8336_09
ABXO8336_10
ABXO8336_12
ABXO8336_12
                                                                                                                                                              kidney failure
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ABX08336 07
Continuation (8 c
                                               Fischer CL,
Lafleur DW,
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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed crivity of (II) as useful in gene therapy techniques to restore normal activity of (II) so to treat disease states involving (II). (II) is useful in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations diagnostics, forensics and products dependent on DNA and am to produce other types of data and products dependent on DNA and amino acid sequences has sets terminal diagnostic contact the second of the contact 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        449 CGTGTGTTAAATTCTCCCATTATTATTGTGGGAGTCTAAGTCTCTTTGTAGATCTCTA 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from NIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           125 AGGICITITGGGITITITATCAGIGIGCTICIGIAGTITICIGAGGAAATCTAAGGCACA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              389 Aggaciricerriargaarcinggigericergiaringgigerataraharahana 333
                                                                                                            Human, chromosome mapping, gene mapping, gene therapy, forensic, food supplement, medical imaging, diagnostic, genetic disorder, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity.
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                                                                       DNA encoding novel human diagnostic protein #6266.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; SEQ ID NO 6266; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: August 4, 2005, 08:31:19
Job time : 203.826 secs
                                                                                                                                                                                                                                                                                 30-MAR-2001; 2001WO-US008631.
                                                                                                                                                                                                                                                                                                                                                                                                               Tang YT,
                                                                                                                                                                                                                                                                                                                    31; MAR-2000; 2000US-00540217
23-AUG-2000; 2000US-00649167
                                      13-FEB-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-639362/73.
P-PSDB; ABG06275.
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les 65; Conserv
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                                                                                                                                                                                                       WO200175067-A2.
                                                                                                                                                                      Homo sapiens
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 AAS70462;
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                                                                                                                                                                                                                       Score 34.4; DB
Pred. No. 13;
0; Mismatches
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Pred. No. 13;
0; Mismatches
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AAS70462 standard; cDNA; 2268 BP.
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17
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Sequence split into
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ADOS0281 00
ADOS0281 01
ADOS0281 02
ADOS0281 04
ADOS0281 05
ADOS0281 06
ADOS0281 06
ADOS0281 06
               ADN9798907
ADN9798908
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ADN9798910
ADN9798911
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ADN9798915
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ADO50281_10
ADO50281_11
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ADOS0281_13
ADOS0281_14
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ADOS0281_16
ADN97989 06
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Continuation (8
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AZ446937 IMOZ4300
CE725189 CH216-73K
CE72518 Light-73K
CE3614654 TAM32-170
AI857124 MBNAAd-23
CL092596 ISB1-22D2
CG226677 OGOCZ03TH
CG360051 OGOEZ60TH
CG360051 OGOEZ60TH
CG222409 OGOFU36TH
CC408138 PUHIF57TB
CC408138 PUHIF57TB
CC408138 PUHIF57TB
CC40813 ZMMBH6000
CL987077 ZMMBH6000
CL987077 ZMMBH6000
CL98353 ZMMBH6000
CL98353 ZMMBH6000
CL985353 ZMMBH6000
CL985353 ZMMBH6000
AZ757570 ew09h011.F
BF604634 Z70544 MA
BBE204633 BBE206633
CR041049 Reverse s
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AZ446937 1M0243N04
CL051289 CH216-73K
                                                                                   August 4, 2005, 04:04:35; Search time 1415.95 Seconds (without alignments) 8064.741 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                               US-09-899-276C-5
300
1 aaggaggaggcagtgggcta......ataaccagggatgaacttct 300
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                       34239544 segs, 19032134700 residues
                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                        OM nucleic - nucleic search, using sw model
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CCL051289
CC314654
AR857124
CC326877
CG320691
CG408141
CC408138
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                                                                                                                                                                                                         IDENTITY NUC Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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gb_htc:..,
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gb_est6:..,
gb_est6:..,
gb_gs81:..,
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Perfect score:
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CG947926 MBEJI67TR CC220759 CH261-83M BE092056 IL2-BT073 BE092021 IL2-BT073 CN887426 010512AAW BE091833 IL2-BT073 CN887915 010512AAW BC091833 IL2-BT073 CN887915 010531AAW BQ890869 AGENCOURT AQ839804 Z60L13-C5 AG277081 Mus muscu BZ154015 CH230-149 AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b AZ124313 T223077b	INTS	<pre>bp DNA linear GSS 06-JUL-2004 rt in 5'HPRT insertion targeting and MHPN114f13, genomic survey sequence. MICER.</pre>	Craniata; Vertebrata; Buteleostomi; Sciurognathi; Muridae; Murinae; Mus. V., Davies,R.M., van der Weyden,L., W., Taylor,R.G., Nishijima,I., Yu,Y.,	Centre, Hinxton, Cambridgeshire, .ac.uk/MICER .sac.uk/MICER		4; DB 9; Length 737; 0.11; .ches 56; Indels 6; Gaps 1;	AAGGAGGAGGCAGTGGGCTAGGAATCGAGATTTTAAACTCAGCCCAGCCA 60 	TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT 120	CTTCTG 155 ATCCGG 4
CG947926 CC365704 CC320759 BE0320759 BE032021 CN887426 BE031833 CN887915 BC081833 AC277081 BZ154035 BZ164035 AZ124334 AZ124334 AZ124334 CNS055BT CNS055BT CNS055BT CNS055BT CNS055BT	ALIGNMENTS	737 clone clone sence;	rdata; entia; Cox,A. lumb,R.	Dmission (20-FBB-2004) Sanger Cd (20-EBB-2004) Sanger of UK. http://www.sanger.el 1737 /organism="Mus musculus" /mol type="genomic DNA" /db_xref="taxon:10090" /clone="MINN14f13"		Score 43.4; Pred. No. 0.1 0; Mismatches	TAGGAGAATCC 3GAGGAAATCA	TTAACATGCCTCAAGTACTCCTATCATATTTGT 	CTAAGGICTTTGGGTTTTTATCAGTGTGCTTCTG
$\sigma \circ \sigma \circ \sigma \circ \sigma \circ \sigma \circ \sigma \circ \sigma \circ \sigma \circ \sigma \circ \sigma \circ$		ad erij 010 7 se		-20/ /Ou/ /Ou/ /Ou/ /Ou/ /Ou/ /Ou/ /Ou/ /O		n 0	39GC	FAC SAG	<u> </u>
899 1024 3955 393 527 527 527 593 649 771 1112 515 515 515 515 515 515 515 515 7613 7613 7613 7613 7613 7613 7613 7613			, Metazoa; Ch Eutheria; Rc Euth 73) , Biggs, P.J. Smith, J., and Bradley,	12 K 0 . 2 6 4 7 7		14.5%; larity 60.0%; Conservative	GCAGTG	CCTCAAG CATGTGA	CTTTGGG
		31209 erse omoso 31209 31209 musc	muscu. aryota nalia; (bases ns, D.J cers, J.	Direct Submitted Submitted CB10 1SA, 1 LG		sh Similarity 93; Conserv	AGGAGGA(AGGATGC	TAACATGO	CTAAGGT(CTAAGGG
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22222222222222222222222222222222222222		CR231209/C LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	ORGANISM REFERENCE AUTHORS	TITLE JOURNAL FEATURES SOUFC		Query Matc Best Local Matches			
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RESULT 2 AZ446937/c

CE290785 AG175765 AZ757570 BF604634 BB620693 CR041049

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Xenopus tropicalis (western clawed frog)
Xenopus tropicalis
Xenopus tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibita; Barrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus; Silurana.

I (bases 1 to 1115)
Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,
Mardis,E. and Wilson,R.
A physical map of the xenopus tropicalis genome
Unpublished (2003)
Contact: Richard K Wilson
Genome Sequencing Center
Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 17500 Seq primer: Sp6 ATTTAGGTGACTATAG
Class: BAC ends
Class: BAC ends
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CE726528
                                                                                                                                                                                          CL051289 1115 bp DNA linear GSS 31-DEC-2003 CH216-73X13 Sp6.1 CH216 Xenopus tropicalis genomic clone CH216-73X13, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_line="Stock 248 F7A2, inbred N7"
/clone_lib="CH216"
/note="Vector: pTARBAC2.1; CHORI-216 Xenopus tropicalis
BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 GGAGGCAGTGGGCTAGGAGATCGAGATCAGAATTTTAAACTCAGCCCAGCCATTAAC
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12.6%; Score 37.8; DB 9; Length 1115;
Best Local Similarity 54.7%; Pred. No. 5.4;
Matches 75; Conservative 0; Mismatches 62; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Xenopus tropicalis"
/mol type="genomic DNA"
/strain="Nigerian frog"
/db.xref="caxon:8364"
/clone="CH216-73K13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence start: 67
High quality sequence stop: 334.
Location/Qualifiers
                      268 GAGCATAGCTGCCATAACCAGGG 290
                                                           193 AAGTATGTCTGTTATAAACAAGG 171
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AZ446937 648 bp DNA linear GSS 04-OCT-2000 1M0243N04R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0243N04 R, genomic survey sequence.
                                                                                                                                                              Mus musculus (house mouse)
Mus musculus
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
(bases 1 to 648)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,
Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von
Niderhausern, A. and Wright, D., Weiss, R.,
Mouse whole genome scaffolding with paired end reads from 10kb
Dlasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="B. Coli strain XL10-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UNGCNM library" /note="Vector: PWD42Lv; Purified genomic DNA from M.musculus GS7BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          148 TGCTTCTGTAGTTTCTGAGGAAATCTAAGGCACAACTGAGGAATGAAGTCAGGCTTTCCA
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Pred. No. 2.1;
0; Mismatches 65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 801 585 5606

Fax: 801 585 7177

Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00

Plate: 0243 row: N column: 04

Seq primer: CACACAGGAAACAGCTATGACC

Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus"
/mol type="genomic DNA"
/strain="C57BL/6J"
/db xref="taxon:10090"
/clone="UUGCIM0243N04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Utah
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Location/Qualifiers
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Best Local Similarity 54.5%;
Matches 78; Conservative
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A1857124

MBNAAA-239SAC Necator americanus (parasitic nemacode) mixed adult
Necator americanus cDNA clone MBNAAG-239 5' similar to from Necator
americanus EST cluster NAC00239, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Bunostominae; Necator. 1 (Bases I to 675) Bubb. 1 (Bases I to 675) Bubb. J., Loukas. A., Pritchard, D. and Blaxter, M. A survey of genes expressed in adults of the hookworm Necator
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/clone_lib="Necator americanus (parasitic nematode) mixed
adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: Lambda Zap Express; Site_1: BcoRI (5'end);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mark.blaxcerged.ac.uk
The Necator americanus EST dataset (including the NAC clustering
Information) is available on the www at http://www.ed.ac.uk/
mbx/NecatorEST.html
PCR PRimers
PCR PRimers
PCRAMAD: M13 Reverse (AGCGGATAACAATTTCACACAGGA)
BACKWARD: M13 Porward (CGCCAGGGTTTTCCACACAGGA)
Seq primer: SAC (GGGAACAAAAGCTGGAG)
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University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      56 AGCCATTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAA
                                                                                                                                                                                                              /cell line="UCD001, inbred 256"
/clone lib="TAM32"
/note="Vector: PECBAC1; Site_1: EcoR1; Site_2: 1
TAM32 Female Chicken library - for library and ordering information: http://www.hbz.tamu.edu"
                                                                                                                                                                                                                                                                                                                                                                                         Length 1043;
                                                                                                                                                                                                                                                                                                                                                                                      Score 37.2; DB 8; Length 1 Pred. No. 8; 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 TGAATTCTAAGGTCTTTGGGTTTTTTATCAGTGTGCTTC 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             111 AGTCCTGCATGGACTTGGGTTTACTATCAAGGTATTTC 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Necator americanus"
                                                                                             /mol_type="genomic_DNA"
/strain="Red_Jungle Fowl"
/db_xref="taxon:9031"
/clone="TAM32-17J9"
                                                                      organism="Gallus gallus"
  ity sequence stop: 535.
Location/Qualifiers
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/db xref="taxon:51031"
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                                                                                                                                                                                            /sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: +44 131 650 6760
Fax: +44 131 670 5450
                                                                                                                                                                                                                                                                                                                                                                                      th 12.4%; Similarity 61.2%; 60; Conservative
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     High quality
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TAM32-17J9_Sp6.1 TAM32 Gallus gallus genomic clone TAM32-17J9,
genomic survey sequence.
                                                                                                                                                                                                                                                                               The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0208
Fax: 301-838-0208
Email: ekirknes@tigr.org
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          304 TTAGAAACACTCCCTAAAAATTATAACTATTCCACAATTCATTAAGGGTCTGTCATAACAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         101 AACAGTTCACTGAAATGAATTCTAAGGTCTTTTGGGTTTTTATCAGTGTGCTTCTGTAGTT 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244 AAATGTACCTTAATGTGAATATTAAGTATTTTATATTTGGACCACTGTGTTTTTCTACAT 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Archosauria, Aves, Neognathae, Galliformes, Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1043)

Kremitzki, C., Higginbotham, J., Wylie, K., Carter, J., McPherson, J., Warren, W., Graves, T., Mardis, E. and Wilson, R.
Gallus, Gallus, BAC, End Reads
Unpublished (2003)

Contact: Richard K. Wilson
                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis. [ (bases 1 to 721) Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="Standard Poodle"
/strain="Standard Poodle"
/bx xref="taxon:9615"
/clone lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
                                                                                                                                       Venter, J.C.
The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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Washington University School of Medicine
Email: submissions@watson.wustl.edu
Insert Length: 152000 Std Error: 0.00
Seq primer: Sp6 ATTTAGGTGACACTATAG
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Canis familiaris"
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Gallus gallus
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Canis familiaris
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ORGANISM
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CG360051 819 bp DNA linear GSS 26-AUG-2003
OG0EZ60TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0703124,
                            OGOCZOSTH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0690A06, GG226877
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 819)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          247 icttrairaaitcactcaattgatctairtccciatggcacaittiririaaatigiaia 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            307 AGACTGAAATTITCTGITAATGGTAACATAATTIGTIGGTTCTITITGTATITTGCTATA 366
                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                             1 (bases 1 to 731)
Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budinan, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Numberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other_GSSs: OGGCZ03TV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 TCAGAATTTTAAACTCAGCCCAGCCATTAACATGCCTCAAGTACTCCTATCATATTTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     155 GIAGTITCTGAGGAAATCTAAGGCACAACTGAGGAATGAAGTCAGGCTTTCCAA 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db.zref="taxon:4577"
/clone="ZMMBMa0690A06"
/clone lib="ZMO.7 1.5_KB"
/note="vector: pBCSK-; Site 1: HincII; 0.7-1.5 ]
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                9712 Medical Center Drive, Rockville, MD 20850, Tel: 301-838-5843
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 9;
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/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: whitelaw@tigr.org
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CG360051
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                                                                                                                                       CG226877.1 GI:34126765
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Class: sheared ends
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                   RESULT 8
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Site_2: XhoI (3'end); Necator americanus is a human hookworm, responsible for debilitating anaemia. The library was constructed from mRNA from N.americanus adults (Nottingham strain) maintained in hamsters."
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                                                                                                                                                                                                                                                                                                                                                                                                                                    CL092596 1114 bp DNA linear GSS 05-JAN-2004 ISB1-22D23_T7.1 ISB1 Xenopus tropicalis genomic clone ISB1-22D23,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus tropicalis (western clawed frog)

Xenopus tropicalis

Xenopus tropicalis

Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;

Xenopodiae; Xenopus; Silurana.

X (Ases 1 to 1114)

Kremitzki,C., Carter,J., McPherson,J., Warren,W., Graves,T.,

Mardis,E. and Wilson,R.

A physical map of the xenopus tropicalis genome

Unpublished (2003)

Contact: Richard K Wilson
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/organism="Xenopus tropicalis"

/mol type="genomic DNA"

/db xref="taxon:836"

/clone="1SB1-22D23"

/clone="1EB1" ISB1"

/note="Wettor: pBeloBAC11; ISB-1 Xenopus tropicalis libbrary Segment 1"
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                                                                                                                                                                                                                                                                                          100 CAACAGTTCACTGAAATGAATTCTAAGGTCTTTGGGTTTTTATCAGTGT
                                                                                                                        12.3%; Score 37; DB 1; Length 675;
.larity 58.7%; Pred. No. 8.2;
Conservative 0; Mismatches 45; Indels
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Mashington University School of Medicine
Email: submissions@wateon.wustl.edu
Insert Length: 75000 Std Error: 0.00
Seq primer: T7 TAATACGACTACTATAGGG
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Pred. No. 9.3;
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High quality sequence start: 5
High quality sequence stop: 323.
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                                                                                                                                                Local Similarity
ses 64; Conserv
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B84 bp DNA linear GSS 19-MAY-2003 PUHIF57TD ZM 0.6_1.0 KB Zea mays genomic clone ZMWBTa457118, genomic survey sequence.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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ktrāln="B73"
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/note="Wocror: PBGSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Mittelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
Bennetzen, J.
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1 Similarity 50.6%; Pred. No. 13;
88; Conservative 0; Mismatches
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/mol_type="genomic DNA"
/strain="B73"
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Class: sheared ends.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
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Other_GSSs: PUHIF57TB
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OG0FU36TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0708F23,
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1 (bases 1 to 849)
Mhitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Nunckenbush, J., Van Aken, S., Utterback, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics
Unpublished (2002)
Other_GSSS: OGOPU36TV
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Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N. Consortium for Maize Genomics Unpublished (2002) Other GSSs: OGGEZ60TV

Contact: Cathy Whitelaw
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/note="Vector: pBGSK-; Site_1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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Fax: 301-838-0208
Email: whitelaw@tigr.org
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CL987077 1027 bp DNA linear GSS 23-SEP-2004
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1 (bases 1 to 1027)

Ma,J., SanMiguel,P., Liu,R., Haller,K., Soderlund,C. and
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                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 985)

Ma,J., Samhiguel,P., Liu,R., Haller,K., Soderlund,C. and Bennetzen,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="immature ear"
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/note="Yector: TOPOpcr4; Site_1: EcoR1; Site_2: EcoR1"
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                                                                                                                                                                                                                                                                                The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, '30602, USA
Tel: 706-542-3698
Fax: 706-583-0972
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50.6%; Pred. No. 14;
tive 0; Mismatches
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/mol_type="genomic DNA"
/cultivar="B73"
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Plate: 0003 row: d column: 22
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Unpublished (2004)
Contact: Jeff Bennetzen
Bennetzen Lab
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Unpublished (2004)
Contact: Jeff Bennetzen
GI:52560075
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Eukaryots; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryots; Vanidiplantae; Streptophyta; Enbryophyta; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea
1 (bases 1 to 935)
Whitelaw, C. A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
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                                                                   449 AGACTGAARTTİTCTGİTAATGĞTAACAİAATTİGİTĞİTGİTİTİTGTATİTİĞĞİATA 508
                           95 AGAGACAACAGTTCACTGAAATGAATTCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTCT 154
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9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
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Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TR
Class: sheared ends.
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Other GSS8: PUHIF57TD
Contact: Cathy Whitelaw
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CC408138.1 GI:30888228
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1 (bases 1 to 1058)
Ma.J., SanMiguel, P., Liu, R., Haller, K., Soderlund, C. and Bennetzen, J.
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The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, GA
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The University of Georgia
Department of Genetics, C426a Life Sciences Building, Athens, 30602, USA
Tel: 706-542-3698
Fax: 706-583-0972
Bmail: maize@uga.edu
Blate: 0003 row: k column: 03
Class: BAC ends.
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Contact: Jeff Bennetzen
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Fax: 706-583-0972
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/clone="ZMMBHe0001e22"
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Job time : 1423.95 secs
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Matches 88; Conserv
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on:

August 4, 2005, 07:01:49; Search time 61.8219 Seconds (without alignments) 7940.282 Million cell updates/sec

US-09-899-276C-5 300

Perfect score: Sequence:

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Minimum DB seq length: 0
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## SUMMARIES

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Score	35.6	. 4	4	34.2	33.8	33.8	33.4	33.4	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.6	32.4	32.2	32.2	32.2	32	32	32	32	32
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Sequence 152883, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

RESULT 2 US-09-949-016-152883/c

Sequence 12705, A	Sequence 17550, A	Sequence 130167,	Sequence 80, Appl	Sequence 16813, A	Sequence 17175, A	Sequence 1957, Ap	Sequence 508, App	Sequence 30, Appl	Sequence 13799, A	Sequence 17, Appl	Seguence 15920, A	Seguence 12553, A	Sequence 13210, A	Sequence 14588, A	Sequence 14589, A	Sequence 17119, A	Sequence 16297, A
US-09-949-016-12705	US-09-949-016-17550	US-09-949-016-130167	US-09-220-132-80	US-09-949-016-16813	US-09-949-016-17175	US-09-583-110-1957	US-09-107-433-508	US-08-569-166-30	US-09-270-767-13799	US-08-961-527-17	US-09-949-016-15920	US-09-949-016-12553	US-09-949-016-13210	US-09-949-016-14588	US-09-949-016-14589	US-09-949-016-17119	US-09-949-016-16297
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## ALIGNMENTS

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Sequence 13355, Application US/09949016

j Batent No. 6812339

j GENERAL INFORMATION:
    PAPLICANT: VENTER,
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
    TITLE OF INVENTION: 2000-04-14
    PRIOR REFERENCE: 2000-04-14
    PRIOR APPLICATION NUMBER: 60/231,768
    PRIOR FILING DATE: 2000-10-20
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-10-03
    PRIOR FILING DATE: 2000-09-08
    NUMBER OF SEQ ID NOS: 207012
    SOCTWARE: FastSEQ for Windows Version 4.0
    SEQ ID NO 13355
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Pred. No. 0.28;
0; Mismatches 74; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 TCTAAGGTCTTTGGGTTTTTTATCAGTGTGCTTCT 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 51.9%;
Matches 80; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13355
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; LOCATION: (1)...(166698); OTHER INFORMATION: n = A,T,C or G US-09-949-016-16038
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60.0%;
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Best Local Similarity 60.0%;
Matches 57; Conservative
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NAME/KEY: misc_feature
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                      , ORGANISM: Human
US-09-949-016-152885
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 166698
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                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: Rastese for Windows Version 4.0
SEQ ID NO 152884
LENGTH: 601
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 103 CAGTICACIGAAATGAATICTAAGGICTITIGGGITTITAATCAGTGTGTGTTCTGTAGTITTC 162
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Pred. No. 0.16;
0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                           Score 34.2; DB 4; Length 601;
Pred. No. 0.16;
0; Mismatches 38; Indels
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FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PILING DATE: 2000-10-3
PRIOR PLICATION NUMBER: 60/231,498
PRIOR PLICATION NUMBER: 60/231,498
PRIOR PLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FBELSEQ for Windows Version 4.0
SEQ ID NO 152883
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US-09-949-016-152885/c
US-09-940-016-152885/s
; Sequence 152885, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 152884, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 60.0%;
Matches 57; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                    11.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 60.0%
Matches 57; Conservative
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US-09-949-016-152884/C
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US-09-949-016-152883
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US-09-949-016-16038/C
; Sequence 16038, Application US/09949016
; Patent No. 6812339
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHEMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT APPLICATION NUMBER: 60/241,755
; PRIOR PILING DATE: 2000-04-14
; PRIOR PILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR PILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFFTWARE: RESELECT FOR Windows Version 4.0
APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,758

PRIOR PILING DATE: 2000-10-23

PRIOR PILING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTH NUMBER: FRASESEQ for Windows Version 4.0

LENGTH: 601
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Pred. No. 0.16;
0; Mismatches 38;
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Sequence 12637, Application US/09949016

Batent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: DOLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WINDER: US/09/949,016

TITLE OF INVENTION NUMBER: 06/241,755

FILE REFERENCE: Z000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: Z000-10-20

PRIOR FILING DATE: Z000-10-20

PRIOR FILING DATE: Z000-10-09

PRIOR PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: Z000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 13113, Application US/09949016

Retent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR PLILICATION NUMBER: 60/237,768
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                                              72 CAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAATTCTAAGGTCTT 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       191 TGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATGTCCCTTGGAA 250
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12 AGTGGGCTAGGAGAATCGAGATCAGAATTTTAAACTCAGCCCAGCCATTAACATGCCT
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Pred. No. 1.8;
0; Mismatches
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Best Local Similarity 48.79
....has 91, Conservative
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US-09-949-016-12637
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US-09-949-016-13143
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                                                                           Sequence 12683, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
Patent No. 6812339
GENERAL INFORMATION:
POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT FILING DATE: 2000-04-14
FRIOR REPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR FILING DATE: 2000-09-08
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NOS: 207012
SEQ ID NO 12683
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APPLICANT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF PILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: us/09/949,016

CURRENT PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-09

PRIOR PILING DATE: 2000-10-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33.8; DB 4; Length 152524; Pred. No. 4.1; 0; Mismatches 82; Indels 0;
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Pred. No. 4.1;
0; Mismatches 82; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 TGGGTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAG 176
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SOFTWARES FastSEQ for Windows Version 4.0
SEQ ID NO 13194
LENGTH: 152524
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Patent No. 6812339
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Best Local Similarity 50.3%;
Matches 83; Conservative C
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Best Local Similarity 50.3%;
Matches 83; Conservative
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; ORGANISM: Human
US-09-949-016-12683
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US-09-949-016-13194
                                                                   -09-949-016-12683
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ORGANISM: Human
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Gaps

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MOLECULE TYPE: DNA (genomic)
           US-08-110-158-5
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                                                                                                                                                                                                                                    11.1%; Score 33.4; DB 4; Length 17764; 48.7%; Pred. No. 1.8;
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; Sequence 5, Application US/08110158
; Patent No. 560581
; GENERAL INFORMATION:
    APPLICANT: McEver, Rodger P.
    APPLICANT: Pan, Juniiang
    TITLE OF INVENTION: Expression Control Sequences of the
    TITLE OF INVENTION: P-Selectin Gene
    NUMBER OF SEQUENCES: 17
    CORRESPONDENCES: 17
    CORRESPONDENCES: 17
    STREET: 1100 Peachtree Street, Suite 2800
    CITY: Allanta
                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDITUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/110,158

FILING DATE: 19930820

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/320,408

FILING DATE: 08-MAR.1989

ATTORNEY/AGENT INFORMATION:

NAME: Pabet, Patrea L.

REGISTRATION NUMBER: 31,284

TELECOMMUNICATION NUMBER: 31,284

TELECOMMUNICATION NUMBER: 31,284

TELERPAK: (404)-815-6508

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CRARACTERISTICS:

LENGTH: 4866 base pairs
                                                                                                                                                                                                                                                                                96;
                                                                                                                                                                                                                                                                              0; Mismatches
  PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 13143
LENGTH: 17764
                                                                                                                                                                                                                                        Query Match
Best Local Similarity 48.77
Matches 91; Conservative
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STRANDEDNESS: single
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ORGANISM: Human
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US-08-110-158-5/c
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US-US-YST-ULD-16142/C

Sequence 16142. Application US/09949016

Sequence 16142. Application US/09949016

Patent NO. 681239

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

ITILE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

ITILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;

FILE REFERENCE: CLOON 1307

CURRENT APPLICATION NUMBER: US/99/949,016

CURRENT APPLICATION NUMBER: 00/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR PLING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

NUMBER OF SEC ID NOS: 207012

SOFTWARE: FRACES F
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: 60/944,755
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR APPLICATION NUMBER: 60/231,768
FRIOR APPLICATION NUMBER: 60/231,768
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR PILING DATE: 2000-10-03
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR APPLICATION NUMBER: 60/231,498
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
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FRIOR FILING DATE: 2000-10-03
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           Length 4866;
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                                                                                                                         44;
Score 32.6; DB 1;
Pred. No. 1.7;
0; Mismatches 44;
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Patent No. 6812339
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Best Local Similarity 57.3%;
Matches 59; Conservative (
     Query Match 10.9%;
Best Local Similarity 57.3%;
Matches 59; Conservative
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US-09-949-016-16142
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RESULT 15
US-09-949-016-17009
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US-09-949-016-17009
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LENGTH: 205163
                                                                                                                                                                                                                    TYPE: DNA
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Fatent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/241,755

PRIOR PELICATION NUMBER: 60/231,498

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FEELSEQ for Mindows Version 4.0
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
                                                                                                                                                                                                                                                                                                                                                                           30938 TTAAAGTCTCCCATTATTATTGTGGGAGTCTAATTCTCTTTGTAGGTCTCTAAGGACT 30879
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72852 TTAAAGTCTCCCATTATTATTGTGTGGGAGTCTAAGTCTTTATATAGGTCTCTAAGGACT 72911
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Pred. No. 8.1;
0; Mismatches 44; Indels 0;
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                                                                                                                                                                                                                                                                                   44; Indels
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                                                                                                                                                                                                                                     Score 32.6; DB 4;
Pred. No. 7.3;
0; Mismatches 44;
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Patent No. 6812339
                                                                                                                                                            ; OTHER INFORMATION: n = A, T, C or G
US-09-949-016-15896
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 57.3%;
Matches 59; Conservative
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Best Local Similarity 57.3%;
Matches 59; Conservative
                                                                                                        NAME/KEY: misc_feature
                                              TYPE: DNA
ORGANISM: Human
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SEQ ID NO 15896
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LENGTH: 92155
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Sequence 17009, Application US/09949016

Fatent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

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10.9%; Score 32.6; DB
Best Local Similarity 55.9%; Pred. No. 12;
Matches 62; Conservative 0; Mismatches
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Pred. No. 8.1;
0; Mismatches
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-3
PRIOR APLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESERG for Windows Version 4.0
SEQ ID NO 12166
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SOFTWARE: FastSEQ for Windows Version 4.0
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Best Local Similarity 57.3%;
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 5, Appli	Sequence 121412,	Sequence 121412,	Sequence 3, Appli	Sequence 4, Appli	Sequence 1625, Ap	Sequence 1626, Ap
ΩΙ	9 US-09-899-276-5	US-10-027-632-121412	US-10-027-632-121412	9 US-10-685-705-3	US-10-685-705-4	US-10-311-455-1625	US-10-311-455-1626
98	6	13	17	19	13	15	15
* Query Match Length DB ID	300	934	934	3221	11793	5926	5926
Query Match	100.0	6.66	6.66	98.9	98.9	68.0	64.8
Score	300	299.6	299.6	296.8	296.8	204	194.4
Result No.	-	7	m	4	S	ø	0

3 32.0 10.9 103219 13 05-10-06/-122-0536 Sequence 0506, 4 32.4 10.8 600 22 US-10-972-079-9599 Sequence 9599, 32.4 10 8 84073 13 IIS-10-087-192-712 Sequence 719	42 32.6 10.9 78025 14 US-10-020-141-9 Sequence 9, A 43 32.6 10.9 105219 13 US-10-087-192-658 Sequence 658,		US-10-027-632-129 US-10-087-632-129 US-10-087-632-129 US-10-087-632-1891 US-10-027-632-1991 US-10-027-632-1991 US-10-027-632-1991 US-10-027-632-1991 US-10-067-514-11 US-10-067-514-11 US-10-07-632-199 US-10-07-632-199 US-10-07-632-199 US-10-07-632-199 US-10-07-632-199 US-10-027-632-199 US-10-027-632-199 US-10-027-632-199 US-10-027-632-199 US-10-027-632-199 US-10-027-632-199 US-10-027-632-104 US-10-027-632-104 US-10-027-632-104 US-10-027-632-104 US-10-027-632-1168 US-10-027-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-632-11168 US-10-07-11601-569 US-10-07-116-10-177	$\begin{array}{cccccccccccccccccccccccccccccccccccc$	22 111 6 1		4 4 M W M W W W W W W W W W W W W W W W	8 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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41 32.6 10.9 53323 21 US-10-741-600-17769 Sequence 1776 42 32.6 10.9 78025 14 US-10-020-141-9 Sequence 9, P	41 32.6 10.9 53323 21 US-10-741-600-17769 Sequence 1776	equence 5695	US-10-741-601	13	53323	10.9	32.6	4
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37 32.6 10.9 201 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 21 US-10-744-601-55435 Seque 40 32.6 10.9 3136 10 US-09-764-891-6999 Seque 41 32.6 10.9 53323 19 US-10-741-601-5695 Seque 42 32.6 10.9 53323 21 US-10-741-600-17769 Seque 42 32.6 10.9 78025 14 US-10-741-600-17769 Seque 53.5 10.9 78025 14 US-10-741-600-17769 Seque 53.5 10.9 78025 14 US-10-020-141-9	37 32.6 10.9 201 19 US-10-41-601-20010 Seque 38 32.6 10.9 201 21 US-10-741-600-55435 Seque 40 32.6 10.9 3139 US-10-744-601-5699 Seque 41 32.6 10.9 53323 21 US-10-741-600-5695 Seque 41 32.6 10.9 53323 21 US-10-741-600-17769 Seque	eque	ΩŜ	11	17918	10.9	32.8	36
36 32.8 10.9 17918 17 US-10-221-613-382 Seque 37 32.6 10.9 2011 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 19 US-10-741-600-55435 Seque 39 32.6 10.9 3195 10 US-09-764-891-6999 Seque 40 32.6 10.9 53323 19 US-10-741-601-5695 Seque 41 32.6 10.9 53323 21 US-10-741-601-7769 Seque 42 32.6 10.9 78025 14 US-10-741-601-7769 Seque 5323 21 US-10-741-601-7769 Seque 542 32.6 10.9 78025 14 US-10-720-141-6	36 32.8 10.9 17918 17 US-10-221-613-382 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 21 US-10-741-600-55435 Seque 40 32.6 10.9 3196 10 US-09-764-891-6999 Seque 41 32.6 10.9 53323 21 US-10-741-601-5695 Seque 41 32.6 10.9 53323 21 US-10-741-600-17769 Seque	Seguence 111626,	US-10-027-632-11162	11	2893	10.9	32.8	35
35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 17918 17 US-10-221-613-382 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 21 US-10-741-600-55435 Seque 39 32.6 10.9 3196 10 US-09-764-891-6999 Seque 41 32.6 10.9 53323 21 US-10-741-601-5695 Seque 42 32.6 10.9 53323 21 US-10-741-601-5695 Seque 42 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-741-601-7769 Seque 54 22.6 10.9 78025 14 US-10-	35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 17918 17 US-10-221-613-382 Seque 37 32.6 10.9 201 19 US-10-741-601-2001 Seque 38 32.6 10.9 201 21 US-10-741-600-55435 Seque 39 32.6 10.9 3196 10 US-09-764-891-6999 Seque 41 32.6 10.9 53323 21 US-10-741-600-17769 Seque 510.9 53323 21 US-10-741-600-17769 Seque	Sequence 111626,	US-10-027-632-11162	13	2893	10.9	32.8	34
34 32.8 10.9 2893 13 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 17918 17 US-10-021-611-38 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 39 32.6 10.9 201 21 US-10-741-600-55435 Seque 40 32.6 10.9 53323 19 US-10-741-600-5699 Seque 41 32.6 10.9 53323 21 US-10-741-600-17769 Seque 42 32.6 10.9 53323 21 US-10-741-600-17769 Seque 532.6 10.9 53323 21 US-10-741-600-17769 Seque 532.6 10.9 53323 19 US-10-741-600-17769 Seque 532.6 10.9 78025 14 US-10-741-600-17769 Seque 532.6 10.9 78025 14 US-10-741-600-17769	34 32.8 10.9 2893 13 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 17918 17 US-10-221-613-382 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 21 US-10-741-600-55435 Seque 40 32.6 10.9 3196 10 US-09-764-891-6999 Seque 41 32.6 10.9 53323 21 US-10-741-601-5695 Seque 510.9 53323 21 US-10-741-600-17769 Seque	Sequence 168400,	US-10-425-115-16840	20	524	10.9	32.8	33
33 32.8 10.9 524 20 US-10-425-115-168400 Seque 34 32.8 10.9 2893 13 US-10-072-632-111626 Seque 35 32.8 10.9 2893 13 US-10-027-632-111626 Seque 36 32.8 10.9 17918 17 US-10-221-613-382 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 19 US-10-741-601-5495 Seque 39 32.6 10.9 31323 19 US-10-741-601-5695 Seque 41 32.6 10.9 53323 10 US-10-741-601-5695 Seque 42 32.6 10.9 53323 21 US-10-741-601-1769 Seque 54 32.6 10.9 53323 10 US-10-741-601-1769 Seque 54 32.6 10.9 78025 14 US-10-741-601-5695 Seque 54 32.6 10.9 78025 14 US-10-741-601-1769 Seque 54 32.6 10.9 78025 14 US-10-20-1769	33 32.8 10.9 524 20 US-10-425-115-168400 Seque 34 32.8 10.9 2893 13 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 17918 17 US-10-221-613-382 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 39 32.6 10.9 201 21 US-10-741-600-55435 Seque 40 32.6 10.9 53323 19 US-10-744-691-6999 Seque 41 32.6 10.9 53323 21 US-10-741-601-5695 Seque Seque	Sequence 9598, Ap	US-10-972-079-9598	22	600	11.0	33	32
32 3 11.0 600 22 US-10-972-079-9598 Seque 34 32.8 10.9 524 20 US-10-0425-115-168400 Seque 34 32.8 10.9 524 20 US-10-0425-115-168400 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 17918 17 US-10-027-632-111626 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 21 US-10-741-601-5999 Seque 44 32.6 10.9 3132 19 US-10-741-601-5999 Seque 44 32.6 10.9 53323 21 US-10-741-601-5695 Seque 42 32.6 10.9 53323 21 US-10-741-601-5695 Seque 54 32.6 10.9 53323 21 US-10-741-601-5695 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-5695 Seque 54 32.6 10.9 78025 14 US-10-741-601-5695 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32.6 10.9 78025 14 US-10-741-601-7769 Seque 54 32 32 32 32 32 32 32 32 32 32 32 32 32	32 33 11.0 600 22 US-10-972-079-9598 Seque 34 32.8 10.9 524 20 US-10-072-079-9598 Seque 34 32.8 10.9 5283 13 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 17918 17 US-10-227-633-1182 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 21 US-10-741-600-55435 Seque 39 32.6 10.9 3196 10 US-09-764-891-6999 Seque 41 32.6 10.9 53323 21 US-10-741-600-5695 Seque Seque 32.6 10.9 53323 21 US-10-741-600-5695 Seque 54 32.6 10.9 53323 21 US-10-741-600-7769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque	Sequence 9597, Ap	US-10-972-079-	22	009	11.0	33	31
31 33 11.0 600 22 US-10-972-079-9597 Seque 32 11.0 600 22 US-10-972-079-9598 Seque 34 32.8 10.9 2893 13 US-10-0472-079-9598 Seque 34 32.8 10.9 2893 13 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 17918 17 US-10-027-632-111626 Seque 37 32.6 10.9 17918 17 US-10-027-632-111626 Seque 38 32.6 10.9 201 19 US-10-741-601-2001 Seque 53 32.6 10.9 3196 10 US-09-764-891-6999 Seque 41 32.6 10.9 53323 21 US-10-741-600-17699 Seque 53 32.6 10.9 53323 21 US-10-741-600-17699 Seque 53 32.6 10.9 53323 21 US-10-741-600-17699 Seque 53 32.6 10.9 53323 21 US-10-741-600-17699 Seque 53 32.6 10.9 53323 21 US-10-741-600-17699 Seque 53 32.6 10.9 53323 21 US-10-741-600-17699 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 10.9 54 32.6 1	31 33 11.0 600 22 US-10-972-079-9597 Seque 32 11.0 600 22 US-10-972-079-9598 Seque 33 11.0 600 22 US-10-972-079-9598 Seque 34 32.8 10.9 524 20 US-10-425-115-168400 Seque 35 32.8 10.9 2893 13 US-10-027-632-111626 Seque 37 32.8 10.9 1991 17 US-10-027-632-111626 Seque 37 32.6 10.9 1991 17 US-10-21-613-182 Seque 37 32.6 10.9 201 19 US-10-741-601-2001 Seque 39 32.6 10.9 3196 10 US-09-764-891-6999 Seque 41 32.6 10.9 53323 21 US-10-741-600-5595 Seque 51 0.9 53323 21 US-10-741-600-17769 Seque 51 0.9 53323 21 US-10-741-600-17769 Seque 51 0.9 53323 21 US-10-741-600-17769 Seque 51 0.9 53323 21 US-10-741-600-17769 Seque 51 0.9 53323 21 US-10-741-600-17769 Seque 51 0.9 53323 21 US-10-741-600-17769 Seque 51 0.9 53323 21 US-10-741-600-17769 Seque 51 0.9 53323 21 US-10-741-600-17769 Seque 51 0.9 53323 21 US-10-741-600-17769	Sequence 334, App	US-10-087-192-	13	4	11.1	33.2	30
30 33.2 11.1 345548 13 US-10-007-192-334 Seque 31 11.0 600 22 US-10-972-079-9597 Seque 32 33 11.0 600 22 US-10-972-079-9597 Seque 33 12.8 10.9 524 20 US-10-972-079-9597 Seque 34 32.8 10.9 524 20 US-10-072-15-168400 Seque 35 32.8 10.9 2893 13 US-10-027-632-111626 Seque 37 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 17918 17 US-10-211-613-382 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 39 32.6 10.9 3139 10 US-10-741-601-599 Seque 40 32.6 10.9 53323 21 US-10-741-601-5695 Seque 41 32.6 10.9 53323 21 US-10-741-601-1769 Seque 51 32.6 10.9 53323 21 US-10-741-601-1769 Seque 51 32.6 10.9 53323 21 US-10-741-601-1769 Seque 51 32.6 10.9 53323 21 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32.6 10.9 78025 14 US-10-741-601-1769 Seque 51 32 US-10-741-601-1769 Seque 51 32 US-10-741-601-1769 Seque 51 32 US-10-741-601-1769 Seque 51 32 US-10-741-601-1769 Seque 51 32 US-10-741-601-1769 Seque 51 32 US-10-741-601-1769 Seque 51 32 US-10-741-601-1769 Seque 51 32 US-10-741-601-1769 Seque 51 32 US-10-741-601-1769 Seq	30 33.2 11.1 34548 13 US-10-087-192-334 Seque 31 11.0 600 22 US-10-972-079-9597 Seque 32 31 11.0 600 22 US-10-972-079-9597 Seque 34 32.8 10.9 524 20 US-10-972-079-9598 Seque 35 32.8 10.9 2893 17 US-10-077-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 19 US-10-741-601-20010 Seque 39 32.6 10.9 3196 10 US-09-744-8999 Seque 40 32.6 10.9 53323 21 US-10-741-601-5699 Seque 41 32.6 10.9 53323 21 US-10-741-601-5699 Seque 510.9 53323 21 US-10-741-601-5699 Seque	Sequence 79, Appl	US-10-764-212-	22	1483	11.1	33.2	7
29 33.2 11.1 1483 22 US-10-764-212-79 30 33.2 11.1 34548 13 US-10-0764-212-79 31 31.0 600 22 US-10-972-079-9594 32 31.0 600 22 US-10-972-079-9598 32 32.8 10.9 524 20 US-10-972-079-9598 35 32.8 10.9 2893 13 US-10-077-632-111626 35 32.8 10.9 2893 17 US-10-027-632-111626 36 32.8 10.9 17918 17 US-10-027-632-111626 37 32.6 10.9 17918 17 US-10-027-632-111626 38 32.6 10.9 10.9 US-10-741-601-5999 32.6 10.9 3132 19 US-10-741-601-5999 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599 32.6 10.9 53323 21 US-10-741-601-599	29 33.2 11.1 1483 22 US-10-764-212-79 Seque 31.2 11.1 34548 13 US-10-0907-192-334 Seque 32 US-10-779-9597 Seque 32 US-10-972-079-9597 Seque 33 11.0 600 22 US-10-972-079-9598 Seque 33 32.8 10.9 524 20 US-10-972-1168400 Seque 34 32.8 10.9 2893 17 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 10.9 10.9 10.9 10.0-10.27-632-111626 Seque 37 32.6 10.9 201 19 US-10-741-601-20010 Seque 39 32.6 10.9 201 21 US-10-741-609-55435 Seque 39 32.6 10.9 31.9 US-10-741-601-5999 Seque 41 32.6 10.9 53323 21 US-10-741-601-5695 Seque 51 22.6 10.9 53323 21 US-10-741-601-5699 Seque 51 22.6 10.9 53323 21 US-10-741-601-5695 Seque 51 22.6 10.9 53323 21 US-10-741-601-5695 Seque 51 22.6 10.9 53323 21 US-10-741-601-7769 Seque 51 22.6 10.9 53323 21 US-10-741-601-7769	Sequence 18166, A	US-10-282-122A-1816	11	693	11.2	33.6	~
28 33.6 11.2 693 17 US-10-282-122A-18166 Seque 3 33.2 11.1 346548 13 US-10-764-212-79 Seque 3 13.2 11.1 346548 13 US-10-087-192-334 Seque 3 11.0 600 22 US-10-772-079-9598 Seque 3 22.8 10.9 524 US-10-972-079-9598 Seque 3 32.8 10.9 2893 13 US-10-425-115-168400 Seque 3 32.8 10.9 2893 17 US-10-027-632-111626 Seque 3 32.8 10.9 2893 17 US-10-027-632-111626 Seque 3 32.8 10.9 2893 17 US-10-221-613-382 Seque 3 32.6 10.9 201 21 US-10-741-601-20010 Seque 3 32.6 10.9 3196 10 US-10-741-601-5999 Seque 4 32.6 10.9 3196 10 US-09-764-891-6999 Seque 4 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-7769 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5999 Seque 5 32.6 10.9 53323 21 US-10-741-601-5099 Seque 5 32.6 10.9 53323 21 US-10-741-601-5099 Seque 5 32.6 10.9 542.6 10.9 53323 21 US-1	28 33.6 11.2 693 17 US-10-222-122A-18166 Seque 3 33.2 11.1 34548 13 US-10-764-212-79 Seque 31.2 11.1 34548 13 US-10-087-192-334 Seque 31.2 11.1 34548 13 US-10-087-192-334 Seque 32.3 11.0 600 22 US-10-972-079-9598 Seque 32.8 10.9 2893 13 US-10-425-115-168400 Seque 34 32.8 10.9 2893 13 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 19 US-10-21-613-382 Seque 37 32.6 10.9 201 19 US-10-741-600-55435 Seque 39 32.6 10.9 201 19 US-10-741-600-55435 Seque 39 32.6 10.9 3196 10 US-10-741-609-599 Seque 41 32.6 10.9 53323 21 US-10-741-600-5695 Seque 510.9 53323 21 US-10-741-600-5695 Seque 510.9 53323 21 US-10-741-600-5695 Seque 510.9 53323 21 US-10-741-600-17769 Seque	Sequence 104612,	US-10-027-632-10461	11	1924	11.3	34	27
27 34 11.3 1924 17 US-10-027-632-104612 Seque 28 33.6 11.2 693 17 US-10-027-632-104612 Seque 29 33.2 11.1 1483 2 US-10-782-122-79 Seque 31.2 11.1 344548 13 US-10-074-192-334 Seque 32 11.0 600 22 US-10-972-079-9597 Seque 33 32.8 10.9 524 20 US-10-972-079-9598 Seque 34 32.8 10.9 2893 13 US-10-027-632-111626 Seque 34 32.8 10.9 2893 13 US-10-027-632-111626 Seque 37 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.8 10.9 17918 17 US-10-027-632-111626 Seque 37 32.6 10.9 17918 17 US-10-120-1699 Seque 37 32.6 10.9 3196 10 US-10-741-600-55435 Seque 41 32.6 10.9 53323 21 US-10-741-600-5695 Seque 42 32.6 10.9 53323 21 US-10-741-600-5695 Seque 52 22 22 22 22 22 22 22 22 22 22 22 22	27 34 11.3 1924 17 US-10-027-632-104612 Seque 28 33.6 11.2 693 17 US-10-027-632-104612 Seque 29 33.2 11.1 344548 12 US-10-782-132-79 Seque 31 33.2 11.1 344548 13 US-10-087-192-334 Seque 32 31.10 600 22 US-10-972-079-9597 Seque 33 32.8 10.9 524 20 US-10-972-079-9599 Seque 34 32.8 10.9 2893 13 US-10-072-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.8 10.9 17918 17 US-10-027-632-111626 Seque 37 32.6 10.9 17918 17 US-10-27-632-111626 Seque 37 32.6 10.9 17918 17 US-10-27-632-111626 Seque 37 32.6 10.9 17918 17 US-10-27-632-111626 Seque 37 32.6 10.9 17918 17 US-10-741-601-20010 Seque 39 32.6 10.9 3196 10 US-10-741-601-5699 Seque 41 32.6 10.9 53323 21 US-10-741-600-5695 Seque 510.9 53323 21 US-10-741-600-17769 Seque	Sequence 104612,	US-10-027-632-10461	13	1924	11.3	34	56
26 34 11.3 1924 13 US-10-077-632-104612 Seque 27 33.1 11.3 1924 17 US-10-027-632-104612 Seque 28 33.6 11.2 1483 22 US-10-282-122A-18166 Seque 33.2 11.1 344548 13 US-10-087-132A-18166 Seque 33.3 11.0 600 22 US-10-972-079-9597 Seque 33.3 11.0 600 22 US-10-972-079-9597 Seque 34 32.8 10.9 524 20 US-10-972-079-9597 Seque 35 32.8 10.9 524 20 US-10-072-079-9597 Seque 35 32.8 10.9 5293 17 US-10-077-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 10.9 10.9 10.9 10.0 10.0 10.0 10.0	26 34 11.3 1924 13 US-10-027-632-104612 Seque 28 33.6 11.2 693 17 US-10-027-632-104612 Seque 29 33.2 11.3 1924 17 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-282-122A-18166 Seque 31.2 11.1 344548 13 US-10-087-134 Seque 31.2 11.1 344548 13 US-10-097-079-9597 Seque 32 31.10 600 22 US-10-972-079-9598 Seque 33 32.8 10.9 524 20 US-10-972-079-9598 Seque 34 32.8 10.9 2893 17 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2091 19 US-10-741-601-20010 Seque 38 32.6 10.9 201 21 US-10-741-609-5435 Seque 32.6 10.9 32.6 10.9 10-741-601-20010 Seque 39 32.6 10.9 32.8 10.9 10-741-601-5099 Seque 41 32.6 10.9 53323 21 US-10-741-601-5695 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-601-5455 Seque 540-	Sequence 4561, Ap	US-10-956-15	21	5923	11.4	34.2	7
25 34.2 11.4 5923 21 US-10-956-157-4561 Seque 27 31.1 1924 13 US-10-027-632-104612 Seque 28 31.6 11.2 1924 13 US-10-027-632-104612 Seque 29 33.6 11.2 693 17 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-0764-2127-9 Seque 31.2 11.1 34548 13 US-10-0764-2127-9 Seque 31.3 11.0 600 22 US-10-972-079-9598 Seque 32.8 10.9 2893 17 US-10-972-079-9598 Seque 32.8 10.9 2893 17 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-227-632-111626 Seque 37 32.6 10.9 2091 19 US-10-741-601-20010 Seque 39 32.6 10.9 201 21 US-10-741-601-5999 Seque 39 32.6 10.9 3196 10 US-10-741-601-5999 Seque 41 32.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5999 Seque 51 22.6 10.9 53323 21 US-10-741-601-5059 Seque 51 22.6 10.9 53323 21 US-10-741-601-5099 Seque 51 22.6 10.9 54028 51 22.6 10.9 54028 51 22.6 1	25 34.2 11.4 5923 21 US-10-956-15-4561 Seque 24 11.3 1924 13 US-10-07-632-104612 Seque 25 33.6 11.3 1924 13 US-10-027-632-104612 Seque 26 33.6 11.2 693 17 US-10-027-632-104612 Seque 29 33.2 11.1 345481 22 US-10-764-127-9 Seque 31 23 11.0 600 22 US-10-79-9594 Seque 32 31.0 600 22 US-10-972-079-9597 Seque 34 32.8 10.9 2893 13 US-10-927-079-9598 Seque 35 32.8 10.9 2893 13 US-10-425-115-168400 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-27-632-111626 Seque 37 32.6 10.9 201 19 US-10-741-600-55435 Seque 38 32.6 10.9 201 21 US-10-741-600-55435 Seque 39 32.6 10.9 3196 10 US-10-741-600-55436 Seque 39 32.6 10.9 3196 10 US-10-741-600-55436 Seque 39 32.6 10.9 3196 10 US-10-741-600-55436 Seque 37.6 10.9 3196 10 US-10-741-600-55436 Seque 37.6 10.9 53323 21 US-10-741-600-5695 Seque 540 32.6 10.9 53323 21 US-10-741-600-5695 Seque 540 5323 21 US-10-741-600-5695 Seque 540 53323 21 US-10-741-600-17769 Seque 540 540 540 540 540 540 540 540 540 540	Sequence 199838,	US-10-027-632	11	618	11.4	34.2	7
24 34.2 11.4 618 17 US-10-027-632-199838 Seque 25 34.2 11.4 5923 21 US-10-956-157-4561 Seque 27 34.1 11.3 1924 17 US-10-027-632-104612 Seque 28 33.6 11.2 1924 17 US-10-027-632-104612 Seque 29 33.2 11.1 134498 13 US-10-027-632-104612 Seque 33 33.2 11.1 134498 13 US-10-072-079-959 Seque 33 31.0 600 22 US-10-764-212-79 Seque 33 32.8 10.9 520 US-10-76-072-079-959 Seque 34 32.8 10.9 2893 13 US-10-072-079-959 Seque 35 32.8 10.9 2893 13 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-11626 Seque 37 32.6 10.9 201 21 US-10-741-600-55435 Seque 37 32.6 10.9 3196 17 US-10-741-600-55435 Seque 37 32.6 10.9 3196 10 US-10-741-600-55435 Seque 37 32.6 10.9 3196 10 US-10-741-600-55435 Seque 41 32.6 10.9 53323 21 US-10-741-600-55435 Seque 53 32.6 10.9 53323 21 US-10-741-600-56435 Seque 53 32.6 10.9 53323 21 US-10-741-600-5695 Seque 53 32.6 10.9 53323 21 US-10-741-600-57435 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-1776 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 53 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 10.9 53323 21 US-10-741-600-17769 Seque 54 32.6 1	24 34.2 11.4 618 17 US-10-027-632-199838 Seque 25 34.2 11.4 5923 21 US-10-956-157-4561 Seque 27 34.1 11.4 5923 21 US-10-956-157-4561 Seque 28 33.6 11.3 1924 17 US-10-027-632-104612 Seque 29 33.6 11.2 1481 22 US-10-027-632-104612 Seque 30 33.2 11.1 144548 13 US-10-028-122A-18166 Seque 31.2 11.1 144548 13 US-10-784-212-79 Seque 32 33.1 10.6 60 22 US-10-78-213-79 Seque 33 32.8 10.9 2893 13 US-10-957-079-9598 Seque 34 32.8 10.9 2893 13 US-10-027-632-111626 Seque 35 32.8 10.9 2893 13 US-10-027-632-111626 Seque 37 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.8 10.9 1998 17 US-10-027-632-111626 Seque 37 32.6 10.9 1998 17 US-10-21-613-38 Seque 37 32.6 10.9 201 19 US-10-741-600-55435 Seque 37 32.6 10.9 3196 17 US-10-741-600-55435 Seque 41 32.6 10.9 53323 21 US-10-741-600-5695 Seque 52.6 10.9 53323 21 US-10-741-600-5695 Seque 52.6 10.9 53323 21 US-10-741-600-17769 Seque 52.6 10.9 53323 21 US-10-741-600-17769 Seque	Sequence 199837,	US-10-027-633	11	618	11.4	34.2	7
23 34.2 11.4 618 17 US-10-077-632-199837 Seque 25 34.2 11.4 618 17 US-10-077-632-199838 Seque 25 34.2 11.4 522 3 1 US-10-0956-157-4561 Seque 27 34 11.3 1924 13 US-10-0956-157-4561 Seque 28 33.6 11.3 1924 17 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-282-122A-18166 Seque 31.2 11.1 34458 13 US-10-087-1374 Seque 31.3 11.0 600 22 US-10-972-079-9597 Seque 32 32.8 10.9 524 20 US-10-972-079-9597 Seque 33 32.8 10.9 524 20 US-10-972-079-9597 Seque 34 32.8 10.9 2893 17 US-10-072-079-9597 Seque 35 32.8 10.9 2893 17 US-10-072-079-9598 Seque 37 32.6 10.9 2893 17 US-10-072-632-111626 Seque 37 32.6 10.9 19 US-10-741-601-2010 Seque 37 32.6 10.9 203 17 US-10-741-601-599 Seque 37 32.6 10.9 31323 19 US-10-741-601-599 Seque 41 32.6 10.9 53323 10 US-10-741-601-599 Seque 42 32.6 10.9 53323 10 US-10-741-601-599 Seque 53323 21 US-10-741-601-599 Seque 53323 21 US-10-741-601-599 Seque 53323 21 US-10-741-601-599 Seque 53323 21 US-10-741-601-599 Seque 540 540 540 540 540 540 540 540 540 540	23 34.2 11.4 618 17 US-10-027-632-199837 Seque 25 34.2 11.4 5223 1 US-10-027-632-199838 Seque 25 34.2 11.4 5223 1 US-10-056-157-4561 Seque 27 34 11.3 1924 17 US-10-056-157-4561 Seque 28 33.6 11.2 1924 17 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-282-122A-18166 Seque 29 33.2 11.1 1483 22 US-10-282-122A-18166 Seque 31.2 11.1 34648 13 US-10-0987-192-34 Seque 32 33 11.0 600 22 US-10-972-079-959 Seque 33 32.8 10.9 524 20 US-10-972-079-959 Seque 34 32.8 10.9 2893 17 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 38 32.6 10.9 2893 17 US-10-741-600-55435 Seque 32.6 10.9 32.8 10.9 US-10-741-600-55435 Seque 32.6 10.9 53323 21 US-10-741-600-5695 Seque 32.6 10.9 53323 21 US-10-741-600-5695 Seque 540-601-7769	Seguence 199838,	US-10-027-63	13	618	11.4	34.2	71
22 34.2 11.4 618 13 US-10-077-632-199838 Seque 24 34.2 11.4 618 17 US-10-027-632-199837 Seque 25 34.2 11.4 618 17 US-10-027-632-199837 Seque 26 34.2 11.4 618 17 US-10-027-632-199837 Seque 26 34.2 11.4 5923 21 US-10-027-632-104612 Seque 27 34 11.3 1924 13 US-10-027-632-104612 Seque 28 33.6 11.2 693 17 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-027-632-104612 Seque 31.2 11.1 1483 22 US-10-077-632-104612 Seque 31.2 11.1 34548 13 US-10-077-192-34 Seque 32 31.0 600 22 US-10-77-9599 Seque 33 31.0 600 22 US-10-972-079-9598 Seque 34 32.8 10.9 2893 17 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-27-632-111626 Seque 38 32.6 10.9 2893 17 US-10-741-601-2099 Seque 37 32.6 10.9 3196 10 US-10-741-601-5999 Seque 37 32.6 10.9 53323 21 US-10-741-601-5999 Seque 37 32.6 10.9 53323 21 US-10-741-601-5999 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37	22 34.2 11.4 618 13 US-10-077-632-199838 Seque 24 34.2 11.4 618 17 US-10-027-632-199837 Seque 25 34.2 11.4 618 17 US-10-027-632-199837 Seque 26 34.2 11.4 618 17 US-10-027-632-199838 Seque 26 34.2 11.4 5923 21 US-10-027-632-104612 Seque 27 34 11.3 1924 13 US-10-027-632-104612 Seque 29 33.2 11.1 1924 17 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-027-632-104612 Seque 31.2 11.1 34548 13 US-10-037-632-104612 Seque 31.2 11.1 34548 13 US-10-037-9598 Seque 32.8 10.9 2893 13 US-10-037-632-111626 Seque 34 32.8 10.9 2893 17 US-10-037-632-111626 Seque 34 32.8 10.9 2893 17 US-10-037-632-111626 Seque 35 32.8 10.9 2893 17 US-10-037-632-111626 Seque 36 32.8 10.9 2893 17 US-10-037-632-111626 Seque 37 32.6 10.9 2893 17 US-10-741-601-2001 Seque 39 32.6 10.9 31.9 10.9 10.741-601-2001 Seque 39 32.6 10.9 31.9 10.741-601-2001 Seque 39 32.6 10.9 53323 21 US-10-741-601-5695 Seque 41 32.6 10.9 53323 21 US-10-741-601-5695 Seque 52 32.8 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-5695 Seque 52 34.0 10.9 53323 21 US-10-741-601-569	Sequence 199837,	US-10-027-633	13	618	11.4	34.2	7
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19 34.4 11.5 1691140 22 US-10-868-397-1 Seque 23 44.2 11.4 549 22 US-10-972-0797-1139 Seque 23 44.2 11.4 618 13 US-10-027-632-199838 Seque 24.2 11.4 618 13 US-10-027-632-199838 Seque 25 34.2 11.4 618 17 US-10-027-632-199838 Seque 25 34.2 11.4 618 17 US-10-027-632-199838 Seque 26 34 11.3 1924 13 US-10-027-632-199838 Seque 26 34 11.3 1924 13 US-10-027-632-199838 Seque 27 34 11.3 1924 13 US-10-027-632-199838 Seque 28 33.2 11.1 1483 22 US-10-027-632-104612 Seque 29 33.2 11.1 34548 13 US-10-027-632-104612 Seque 31 11.0 600 22 US-10-972-079-9598 Seque 32.8 10.9 2893 17 US-10-027-632-111626 Seque 34 32.8 10.9 2893 17 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 3332 19 US-10-741-601-599 Seque 37 32.6 10.9 3332 19 US-10-741-601-599 Seque 37 32.6 10.9 53323 21 US-10-741-601-599 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32.6 10.9 53323 21 US-10-741-601-5695 Seque 37 32 US-10-741-601-5695 Seque 37 32 US	19         34.4         11.5         1691140         22         US-10-868-397-1         Seque           20         34.2         11.4         549         22         US-10-972-079-71139         Seque           21         34.2         11.4         618         13         US-10-027-632-199837         Seque           23         34.2         11.4         618         17         US-10-027-632-199837         Seque           24         34.2         11.4         618         17         US-10-027-632-199837         Seque           25         34.2         11.4         618         17         US-10-027-632-199837         Seque           26         34.2         11.4         618         17         US-10-027-632-199837         Seque           26         34.1         11.3         1924         13         US-10-027-632-104612         Seque           27         34         11.3         1924         13         US-10-027-632-104612         Seque           28         31.2         11.1         1483         22         US-10-027-632-104612         Seque           39         31.1         603         17         US-10-027-632-104612         Seque           31	5 5	US-10-419-723-	17	169113	11.5	34.4	18
18 34.4 11.5 1691139 17 US-10-419-723-1 Seque 24.2 11.4 11.5 1691139 17 US-10-668-397-1 Seque 24.2 11.4 618 13 US-10-027-632-199837 Seque 25 34.2 11.4 618 13 US-10-027-632-199837 Seque 25 34.2 11.4 618 17 US-10-027-632-199837 Seque 25 34.2 11.4 618 17 US-10-027-632-199837 Seque 26 34.2 11.4 618 17 US-10-027-632-199837 Seque 27 34 11.3 1924 13 US-10-027-632-199838 Seque 27 34 11.3 1924 13 US-10-027-632-199838 Seque 28 33.6 11.2 693 17 US-10-027-632-194612 Seque 29 33.2 11.1 1483 22 US-10-027-632-194612 Seque 29 33.2 11.1 1483 22 US-10-077-632-194612 Seque 29 33.2 11.1 34548 US-10-077-632-104612 Seque 29 33.2 11.0 600 22 US-10-972-9598 Seque 29 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2893 17 US-10-027-632-111626 Seque 20 32.8 10.9 2833 17 US-10-741-601-5939 Seque 20 32.8 10.9 2333 17 US-10-741-601-5695 Seque 20 32.8 10.9 23323 17 US-10-741-601-5695 Seque 20 32.8 10.9 23323 17 US-10-741-601-5695 Seque 20 32.8 10.9 23323 17 US-10-741-601-5695 Seque 20 32.8 10.9 23323 17 US-10-741-601-5695 Seque 20 32.8 10.9 23323 17 US-10-741-601-5695 Seque 20 32.8 10.9 23323 17 US-10-741-601-5695 Seque 20 32.8 10.9 20.2 US-10-741-601-5695 Seque 20 32.8 10.9 20.2 US-10-741-601-5695 Seque 20 32.8 10.9 20.2 US-10-741-601-5695 Seque 20 32.8 10.9 20.2 US-10-741-601-5695 Seque 20 32.8 10.9 20.2 US-10-741-601-5695 Seque 20 32.8 10.9 20.2 US-10-741-601-5695 Seque 20 32.8 10.9 20.2 US-10-741-601-5695 Seque 20 32.8 10.9 20.2 US-10-741-601-5695 Seque 20 32.8	18 34.4 11.5 1691139 17 US-10-419-723-1 Seque 24.2 11.4 11.5 1691139 17 US-10-668-397-1 Seque 24.2 11.4 618 13 US-10-027-632-199837 Seque 24.2 11.4 618 13 US-10-027-632-199837 Seque 25.3 34.2 11.4 618 17 US-10-027-632-199837 Seque 25.3 34.2 11.4 618 17 US-10-027-632-199837 Seque 25.3 34.2 11.4 618 17 US-10-027-632-199837 Seque 26.3 34.2 11.4 5923 21 US-10-027-632-199838 Seque 27.3 34 11.3 1924 13 US-10-027-632-199838 Seque 27.3 34 11.3 1924 13 US-10-027-632-199838 Seque 29.3 32.1 11.1 34548 13 US-10-027-632-104612 Seque 29.3 32.2 11.1 34548 13 US-10-027-632-104612 Seque 33.3 11.0 600 22 US-10-972-079-9598 Seque 33.2 11.0 500 22 US-10-972-079-9598 Seque 33.3 11.0 500 22 US-10-972-079-9598 Seque 34.2 10.9 2893 17 US-10-027-632-111626 Seque 34.3 32.8 10.9 2893 17 US-10-027-632-111626 Seque 35.2 10.9 2893 17 US-10-027-632-111626 Seque 36.3 32.6 10.9 2893 17 US-10-077-632-111626 Seque 37.6 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-077-632-111626 Seque 37.8 10.9 2893 17 US-10-741-601-5099 Seque 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9 27.8 10.9	Sequence 930, App	US-09-973-278-5	11	38855	11.7	35	-
16 35 11.7 38855 11 US-09-973-278-930 Seque 18 34.4 11.5 1691139 14 US-10-067-514-1 Seque 18 34.4 11.5 1691139 14 US-10-067-514-1 Seque 19 34.4 11.5 1691139 17 US-10-067-5113 Seque 20 34.2 11.4 618 13 US-10-027-632-19983 Seque 23 34.2 11.4 618 13 US-10-027-632-19983 Seque 24 34.2 11.4 618 17 US-10-027-632-19983 Seque 25 34.2 11.4 618 17 US-10-027-632-19983 Seque 26 34.2 11.4 618 17 US-10-027-632-19983 Seque 27 34.2 11.4 618 17 US-10-027-632-19983 Seque 27 34.2 11.4 618 17 US-10-027-632-19983 Seque 28 33.6 11.2 693 17 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-027-632-104612 Seque 31 11.1 1483 22 US-10-037-632-104612 Seque 31 11.0 500 22 US-10-9598 Seque 32 11.0 500 22 US-10-9598 Seque 33 32.8 10.9 2893 17 US-10-027-632-111626 Seque 34 32.8 10.9 2893 17 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 38 32.6 10.9 2893 17 US-10-037-632-111626 Seque 39 32.6 10.9 2833 12 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 37 2.0 US-10-741-601-5999 Seque 38 2.0 US-10-741-601-5999 Seque 38 2.0 US-10-741-601-5999 Seque 38 2.0 US-10-741-601-5999 Seque 38 2.0 US-10-741-601-5999 Seque 38 2.0 US-10-741-601-5999 Seque 38 2.0 US-10-741-601-5999 Seque	16 35 11.7 38655 11 US-09-973-278-930 Seque 18 34.4 11.5 1691139 14 US-010-067-514-1 Seque 18 34.4 11.5 1691139 17 US-10-067-514-1 Seque 20 34.2 11.4 11.5 1691139 17 US-10-067-511.9 Seque 21 34.2 11.4 618 13 US-10-027-632-199837 Seque 22 34.2 11.4 618 13 US-10-027-632-199837 Seque 23 34.2 11.4 618 17 US-10-027-632-199837 Seque 24 34.2 11.4 618 17 US-10-027-632-199838 Seque 25 34.2 11.4 618 17 US-10-027-632-199838 Seque 26 34 11.3 1924 13 US-10-027-632-199838 Seque 27 34 11.3 1924 13 US-10-027-632-199838 Seque 28 33.6 11.2 693 17 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-027-632-104612 Seque 29 33.2 11.1 1483 22 US-10-027-632-104612 Seque 31.3 11.0 600 22 US-10-972-079-9598 Seque 32.8 10.9 2893 13 US-10-037-632-111626 Seque 34 32.8 10.9 2893 13 US-10-027-632-111626 Seque 35 32.8 10.9 2893 13 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-077-632-111626 Seque 37 32.6 10.9 2893 17 US-10-077-632-111626 Seque 37 32.6 10.9 2893 17 US-10-077-632-111626 Seque 37 32.6 10.9 2893 17 US-10-077-632-111626 Seque 37 32.6 10.9 2893 17 US-10-077-632-111626 Seque 37 32.6 10.9 2893 17 US-10-077-632-111626 Seque 37 32.6 10.9 2893 17 US-10-741-601-2099 Seque 37 32.6 10.9 2333 17 US-10-741-601-5099 Seque 37 32.6 10.9 23323 21 US-10-741-601-5699 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-741-601-5099 Seque 27 20 US-10-74	Sequence 102218,	US-10-027-632-10221	17		11.7	35.2	Н
15   35.2   11.7   2286   17   US-10-027-632-102218   Seque   17   34.4   11.5   1691139   14   US-09-973-278-930   Seque   18   34.4   11.5   1691139   17   US-09-973-278-930   Seque   23   34.4   11.5   1691139   17   US-10-667-514-1   Seque   24.2   11.4   51991140   22   US-10-8679-71139   Seque   23   34.2   11.4   618   13   US-10-072-632-199837   Seque   24.2   11.4   618   13   US-10-077-632-199837   Seque   25   34.2   11.4   618   17   US-10-077-632-199838   Seque   25   34.2   11.4   618   17   US-10-077-632-199838   Seque   25   34.2   11.4   5923   10.5   10.027-632-199838   Seque   25   34.2   11.4   5923   13   US-10-027-632-199838   Seque   25   34.2   11.4   5923   13   US-10-027-632-199838   Seque   25   33.5   11.3   1924   17   US-10-027-632-199838   Seque   25   33.5   11.1   1483   22   US-10-972-104612   Seque   25   33.3   11.0   600   22   US-10-972-079-9594   Seque   25   32   33   33   33   33   33   33	15         35.2         11.7         2286         17         US-10-072-632-102218         Seque           16         35         11.7         138655         11         US-09-973-278-930         Seque           17         34.4         11.5         1691139         14         US-10-067-514-1         Seque           18         34.4         11.5         1691139         17         US-10-067-514-1         Seque           20         34.2         11.4         618         13         US-10-079-71139         Seque           21         34.2         11.4         618         13         US-10-077-632-199837         Seque           22         34.2         11.4         618         17         US-10-077-632-199838         Seque           23         34.2         11.4         618         17         US-10-077-632-199838         Seque           24         34.2         11.4         618         17         US-10-077-632-199838         Seque           25         34.2         11.4         618         17         US-10-077-632-199838         Seque           26         34.2         11.4         618         17         US-10-077-632-199838         Seque	Sequence 102218,	US-10-027-632-10221	13		11.7	35.2	_
14 35.2 11.7 2286 13 US-10-077-632-102218 Seque 15 35.2 11.7 3286 11 US-10-077-632-102218 Seque 17 US-10-077-632-102218 Seque 18 34.4 11.5 1691139 14 US-10-067-514-1 Seque 18 34.4 11.5 1691139 14 US-10-067-514-1 Seque 19 34.4 11.5 1691140 22 US-10-686-397-1 Seque 21 34.2 11.4 618 13 US-10-077-632-199837 Seque 22 34.2 11.4 618 13 US-10-077-632-199837 Seque 23 34.2 11.4 618 17 US-10-077-632-199837 Seque 24 34.2 11.4 618 17 US-10-077-632-199837 Seque 25 34.2 11.4 618 17 US-10-077-632-199837 Seque 25 34.2 11.4 618 17 US-10-077-632-199838 Seque 25 34.2 11.4 618 17 US-10-077-632-199837 Seque 26 34 11.3 1924 17 US-10-077-632-199838 Seque 27 34 11.3 1924 17 US-10-077-632-199838 Seque 28 33.6 11.1 1483 22 US-10-956-157-4561 Seque 29 33.2 11.1 34458 13 US-10-097-079-9597 Seque 29 33.2 11.1 34458 13 US-10-097-079-9597 Seque 29 33.2 11.1 34458 13 US-10-077-079-9597 Seque 29 32.8 10.9 2893 17 US-10-072-079-9597 Seque 29 32.8 10.9 2893 17 US-10-072-079-9597 Seque 20 32.8 10.9 2893 17 US-10-072-632-111626 Seque 20 32.8 10.9 2893 17 US-10-072-632-111626 Seque 20 32.8 10.9 2893 17 US-10-072-632-111626 Seque 20 32.8 10.9 2893 17 US-10-072-632-111626 Seque 20 32.8 10.9 2893 17 US-10-072-632-111626 Seque 20 32.8 10.9 2893 17 US-10-072-632-111626 Seque 20 32.8 10.9 2893 17 US-10-072-632-111626 Seque 20 32.8 10.9 2893 17 US-10-072-632-111626 Seque 20 32.8 10.9 2893 17 US-10-072-632-111626 Seque 20 32.8 10.9 2893 17 US-10-074-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5999 Seque 20 32.8 10.9 23323 11 US-10-741-601-5499 Seque 20 32.8 10.9 23323 11 US-10-741-601-5499	14 35.2 11.7 2286 13 US-10-027-632-102218 Seque 15 35.2 11.7 2286 11 US-0-027-632-102218 Seque 17 3865 11 US-0-027-632-102218 Seque 18 34.4 11.5 1691139 14 US-10-067-514-1 Seque 18 34.4 11.5 1691139 14 US-10-067-514-1 Seque 19 34.4 11.5 1691140 22 US-10-667-514-1 Seque 21 34.2 11.4 618 13 US-10-067-632-199837 Seque 22 34.2 11.4 618 13 US-10-027-632-199837 Seque 23 34.2 11.4 618 17 US-10-027-632-199837 Seque 25 34.2 11.4 618 17 US-10-027-632-199837 Seque 25 34.2 11.4 618 17 US-10-027-632-199837 Seque 25 34.2 11.4 523 21 US-10-027-632-199837 Seque 25 34.2 11.4 523 21 US-10-027-632-199837 Seque 26 34 11.3 1924 17 US-10-027-632-199837 Seque 27 34 11.3 1924 17 US-10-027-632-199837 Seque 28 33.2 11.1 1483 22 US-10-027-632-199838 Seque 28 33.2 11.1 344548 13 US-10-027-632-104612 Seque 29 33.2 11.1 344548 13 US-10-027-632-11626 Seque 33 32.8 10.9 524 20 US-10-972-079-9597 Seque 34 32.8 10.9 524 20 US-10-972-079-9597 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 35 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 36 32.8 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 38 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 37 32.6 10.9 2893 17 US-10-027-632-111626 Seque 38 32.6 10.9 2893 17 US-10-027-632-111626 Seque 38 32.6 10.9 2893 17 US-10-027-632-111626 Seque 38 32.6 10.9 2893 17 US-10-027-632-111626 Seque 38 32.6 10.9 2893 17 US-10-027-632-111626 Seque 38 32.6 10.9 2893 17 US-10-027-632-111626 Seque 39 32.6 10.9 2893 17 US-10-027-632-111626 Seque 39 32.6 10.9 2893 17 US-10-027-632-111626 Seque 39 32.6 10.9 2893 17 US-10-027-632-111629 Seque 39 32.6 10.9 2833 12 US-10-27-632-111629 Seque 39 32.6 10.9 23223 21 US-10-27-632-111629 Seque 50 22 US-10-27-632-111629 Seque 50 22 US-10-27-632-111629 Seque 50 22 US-10-27-632-111629 Seque 50 22 US-10-27-632-111629 Seque 50 22 US-10-27-632-111629 Seque	Sequence 89184, A	US-10-027-632-8	11		11.7	35.2	13
13 35.2 11.7 403 17 US-110-027-632-89184 Seque 15 35.2 11.7 2286 13 US-10-027-632-102218 Seque 15 35.2 11.7 2286 13 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 18 34.4 11.5 1691139 14 US-10-067-514-1 Seque 19 34.4 11.5 1691139 14 US-10-067-514-1 Seque 19 34.2 11.4 618 13 US-10-027-632-199837 Seque 23 34.2 11.4 618 13 US-10-027-632-199837 Seque 24 34.2 11.4 618 13 US-10-027-632-199837 Seque 25 34.2 11.4 618 13 US-10-027-632-199837 Seque 26 34.2 11.4 618 17 US-10-027-632-199837 Seque 26 34.2 11.4 618 17 US-10-027-632-199837 Seque 27 34.2 11.4 618 17 US-10-027-632-199837 Seque 28 33.2 11.3 1924 13 US-10-027-632-199837 Seque 29 33.2 11.3 1924 13 US-10-027-632-199837 Seque 29 33.2 11.1 1448 22 US-10-027-632-199837 Seque 29 33.2 11.1 34488 13 US-10-027-632-194612 Seque 29 33.2 11.1 34488 13 US-10-027-632-104612 Seque 29 33.2 11.1 34488 13 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-027-632-11626 Seque 20 02 US-10-	13         35.2         11.7         403         17         US-10-027-632-89184         Seque           14         35.2         11.7         2286         13         US-10-027-632-102218         Seque           15         35.2         11.7         2286         13         US-10-027-632-102218         Seque           17         34.4         11.5         1691139         14         US-10-067-514-1         Seque           19         4.4         11.5         1691139         17         US-10-067-514-1         Seque           20         34.4         11.5         1691139         17         US-10-067-513-1         Seque           21         34.4         11.5         1691139         17         US-10-07-032-19983         Seque           22         34.2         11.4         618         13         US-10-027-632-19983         Seque           23         34.2         11.4         618         17         US-10-027-632-19983         Seque           24         34.2         11.4         618         17         US-10-027-632-19983         Seque           25         34.2         11.4         618         17         US-10-027-632-19983         Seque	89184,	US-10-027-632-8	13		11.7	35.2	12
12 35.2 11.7 403 13 US-10-077-632-89184 Seque 13 55.2 11.7 2286 13 US-10-027-632-89184 Seque 14 35.2 11.7 2286 13 US-10-027-632-102218 Seque 15 11.7 2286 11 US-10-027-632-102218 Seque 17 2286 11 US-10-027-632-102218 Seque 17 2286 11 US-10-027-632-102218 Seque 18 34.4 11.5 1691139 17 US-10-67-514-1 Seque 18 34.4 11.5 1691139 17 US-10-67-514-1 Seque 18 34.2 11.4 618 13 US-10-972-079-71139 Seque 23 34.2 11.4 618 13 US-10-077-632-199837 Seque 24 34.2 11.4 618 13 US-10-077-632-199837 Seque 25 34.2 11.4 618 17 US-10-077-632-199838 Seque 25 34.2 11.4 5923 1 US-10-027-632-199838 Seque 26 34.2 11.4 5923 1 US-10-027-632-199838 Seque 27 34.2 11.4 5923 1 US-10-027-632-199838 Seque 28 33.6 11.3 1924 13 US-10-027-632-199838 Seque 28 33.6 11.3 1924 13 US-10-027-632-199838 Seque 29 33.2 11.1 1483 22 US-10-027-632-199838 Seque 29 33.2 11.1 34548 13 US-10-027-632-104612 Seque 29 33.2 11.1 34548 13 US-10-077-032-104612 Seque 29 32.8 10.9 2893 17 US-10-972-079-9597 Seque 39 32.8 10.9 2893 17 US-10-972-079-9597 Seque 39 32.8 10.9 2893 17 US-10-972-079-9597 Seque 39 32.8 10.9 2893 17 US-10-972-079-9598 Seque 39 32.8 10.9 2893 17 US-10-972-079-9598 Seque 39 32.8 10.9 2893 17 US-10-972-079-9599 Seque 39 32.8 10.9 2893 17 US-10-21-61-382 Seque 39 32.8 10.9 2833 11 US-10-741-601-2010 Seque 39 32.8 10.9 2833 11 US-10-741-601-5895 Seque 40 32.6 10.9 53323 21 US-10-741-601-5895 Seque 41 32.6 10.9 53323 21 US-10-741-601-5895 Seque 41 32.6 10.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque 50 0.9 53323 21 US-10-741-601-5895 Seque	12 35.2 11.7 403 13 US-10-077-632-89184 Seque 135.2 11.7 2286 17 US-10-027-632-102218 Seque 14 35.2 11.7 2286 17 US-10-027-632-102218 Seque 15 35.2 11.7 2286 17 US-10-027-632-102218 Seque 15 35.2 11.7 38855 11 US-00-937-238-930 Seque 16 34.4 11.5 1691139 17 US-10-0419-723-1 Seque 17 US-10-10-10-10-10-10-10-10-10-10-10-10-10-	6887,	US-10-719-993-6	20	5	12.3	36.8	-
11 36.8 12.3 290367 20 US-10-719-993-6887 Seque 12 35.2 11.7 403 13 US-10-027-632-89184 Seque 13 55.2 11.7 2286 13 US-10-027-632-102218 Seque 13 55.2 11.7 2286 13 US-10-027-632-102218 Seque 13 51.2 11.7 2286 11 US-00-027-632-102218 Seque 17 38.4 11.5 1691139 14 US-10-027-632-102218 Seque 17 38.4 11.5 1691139 17 US-10-067-514-1 Seque 18 34.2 11.4 618 13 US-10-067-512-199837 Seque 23 34.2 11.4 618 13 US-10-027-632-199837 Seque 23 34.2 11.4 618 13 US-10-027-632-199837 Seque 24 34.2 11.4 618 17 US-10-027-632-199837 Seque 25 34.2 11.4 618 17 US-10-027-632-199837 Seque 25 34.2 11.4 618 17 US-10-027-632-199838 Seque 25 34.2 11.4 618 17 US-10-027-632-199838 Seque 26 34.2 11.4 618 17 US-10-027-632-199838 Seque 27 34.2 11.4 618 17 US-10-027-632-199838 Seque 28 33.6 11.3 1924 13 US-10-027-632-199838 Seque 28 33.6 11.1 1483 22 US-10-927-032-104612 Seque 29 33.2 11.1 34458 13 US-10-027-632-104612 Seque 29 33.2 11.1 34458 13 US-10-027-632-104612 Seque 29 33.2 11.1 34458 13 US-10-027-632-104612 Seque 29 33.2 11.1 34458 13 US-10-027-632-104612 Seque 29 33.2 11.1 34458 13 US-10-027-632-104612 Seque 20 0.0 2 US-10-932-0.0 9.5 9.5 8 0.0 9.2 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0.0 0	11         36.8         12.3         290367         20         US-10-719-997-6887         Seque           12         35.2         11.7         403         13         US-10-027-632-89184         Seque           13         35.2         11.7         403         13         US-10-027-632-102218         Seque           14         35.2         11.7         2286         13         US-10-027-632-102218         Seque           15         31.7         11.7         38855         11         US-10-027-632-102218         Seque           17         34.4         11.5         1691139         14         US-10-027-632-102218         Seque           20         34.2         11.4         11.5         1691140         2         US-10-067-514-1         Seque           21         34.2         11.4         618         13         US-10-067-514-1         Seque           22         34.2         11.4         618         13         US-10-067-512-109833         Seque           23         34.2         11.4         618         13         US-10-027-632-199833         Seque           24         34.2         11.4         618         13         US-10-027-632-199833         Seque <td>958, A</td> <td>US-10-087-192-958</td> <td>13</td> <td>20</td> <td>12.3</td> <td>36.8</td> <td>-</td>	958, A	US-10-087-192-958	13	20	12.3	36.8	-
10 36.8 12.3 204621 13 US-10-087-192-958 Seque 12.3 20367 20 US-10-719-993-6887 Seque 13.5.2 11.7 2286 13 US-10-027-632-102218 Seque 13.5.2 11.7 2286 13 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 17 US-10-027-632-102218 Seque 18 US-10-027-632-103218 Seque 19 US-10-027-632-103218 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-10331 Seque 19 US-10-027-632-104612 Seque 19 US-10-037-632-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-037-032-104612 Seque 19 US-10-038-1038-10	10 36.8 12.3 204621 13 US-10-087-192-958 Seque 12.3 20367 20 US-10-719-993-6887 Seque 13.5.2 11.7 2286 13 US-10-027-632-102218 Seque 14.5.2 11.7 2286 13 US-10-027-632-102218 Seque 17.3 2286 11.7 2286 13 US-10-027-632-102218 Seque 17.3 2286 11.7 2286 13 US-10-027-632-102218 Seque 17.3 11.7 2286 13 US-10-027-632-102218 Seque 17.4 11.5 1691139 14 US-10-027-632-102218 Seque 17.4 11.5 1691139 14 US-10-027-632-19913 Seque 17.4 11.5 1691139 14 US-10-027-632-19913 Seque 17.4 11.5 1691139 14 US-10-027-632-19913 Seque 17.4 11.5 1691139 14 US-10-027-632-19913 Seque 17.4 11.4 618 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-19913 Seque 17.4 11.3 1924 13 US-10-027-632-111626 Seque 17.4 11.3 1924 13 US-10-027-632-111626 Seque 17.4 11.3 1924 13 US-10-027-632-111626 Seque 17.4 11.3 1924 13 US-10-027-632-111626 Seque 17.5 11.5 11.5 11.5 11.5 11.5 11.5 11.5	129675	US-10-027-632-12967	17		13.5	40.4	
9 40.4 13.5 563 17 US-10-027-632-129675 Sequence 1290 10 36.8 12.3 204621 13 US-10-019-939-6887 Sequence 6980 11 36.8 12.3 204621 13 US-10-019-939-6887 Sequence 6981 12 35.2 11.7 2286 13 US-10-027-632-89184 Sequence 8910 13 35.2 11.7 2286 13 US-10-027-632-89184 Sequence 1021 14.4 11.5 1691139 14 US-10-027-632-102218 Sequence 1021 15 34.4 11.5 1691139 14 US-10-027-632-102218 Sequence 1021 16 34.4 11.5 1691139 17 US-10-027-632-103018 Sequence 1021 17 34.4 11.5 1691139 17 US-10-027-632-19931 Sequence 1031 18 34.4 11.5 1691139 17 US-10-027-632-19931 Sequence 1031 18 34.2 11.4 618 13 US-10-027-632-19933 Sequence 1031 18 34.2 11.4 618 17 US-10-027-632-19933 Sequence 1031 18 34.2 11.4 618 17 US-10-027-632-19933 Sequence 1031 18 34.2 11.4 618 17 US-10-027-632-19933 Sequence 1031 18 34.2 11.4 618 17 US-10-027-632-19933 Sequence 1031 18 32.1 11.3 1924 13 US-10-027-632-19933 Sequence 1031 18 32.1 11.3 1924 13 US-10-027-632-19933 Sequence 1031 18 32.1 11.3 1924 13 US-10-027-632-19933 Sequence 1031 18 32.1 11.3 1924 13 US-10-027-632-19933 Sequence 1031 18 32.8 10.9 2893 17 US-10-92-34 Sequence 1031 18 32.8 10.9 2893 17 US-10-92-34 Sequence 1031 18 32.8 10.9 2893 17 US-10-92-34 Sequence 1031 18 32.8 10.9 2893 17 US-10-027-632-111626 Sequence 1031 18 32.8 10.9 2893 17 US-10-027-632-111626 Sequence 5931 18 32.8 10.9 2893 17 US-10-027-632-111626 Sequence 5931 18 32.8 10.9 10-91-91-91 US-10-91-699 Sequence 5931 18 32.8 10.9 10-91-91-91 US-10-91-699 Sequence 5931 18 32.8 10.9 10-91-91-91 US-10-91-699 Sequence 5931 18 32.8 10.9 10-91-91-91-91-91-91-91-91-91-91-91-91-91-	9 40.4 13.5 563 17 US-10-027-632-129675 Seque 10 36.8 12.3 200467 1 13 US-10-079-9518 Seque 11.3 200467 1 13 US-10-079-951-887 Seque 11.3 20047 1 13 US-10-077-632-89184 Seque 11.3 2286 11.7 403 17 US-10-027-632-89184 Seque 11.5 16311.7 2286 17 US-10-027-632-102218 Seque 12.3 211.7 2286 17 US-10-027-632-102218 Seque 12.3 11.7 2286 17 US-10-027-632-102218 Seque 12.3 11.7 2286 17 US-10-027-632-102218 Seque 12.3 11.7 2286 17 US-10-027-632-102218 Seque 12.3 11.7 2286 17 US-10-027-632-102218 Seque 12.3 11.4 618 17 US-10-027-632-19983 Seque 12.3 11.4 618 17 US-10-027-632-19983 Seque 12.3 11.4 618 17 US-10-027-632-19983 Seque 12.3 11.4 618 17 US-10-027-632-19983 Seque 12.3 11.3 1924 13 US-10-027-632-19983 Seque 12.3 11.3 1924 13 US-10-027-632-19983 Seque 12.3 11.3 1924 13 US-10-027-632-19983 Seque 12.3 11.3 1924 13 US-10-027-632-19983 Seque 12.3 11.3 1924 13 US-10-027-632-19983 Seque 12.3 11.3 1924 13 US-10-027-632-19983 Seque 12.3 11.3 1924 13 US-10-027-632-19983 Seque 12.3 11.3 1924 13 US-10-027-632-19983 Seque 13.3 11.0 600 22 US-10-92-929 Seque 13.3 11.0 600 22 US-10-92-929 Seque 13.3 11.0 600 22 US-10-92-02-92-92-92-92-92-92-92-92-92-92-92-92-92	mence 12967	US-10-027-632-12967	13		13.5	40.4	

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APPLICANT: Finzer, Patrick
APPLICANT: Delius, Hajo
APPLICANT: Delius, Hajo
APPLICANT: Delius, Hajo
APPLICANT: Delius, Hajo
APPLICANT: Durkaka, Annemarie
APPLICANT: Zur Hausen, Harald
APPLICANT: Patzelt, Andrea
TITLE OF INVENTION: No. US20020106355Alel Regulatory Sequences of the MCP-1 Gene
TITLE OF INVENTION: NUMBER: US/09/899,276
CURRENT APPLICATION NUMBER: US/09/899,276
CURRENT FILING DATE: 2001-07-06
MUMBER OF SEQ ID MOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 300
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100.0%; Score 300; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 5e-88;
Matches 300; Conservative 0; Mismatches 0; Indels
Sequence 5, Application US/09899276 Patent No. US20020106355Al GENERAL INFORMATION:
                                                                                    APPLICANT: Rosl, Frank
APPLICANT: Soto, Ubaldo
APPLICANT: Coy, Johannes
APPLICANT: Finzer, Patrick
APPLICANT: Delius, Hajo
APPLICANT: Poustka, Annemarie
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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265 AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG 324

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Pred. No. 1.2e-87;
1; Mismatches 0
                                                                                                                  US-10-027-632-121412
; Sequence 121412, Application US/10027632
; Publication No. US20030204075A9
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Best Local Similarity 99.77
Matches 299; Conservative
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                                                                           61 TIAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT 120
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Sequence 121412, Application US/10027632

Publication No. US2020198371A1

GENERAL INFORMATION:

GENERAL INFORMATION:

GENERAL INFORMATION:

FAPLICATION

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION WUMBER: US 60/218,006

PRIOR FILING DATE: 2000-00-12

PRIOR FILING DATE: 2000-04-20

PRIOR PLING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/185,218

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 1909-11-23

PRIOR FLING DATE: 1999-109-28

PRIOR FLING DATE: 1999-109-28

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-09-08

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-09

PRIOR PLING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SEQ ID NO 121412

LENGTH 1934
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                                    1 AAGGAGGAGGCAGTGGCTAGGAGAATCGAGAGATCAGAATTTTAAACTCAGCCCAGCCA
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Pred. No. 1.2e-87;
1; Mismatches 0;
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Best Local Similarity 99.7%;
Matches 299; Conservative
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RESULT 4
US-10-685-705-3
Sequence 3, Application US/10685705
Sequence 3, Application No. US20040177387A1
GENERAL INFORMATION:
APPLICANT: UNIVERSITY of Kentucky Research Foundation
APPLICANT: UNIVERSITY, of Ambati
TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ICTAAGGICTITIGGGITTITIATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGCAC 180
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Tentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: POLYMORPH: US/10/027,632
CURRENT FILING DATE: 2002-04-30
FRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR PETLING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-24
PRIOR FILING DATE: 1909-01-24
PRIOR PETLING DATE: 1999-11-23
PRIOR PETLING DATE: 1999-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detern
TITLE OF INVENTION: cytosine methylation
FILE REFERENCE: 5013-1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR APPLICATION NUMBER: DET/EP01/07537
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3813 TTTAAGGTTTTTTGGGTTTTTTATAGTGTGTTTTTGTAGTTTTTGAGGAAATTTAAGGTAT 3872
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                         6369 TCTAAGGTCTTTGGGTTTTTTATCAGTGTGCTTCTGTAGTTTCTGAGGAAATCTAAGGCAC
                                                                                                      5429 AACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG
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                                                                                 AACTGAGGAATGAAGTCAGGCTTTCCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1625
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80.0%; Pred. No. 8e-56;
ive 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                     ; Sequence 1625, Application US/10311455; Publication No. US20030143606A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1626, Application US/10311455; Publication No. US20030143606A1; GENERAL INFORMATION: APPLICANT: OLEK, Alexander APPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 80.04
Matches 240; Conservative
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US-10-311-455-1626/c
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US-10-311-455-1625
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                                                                                                                                                                                                                                                                                  98.9%; Score 296.8; DB 19; Length 3221; 99.3%; Pred. No. 1.7e-86;
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                                                                                                                                                                                                                                                                                                                          0; Mismatches
            FILE REFERENCE: 050229-0415
CURRENT APPLICATION NUMBER: US/10/685,705
CURRENT FILING DATE: 2003-10-16
FRIOR APPLICATION NUMBER: 60/422,096
PRIOR FILING DATE: 2002-10-30
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
LENGTH: 3221
TITLE OF INVENTION: Degeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
LENGTH: 11793
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Matches 298; Conservative
                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; ORGANISM: Homo sapiens
US-10-685-705-4
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GAAGTAGCCGCACAACCTACAATAATCATTTCACTTCTGTTGTTTCATTTGTAAAG 412
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US-10-027-032-129-05.

Sequence 129675, Application US/10027632

Publication No. US20030204075A9

GENERAL INFORMATION:

GENERAL INFORMATION:

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: Polymorphisms in the Human Genome

CURRENT APPLICATION NUMBER: US 60/128,006

PRIOR FILING DATE: 2002-04-30

PRIOR FILING DATE: 2000-07-20

PRIOR PELICATION NUMBER: US 60/198,676

PRIOR PELICATION NUMBER: US 60/198,676

PRIOR PELICATION NUMBER: US 60/198,676

PRIOR PELICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-24

PRIOR PELING DATE: 1999-01-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-08-08

PRIOR FILING DATE: 1999-08-08

PRIOR FILING DATE: 1999-08-08

PRIOR FILING DATE: 1999-08-09

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PRIOR FILING DATE: 1999-08-08

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     352 ATCATTAAGGACAGTIGGAGCAGGGCTGAAAATGAAAGGAGAAATTCTGCTTCCCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   411 GGAAATACTTGAATAAATTAAATGCAACTGCCTCTTTCAACTCAT-TCTATAATATTGTG
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                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                   Score 40.4; DB 13;
Pred. No. 0.018;
0; Mismatches 121;
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                                                                                                                                                                                          13.5%;
52.3%;
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Best Local Similarity 52.3
Matches 137; Conservative
                                                                                                                                                                                              Query Match 13.59
Best Local Similarity 52.33
Matches 137; Conservative
                                 ; IENGTH: 563
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-129675
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US-10-027-632-129675
   SEQ ID NO 129675
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APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Determ
TITLE OF INVENTION: Cytosine methylation
FILE REPRENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT APPLICATION NUMBER: Diagnosis of PRIOR APPLICATION NUMBER: Diagnosis of PRIOR APPLICATION NUMBER: Diagnosis of PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 1626
LENGTH: 5926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTAACATGCCTCAAGTACTCCTATCATATTTGTAAGAGACAACAGTTCACTGAAATGAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181 AACTGAGGAATGAAGTCAGGCTTTCCCAATTCCCGAAATACTCCTCCACTGCTTACTCATG 240
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILTE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2000-04-30
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR APPLICATION NUMBER: US 60/199,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,318
PRIOR PELING DATE: 2000-03-24
PRIOR PELING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens) US-10-311-455-1626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 194.4; DB 15; Length
Pred. No. 1.1e-52;
0; Mismatches 66; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 129675, Application US/10027632 Publication No. US20020198371A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 64.8%;
Best Local Similarity 78.0%;
Matches 234; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-027-632-129675/c
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Query Match
Best Local Similarity 61.1%;
Matches 55; Conservative
                                                                                                                                                                                                                      Best Local Similarity 58.0
Matches 65; Conservative
           ORGANISM: Homo sapiens
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US-10-027-632-89184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-10-027-632-89184
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US-10-027-632-89184
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Publication No. US20040265849A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: ALZHEIMER'S DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION NUMBER: US/10/719,993
CURRENT FILING DATE: 2003-11-24
NUMBER OF SEQ ID NOS: 55342
SOFTWARE: FRASES for Windows Version 4.0
SEQ ID NO 6887
LENGTH: 290367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105675 TTCACAGTCAACACGCAATGAAAGTTTATGAATTTCTCTTTTTATGCTTTGAAGACATA 105616
292 recrercicace---raarrreacrecirigagaaccageraagareragaagerereer 236
                                                                                                                                    352 Arcatiaaksakcastresassaksaksakaraaarisaaaaritstestressasa 293
                                                                                                                                                                                          42 TITAAACTCAGCCCAGCCATTAACAIGCCTCAAGTACTCCTATCATATITGTAAGAGACA
                                                                                 158 GTTTCTGAGGAAATCTAAGGCACAACTGAGGAATGAAGTCAGGCTTTCCAATTCCCGAAA
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APPLICANT: Engelhard, Eric K.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: OCANCER
FILE REFERENCE: 529452000122
CURRENT APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR APPLICATION NUMBER: 2010-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PRESEQ for Windows Version 4.0
LENGTH: 204621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
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12.3%; Score 36.8; Di
Best Local Similarity 58.0%; Pred. No. 4.4;
Matches 65; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                   278 GCCATAACCAGGGATGAACTTC 299
                                                                                                                                                                                                                                                                                                                                          235 TCCATAGCAAGGTATAYATTTC 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 958, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
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OTHER INFORMATION: n = A,T,C or
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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FEATURE:
NAME/KEY: misc feature
LOCATION: (1)....(290367)
COTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1 US-10-719-993-6887)
                                                                                                                                                                                                                                                                                                                                                                                     202461 TTCACAGTCAACACAGCAATGAAAGTTTATGAATTTCTCTTTTTATGAGATTA 202402
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Publication No. US20020198371A1

JERREAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

FRIOR PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-02-26

PRIOR PLING DATE: 1000-02-26

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PLING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PLING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-08

NUMBER OF SEQ ID NOS: 325720

SOFTWARE FREERENCE FREESEQ FOR WINDOWS VERSION 4.0
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                                                                                                                                                                                                                                                                      Gaps
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; Publication No. US2030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        102 ACAGITCACIGAAATGAATICTAAGGICTTTTGGGTTTTTTATCAGTGTGCTTC 153
                                                                                                                                                                                                    Length 290367;
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                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                 12.3%; Score 36.8; DB 20; 58.0%; Pred. No. 5.2; ive 0; Mismatches 47;
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Pred. No. 0.77;
1; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99 ACAACAGTTCACTGAAATGAATTCTAAGGT 128
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APPLICANT: Wang, David G.;
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Identification in the Human Genome
TITLE OF INVENTION: IDENT
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        Polymorphisms in the Human Genome
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61.1%; Pred. No. 0.77;
iive 1; Mismatches 34;
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FILE REFERENCE: 108927.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-12
PRIOR PLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-34
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-38
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Publication No. US20020198371A1
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Matches 55, Conservative
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ORGANISM: Human
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11.7%; Score 35.2; DB 13; Length 2286;

Query Match

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99 ACAACAGTICACTGAAATGAATTCTAAGGTCTTTGGGTTTTTATCAGTGTGCTTCTGTAG 158
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GENERAL INFORMATION:
GENERAL INVESTION:
JETLE OF INVESTION: Identification and Mapping of Single Nucleotide
TITLE OF INVESTION: Polymorphisms in the Human Genome
FILER REFERENCE: 10827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PILING DATE: 2000-07-12
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Best Local Similarity 50.0%; Pred. No. 1.8;
Matches 115; Conservative 0; Mismatches 113; Indels 2;
   ilarity 50.0%; Pred. No. 1.8; Conservative 0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 102218, Application US/10027632; Publication No. US20030204075A9; GENERAL INFORMATION:
Best Local Similarity
Matches 115; Conserv
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Search completed: August 4, 2005, 15:54:22 Job time : 541.142 secs

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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SOURCE
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JOURNAL
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54 Sequence
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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2740 AATGGCACTTAACTACTTGGAGGTCATGGATGCCTTTGCTAATCTAATAGAAGCTACTGA 2799
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Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.
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                                                                                                                                                                                                                                                                                                                 2560 CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGGAGCAGATAGTGC 2619
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
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                                                                                                        Length 11793;
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; Pred. No. 2.7e-76;
0; Mismatches 0;
8968. .>9073
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/number=3
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                                                                                                               Query Match
Best Local Similarity 100.0%;
Matches 300; Conservative 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Finzer,P., Soto,U., Delius,H., Patzelt,A., Coy,J.F., Poustka,A., zur Hausen,H. and Rosl,F.

zur Hausen,H. and Rosl,F.

zur Hausen,H. and Rosl,F.

poliferential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HPV 18 positive cells: the role of the chromatin extructure and AP-1 composition

structure and AP-1 composition

oncogene 19 (29), 3235-3244 (2000)
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Submitted (15-APR-1999) F. Roesl, Applied Tumor Virology, DKFZ
German Cancer Research Institute), Im Neuenheimer Feld 506, 69120
Heidelberg, FRG
                                                                                241 ANTGGCACTTAACTACTTGGAGGTCATGGATGCCTTTGCTAATCTAATAGAAGCTACTGA 300
                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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'gene="MCP-1"
                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                   Y18933.1 GI:10933860
MCP-1 gene; monocyte chemoattractant protein-1.
Homo sapiens (human)
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Homo sapiens MCP-1 gene and enhancer region.
Y18033
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HSY18933
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7119. 716
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337. .7636
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   Only the first 147416 bases of this clone are being submitted. Bases 145417-155040 overlap accession number AC004147 (WICGR project 1228). The first 200 of the overlapping region are submitted to confirm overlap. Location/Qualifiers
 Lehoczky, J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             clone="hRPK.215 E 13"
clone_lib="RPCI-11 human BAC library"
Jacotot, L., Jones, C., Kann, L., Karatas, A.
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6574. .6600
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1291. .1390
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2980. .3131
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5406. .6455
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ACC21222 177426 bp DNA linear HTG 07-JUL-2000
Homo sapiens chromosome 11 clone RP11-567M21, WORKING DRAFT
SEQUENCE, 30 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variation, R.H.
Direct Submission
Submitted (15-JAN-2000) Genome Sequencing Center, Washington
Submitted (15-JAN-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On May 12, 2000 this sequence version replaced gi:7233676.
              TICAATGGCACTTAACTACTTGGAGGTCATGGATGCCTTTGCTAATCTAATAGAAGCTAC 297
                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 177426)
Waterston, R.H.
IGAAGCCCAGAACTCTCTGATAAA
                                                                       arbitrary. Gaps between the contige are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This is a 'working draft' sequence. It currently consists of 30 contigs. The true order of the pieces is not known and their order in this sequence record is
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1144: gap of unknown length
2529: contig of 1385 bp in length
2629: gap of unknown length
3739: contig of 1110 bp in length
5188: contig of 1349 bp in length
      178 ATAMAMATGCAGACTGTGATTCAGCAGGTCTGGGT
                                                                                                                                                                                                                                                                                                                                                                                                       The sequence of Homo sapiens clone Unpublished
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HTG; HTGS PHASE1; HTGS_DRAFT.
Homo sapiens (human)
Homo sapiens
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1. .5926
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                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AAAAATGCAGACTGTGATTCAGCAGGTCTGGAGTTGAAGCCCCAGAACTCTCTGATAAATTC
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1625 03-JAN-2002;
Epigenomics AG (DE)
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                                                                                                                                                                                                          Length 147416;
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Best Local Similarity 100.0%; Pred. No. 2.9e-76;
Matches 300; Conservative 0; Mismatches 0;
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Sequence 1625 from Patent WO0200928.
AX346554
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4781. 44811

419. family="AT_rich"

4184. 46296

/rpt family="MIR"

complement (4705. 47140)

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complement (47266. 47307)

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complement (47266. 34742)

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Tue Aug

100080 CTGAGACAGGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAGTGAGCCGAGATCGCAC 100021 61 CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG Gapa ö Query Match 54.7%; Score 164; DB 2; Length 177426; Best Local Similarity 84.1%; Pred. No. 9e-37; Matches 185; Conservative 0; Mismatches 35; Indels 0; 99960 AAAAAAAAGAATGCTAAGCAACAGGCCAGGCATGGTGGC 99921 AAAAATGCAGACTGTGATTCAGCAGGTCTGGGTTGAAGCC 220 15740. .18805 / note="assembly_name:Contig21" | 18906. .21750 / note="assembly_name:Contig21" | 21851. .24673 / note="assembly_name:Contig22" / note="assembly_name:Contig23" / 24774. .27874 clone end: T7 vector_side:left"
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RESULT 6 AP003041/c

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Homo sapiens genomic DNA
Homo sapiens genomic DNA
L Homblished Only in Database (2000)
E 2 (bases 1 to 188172)
RS Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fuliyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
AL Submitted (11-DEC-2000) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Submiro-chou,Turumi,Vu, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-911/, Fax:81-45-503-9170)
On Aug 9, 2002 this sequence version replaced gi:20334333.

Location/Qualifiers
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| Mol_type="genomic DNA" |
| Map="HIM" |
| Map="HIM" |
| Map="HIM" |
| Clone="RP11-567W21" |
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Homo sapiens genomic DNA, chromosome 11 clone:RP11-567M21, complete
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1 (bases 1 to 238472)

DOE Joint, Genome Institute and Stanford Human Genome Center.
                                                                                                                                      Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalla; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens chromosome 5 clone CTB-125B20, complete sequence.
ACO10290
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Pred. No. 9e-37;
); Mismatches 35; Indels 0;
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Unpublished
2 (bases 1 to 238472)
DOE Joint Genome Institute.
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                                                                          AP003041.3 GI:22202826
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                                                                                                           Homo sapiens (human)
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171312 AAAATACAAAATTAGCCAGGTGTGATGGCATGTGACTGTAGTCCCCAGCTACTAGGGAGG 171253
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On Mar 7, 1999 this sequence version replaced gi:4056528.

On Mar 7, 1999 this sequence are compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation may not be found in the sequence submission variation on the overlapping clone, as we submit sequences with only a small overlap as described above.

The following abbreviations are used to associate primary accession the following abbreviations are used to associate primary accession
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Human DNA sequence from clone RP1-28H20 on chromosome 20q13.1
Contains the SLC2A10 gene encoding a solute carrier family 2
(facilitated glucose transporter) member 10, the 5' end of a novel
gene, BSTs, STSs, GSSs and three CpG islands, complete sequence.
AL031055.1 dg:4375937
HTG; CpG island; SLC2A10.
Homo sapiens (human)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 127418)
Ramsay,H.
Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 238472)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                      Direct Submission
Submitted (23-OCT-2001) DOB Joint Genome Institute, 2800 Mitchell
Submitted (23-OCT-2001) DOB Joint Genome Institute, 2800 Mitchell
Direc, Walnut Creek, CA 94598, USA
On Oct 23, 2001 this sequence version replaced gi:7711412.
Draft Sequence Produced by DOB Joint Genome Institute
Www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
Www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.7% of Sequence;
Estimated Total Number of Errors is 0.5.
I. 238472
I. 238472
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
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Pred. No. 9.1e-37;
0; Mismatches 35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171132 AAAAAAAAAAAAGAATGCTAAGCAACAAGGCCAGGCATGGTGGC 171093
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol type="genomic DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="CTB-125B20"
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nilarity 84.1%;
Conservative 0
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3963. .5655
/note="LIMA8 repeat: matches 4532. .6270 of consensus"
5669. .5895
/note="LIME repeat: matches 5501. .5739 of consensus"
6332. .6548
/note="LI repeat: matches 2524. .2746 of consensus"
                                                                                                                                                                    .391 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="LTR16C repeat: matches 126. .316 of consensus"
0631. .10690
note="MLT1D repeat: matches 445. .505 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="MLTID repeat: matches 445. .505 of consensus" 0691. .10995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="AluJb repeat: matches 1. .295 of consensus" 10996. .11200 / note="MLT1D repeat: matches 248. .445 of consensus" 11322. .11634 / note="MSTB repeat: matches 2. .409 of consensus" 11670. .11761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="MLTID repeat: matches 128. .192 of consensus"
1762. .12062
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12063. .12180
/note="WirID repeat: matches 1. .128 of consensus"
complement(12181. .12344)
/note="match: GSS: Em:AQ190762"
13011. .13129
/note="WirIJ repeat: matches 252. .368 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 864. .7934
note="MLT1I repeat: matches 311. .382 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1685. 8793
note="MLT1J repeat: matches 271. .366 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="MIR repeat: matches 104. .146 of consensus" 3660. .13783 repeat: matches 330. .452 of consensus" note="LTR33 repeat: matches 330. .452 of consensus"
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/note="MERS8A repeat: matches 42. 220 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="AluJo repeat: matches 74. .306 of consensus"
0038. .10206
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14446. .14525
/note="4 copies 20 mer 76% conserved"
15752
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1note="L2 repeat: matches 2389. .2513 of consensus"
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/note="L2 repeat: matches 2657. .2744 of consensus"
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note="MIR repeat: matches 102. .242 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            .290 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .312 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8347. .8647
/note="AluSq repeat: matches 1. .300 of consensus"
8685. .8793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    457. .7623 <sup>-</sup>
'note="MIR repeat: matches 93. .262 of consensus"
'864. .7934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .62 of consensus"
                                                                                                                                  1865. .3962
/note="MER21B repeat: matches 299.
                                                                                                                                                                                                                                                                                                                                                                                                                 6626. .6915
/note==#AluSx repeat: matches 3.
6918. .6980
/note==#RER94 repeat: matches 1.
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/note="AluJo repeat: matches 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8046. .8240
/note="MLT1J repeat: matches 9.
8347. .8647
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note="L2 repeat: matches 2170.
                                                                                        /note="match: STS: Em:G15621"
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'note="MER20 r
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numbers given in the feature table with their source databases:
Em:, EMBL; Sw.; SWISSROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C elegans/wormpep This sequence
thromosome 20, constructed by the Sanger Centre Chromosome 20
chromosome 20, constructed by the Sanger Centre Chromosome 20
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr20
This sequence is the entire insert of clone RPI-28H20 This sequence
was finished as follows unless otherwise noted: all regions were
cither double-stranded or sequenced with an alternate chemistry or
covered by high quality data (i.e., phred quality >= 30); an
attempt was made to resolve all sequencing problems, such as
compressions and repeats; all regions were covered by at least one
plasmid subclone or more than one M13 subclone; and the assembly
was confirmed by restriction digser. RPI-28H20 is from the library
Application or more than one M15 subclone; and the all brance and the second and the second and the second and the second and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="dJ28H20.2 (novel protein)"
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Em:AA60132 Em:AA483490 Em:AA646575"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [251. 1353 Table matches 50. 151 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .262 of consensus"
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note="MIR repeat: matches 8. .135 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /evidence=not_experimental
18. .494
10. .494
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continues in Em:ALi33520 as dJ101A2.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .135 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EAFLKSYSTSSKKARPVLKKLDEVRLRGRKRSMVG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(join(<1. .562,2463.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .855. .2079
note="MIR repeat: matches 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="MIR repeat: matches 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP1-28H20"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="CpG island"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /chromosome="20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="Epsilon-COP"
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/note="Clathrin-ordered protein; identified by sequence
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12465. 12590)
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/note="Clathrin -ordered protein; Identified through
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(87% identity; 232554) and B. taurus (89% identity;
X76980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="LL19NCO3 cosmid library constructed at LLNL from flow-sorted chromosomes from hybrid 5HL2-B, which carries chromosome 19 as its only human chromosome."
                                                                                                                                                                                                                        Cosmid R27090 overlaps cosmid R32469 to the left and cosmid R31317 to the right.
                                                                                       Lamerdin, J.B.
Direct Submission
Submitted (22-OCT-1997) Human Genome Center, Lawrence Livermore Submitted (12-OCT-1997) Human Genome Center, Cay 94551, USA National Laboratory, 7000 East Ave., Livermore, CA 94551, USA Map and sequence oriented from p telomere to centromere.
Submitted (29-SEP-1997) Human Genome Center, Lawrence Livermore National Laboratory, 7000 East Ave., Livermore, CA 94551, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_lib="LL19NC03 R chromosome 19-specific cosmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /map="19p12 between UBA52 and D19S451"
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3583. .327
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8300. .847
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complement(7998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="Alu"
complement(2762.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'clone="R27090"
                                                                (bases 1 to 38041)
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                                                                REFERENCE
AUTHORS
                                                                                                                     TITLE
JOURNAL
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                JOURNAL
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1 (Dases I to 3804).

1 (Dases I to 3804).

1 (Dases I. To Saloi, Morceady, P.M., Adamson, A.W., Burkhart-Schultz, K., Garcia, E., Kyle, A., Ramirez, M., Stilwagen, S., Garnes, J., Danganan, L., Bruce, R., Quan, G., Montgomery, M., Ow, D., Kobayashi, A., Olsen, A.O. and Carrano, A.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AC002985 38041 bp DNA linear PRI 22-OCT-1997
Human DNA from chromosome 19-specific cosmid R27090, genomic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="LiMA10 repeat: matches 6162. .6284 of consensus"
16804. .17190
/note="MER57B repeat: matches 1. .403 of consensus"
17198. .17297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAATAGTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19343. .19485
//note="MERS2 repeat: matches 2. .180 of consensus"
19721. .20190
//note="LTR8 repeat: matches 251. .691 of consensus"
20238. .20493
                                                                                                     .2657 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="AluJb repeat: matches 1. .296 of consensus" 6600. .16635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 127418;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                  note="5 copies 20 mer 71% conserved"
.7204. .17297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 163.4; DB 9
Pred. No. 1.3e-36;
                                                                                                  /note="L2 repeat: matches 2617.
16641. .16803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
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2 (bases 1 to 38041)
Lamerdin, J.E.
Direct Submission
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ilarity 82.1%;
Conservative
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Homo sapiens
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Best Local Similarity
Matches 188; Conserv
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AUTHORS
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                                                                                         /product="R27090_3"
/protein_id="AABB1545.1"
/db_xref="G1:2443811"
/translation="WATAREQPIFSTRAHVPQIDPATKRNWIPAGKHALTVSYFYDAT
/translation="WATAREQPIFSTRAHVPQIDPATKRNWIPAGKHALTVSYFYDAT
RNVYRIISIGGAKAIINSTVTPDNWTPTKTSQKFGQWADSRANTVYGLGFASEQHLTQF
                                                                                                                                                                                                                                     AEKFQEVKEAARLAREKSQDGGELTSPALGLASHÕVSTPYSPMPAWAPVPPSPLVSÄN
GPGEEKLFRSQSADAPGPTERERLKKMLSEGSVGEVQWEAEFFALQDSNNKLAGALRE
ANAAAAQWRQQLEAQRAEAERLRQRVAELEAQAASEVTPTGEKEGLGQGGSLEQLEAL
                                                                                                                                                                                                                                                                                                                     votkdobiotilksotgeprealegaereetookvodietrnaeleholpamereleea
raereraraevoraaolldvslfelselregiarlaeaap"
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Homo sapiens chromosome 3 clone RP11-10315, *** SEQUENCING IN
PROGRESS ***, 21 unordered pieces.
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I (bases I to 80952)
Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Ayele, M., Banks, T., Bancen, J., Bancon, J., Balmage, K., Bankenburg, K., Bonnin, D., Buock, J., Bowie, S., Brieva, M., Brown, B., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27125 AAAATACAAAAATTAGCCAGGCGTGGTGGCATGCGCCTGTAGTCCCAGCTACTCGGGAGG
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AA202832,AA246370"
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Pred. No. 7.3e-36;
0; Mismatches 27; Indels
                                                                                                                                                                                                                                                                                                                                                                        Complement (23068. .23216)
/rpt family="Alu"
23531. .23507
/rpt family="Alu"
23535. .24266
/rpt family="Alu"
/rpt family="Alu"
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/rpt_family="Alu"
/s950. .30567
/rpt_family="Alu"
30657. .30931
/rpt_family="Alu"
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86.8%;
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Best Local Similarity 86.8<sup>3</sup>
Matches 177; Conservative
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AC012094/c
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// note="BLASTN similarity to 241188 (1. 67); match: 0.94,
score: 8.5e-89; database searched: e6t; H. sapiens partial
cDNA sequence.

complement (join(22685. 22876,24567. 24653,24751. 24867,
25218. 22374,28166. 26287,27566. 27652,31595. 31726,
31970. 32126,32211. 332244)

// note="Hypothetical 41.3 kDa human protein most similar to
veal and GLGF proteins of rat; Residues 1-128 of
hypothetical protein 827090 3 are 81% identical to Rat
GLGF protein (1092079) and 83% identical to Rat veal
protein (AB003726), both proteins are expressed in brain
and upregulated during seizures.

Human EST matches: M42820, AA121538, W42730, AA127702

MOUSE EST matches: AA407944, AA408331, AA013888, AA035853,
/rpt_family="MLTI"

complement(10611. .10904)

/rpt_family="Alu"

ll160 .11445

/rpt_family="Alu"

complement(11721. .11961)

/rpt_family="Alu"

join(12984. .13098.13822. .13945,14905. .14990,15085. .15206,

15568. .15755,15846. .15986,17475. .17550,17865. .17941,

18124. .18221,19545. .19619,21008. .21096,21207. .21278,
                                                                                                                                                                                                                                                                                     21370. .21558)
/ note="Hypochetical 56kDa human ATP-dependent RNA helicase; Putative ATP-dependent RNA helicase of DEAD box family. Most similar (F7* identical) to probable ATP-dependent RNA helicase Dbp45A (S38329) - fruit fly (Drosophila melanogaster)
Human BST matches: AA534472, H08289, AA464032, AA196836, AA569862, AA573466, AA64741, W46150, AA535538, AA488261, W46162, R00974, AA378518, R26194, R15246, AA359638, etc. Mouse EST matches: AA271508
Drosophila BST matches: AA540379
Rat EST match: H35240"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="BidSTN similarity to Z41188 (216. 289); match:
0.85, score: 3.5e-33; database searched: est; H. sapiens
partial CDNA sequence"
complement (21611. 21871)
/note="BiASTN similarity to T16014 (1. 261); match: 0.94,
score: 1.1e-90; database searched: est; IB2449 Infant
brain, Bento Soares Homo sapiens cDNA 3'end."
complement (21615. 21825)
/note="BiASTN similarity to Z41188 (42. 252); match: 0.92,
score: 8.5e-89; database searched: est; H. sapiens partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MAGFAELGLSSWLVBQCRQLGLKQPTPVQLGCIPALLEGRDCLG
CAKTGSGKTAARVLPINGLSEDPYGIFCLUTPTRELAYQIARQFRYLGKPLGLKDC
CAKTGSGKTAARVLPINGLSEDPYGIFCLUTPTRELAYQIARQFRYLGKPLGLKDC
GCTGFTVDLEAXILAAVDARRQTLFSANTLTDTLRELQGLATNQPFFREAQAPVSTVBG
LDQRYLLVPEKVKDAYLVHLIQRFQDEHEDWSIIIFTNTCKTCQILCWMLRKFSFPTV
ALHSWMKQKBRRPAALAKFKSSIYRILLATDVAASRGLDIPTVQVVINHYTPGLRYIYIH
RVGRTARAGRQGQAITLUVTQYDIHLVHAIEGQIKKKLBEFSVBEAEVLQILTQVNVVN
RECEIKLBAAHFDERKEINKRKQLILEGKDPDLGAKKKAEFFSVBEAEVLQILTQVNVVN
RECEIKLBAAHFDERGHKGRPFRLEGROPDLGAKKAAELAKIKQKORRFKEKVEFT
LARQCAGGAHKGRPPRTPSGSHSGPVPSQGLV"
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/rpt family="Alu"
complement (17052.
/rpt family="Alu"
18360. 18802
/rpt family="Alu"
/rpt family="Alu"
/rpt family="Alu"
/rpt family="Alu"
complement (21577. 21650)
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/product="R27090_2"
/protein_id="AABB1544.1"
/db_xref="GI;2443870"
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'rpt_family="Alu"
                                      repeat_region
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Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, R., Chen, R., Chowdhry, I., Christopoulos, C., Chel, G., Chen, R., Coyle, M.D., Daud, J.B., David, R., David, R., David, M.L., David, C., David, M.L., David, C., David, R., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.R., Delgado, O., Denn, A.L., Ding, Y., Dinh, H.H., Delaney, K.J., Erraguto, D., Plagg, N., Ford, J., Foster, P., Frantz, P., Farlbar, C., Edagia, A., Garza, M., Gill, R., Gao, J., Garcia, A., Garrer, T., Garza, N., Gill, R., Harris, C., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, K., Harris, C., Hollins, B., Honsi, F., Howard, S., Huber, J., Holloway, C., Hollins, B., Jackson, E., Ralsson, E., Ralson, R., Kally, K., Harris, M., Holloway, C., Joudah, S., Karlsson, E., Ralson, E., Rally, S., Huber, J., Ully, K., Johason, R., Jolivet, S., Joudah, S., Karlsson, E., Rarison, E., Rahi, M., Landry, N., Hulyk, S., Huber, J., Lid, Y., Lulu, W., Loulseged, H., Li, J., Liz, Lichtarge, O., Lieu, C., Liu, J., Liu, W., Loulseged, H., Lorado, R., Ju, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Marston, D., Maner, G., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Sodergran, R., Nocken, R., Pator, P., Martin, R., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, H., Stone, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R., Martin, R.
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Submitted (08-JAN-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Apr 24, 2002 this sequence version replaced gi:18449890.

Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu

Center project Information
Center project Information
Center project name: RPII-10315

Center project name: RPII-10315

Center project name: Phrap; version 0.990329
Assembly program: Phrap; version 0.990329
Consensus quality: 70276 bases at least Q40
Consensus quality: 70276 bases at least Q30
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Consensus quality: 70276 bases at least Q30
Consensus quality: 70276 bases; agarose-fp estimation
Quality coverage: 1x in Q20 bases; sum-of-contigs estimation
Quality coverage: 2x in Q20 bases; sum-of-contigs estimation
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (20-OCT-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 80952)
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Direct Submission
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consists of 21 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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628 65727: gap of unknown le
728 73013: contig of 728 bj
014 73113: gap of unknown le
114 80952: contig of 7839 bj
Location/Qualifiers
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/clone="RP11-10315"
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1. (bases 1. o. 16213)

1. (bases 1. o. 16213)

1. Hilier, W., Fulton, R.S., Fulton, L.A., Graves, T.A., Pepin, K.H., Wagner-McPherson, C., Layman, D., Maas, J., Jaeger, S., Walker, R., Walle, K., Schon, M., Becker, M.C., O'Laughlin, M.D., Schaller, M.E., Fewell, G.A., Delehauuty, K.D., Miner, T.L., Nash, W.E., Cordes, M., Isak, A., Vambrunt, A., Nauyen, C., Du, L., Lamer, B., Courtney, L., Kalicki, J., Ozersky, P., Balaicki, L., Scott, K., Holmes, A., Harkins, R., Harris, A., Strong, C.M., Hou, S., Tomlinson, C., Dauphin-Kohberg, S., Kozlowicz, Reilly, A., Leonard, S., Rohlfing, T., Strowmatt, C., Latreille, P., Miller, N., Johnson, D., Murray, J., Woessner, J.B., Wenth, M., Spieth, J., Beri, T.A., Nelson, J.O., Berkowicz, N., Wohldmann, P.E., Cook, L.L., Hickenbotham, M.T., Eldred, J., Williams, D., Bedell, J.A., Maugen, E., Gillett, W., Zhou, Y., James, R., Phelps, K., Iadanoto, S., Bork, P., Suyma, M., Bailey, J.A., Portnoy, M.E., Torrents, D., Chinwalla, A.T., Gish, W.R., Eddy, S.R., McPherson, J.D., Olson, M.V., Eichler, E., Green, E. D., Watterston, R., Chiner, E., Green, E. D., Watterston, R., and Wilson, R.K., The DNA sequence of human chromosome 7

In Nature 424 (6945), 157-164 (2003)
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The sequence of Homo sapiens BAC clone RP11-84K19
Watersten,R.H.
Watersten,R.H.
Submitted (15-SEP-1998) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, Waterston,R.H.
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Submitted (07-027-2000) Department of Genetics, Washington

Bubwrstlty, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

(Dasses 1 to 162139)
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University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                          ACO05682 162139 bp DNA linear PRI 30-J
Homo sapiens BAC clone RP11-84K19 from 7, complete sequence.
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181 AAAATGCAGAC 192
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The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see http://www.nhgri.nih.gov/DRIK/GTPCHR7, send mailto:egreen@nhgri.nih.gov, or see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The clone sequenced to the left is RPI1-319F3. Actual start of this clone is at base position 52619 of RPI1-319F3 actual end is at base position 162139 of RPI1-84K19.

Location/Qualifiers
                                                                                                                                      NOTICE: This sequence may not represent the entire insert of this forms. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The RPCI-11 human BAC library was made from the blood of one male donor, as described by Gosegawa, K., Woon, P.Y., Zhao, B., Frengen, E. Tatoo, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                  This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.
Contact: sapiens@watson.wustl.edu
                                                     Center project name: H_NH0084K19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     744. .764
/rpt_family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="AT_rich" 718. .1798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone lib="RPCI-11"
100. 207
/rpt family="L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone="RP11-84K19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2137. .2441
/rpt_family="Alu"
2765. .23657
/gene="DRCTNNBIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="Alu"
1659. .1702
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1399. .1657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /rpt_family="L1"
.267. .1330
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1822. .2049
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2137. .2441
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VECTOR: pBACe3.6
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Submitted (20-APR-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Cambridgeshire, CB10 18A, UK. E-mail enquiries:

Numquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk

Numquery@sanger.ac.uk clone requests: clonerequest@sanger.ac.uk

Numquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations

rogether with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; WORMPEP; Information on the WORMPEP there is now the submitted of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the content of the
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http://www.sanger.ac.uk/HGP/Chr1
RP11-91A18 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm

VECTOR: DAAGE3.6.

Location/Qualifiers
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                               AL445685 142790 bp DNA linear PRI 21-APR-2002
Human DNA sequence from clone RPI1-91A18 on chromosome 1, complete
sequence.
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     Bukaryoča; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
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/clone_lib="RPCI-11.1"
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AL445685.18 GI:20302179
                                                                                                                                                                   96082 AAATATATACAC 96071
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                                                                                                                   181 AAAAATGCAGAC 192
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AL445685/c
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AUTHORS
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JOURNAL
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KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                             ISRNAVTSMSIRGHRWKRHGNTELTGQEBLMEISEVDEGFYSRAASSTSGSGLENSSH
NCSKRESIGKNHRRSGGSKTGGKEKETTGESCKDHFARKGTQRAQSENLELSLKRLT
LTTSQSLPKPSSHGLAKTAATVFSKSFEQVSGVTVPHNPSSAVGCGAGTDANRFSACS
LQEEKLIYVSERTELPMKHQSGQQRPPSISITLSTD"
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/protein id="AAS01991.1"
/db_xref="G1:41393460"
/translation="ICVCGYPRQHVRKYKGISSRIPVSSGFMVQMLTGIYFAFYNGEW
/translation="ICVCGYPRQHVRKYKGISSRIPVSSGFMVQMLTGIYFAFYNGEW
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                                                                                                 .21707)
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.23657)
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                                                                                            join(<2765. __2881,5974. .6061,6881. .7040,21133. ./gene="DRCTNNB1A"
/ gene="DRCTNNB1A"
/ note="Homo sapiens down-regulated by Ctnnb1, a (DRCTNB1A), mRNA.; H NH0084K19.1
This gene was based on gi(14211900 17511708)
                                                                                                   .7040,21133.
oin(2765. .2881,5974. .6061,6881. .7040,21133.
                                               .7040,21133.
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                     gene="DRCINNBIA"
|oin(2765. .2881,5974. .6061,6881.
|gene="DRCINNBIA"
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19730. .19771
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/rpt_family="MER1_type"
3710. .5258
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1584 family="L1"

1584 family="L1"

1587 ...1587 rich"

15973...1601

16837...1772
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/rpt_family="L1"
5403...5469
/rpt_family="(CA)n"
6225..6528
/rpt_family="Alu"
/rpt_family="Alu"
/rpt_family="Alu"
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7rpt family="AT_rich"

9242...9365

7rpt family="AT_rich"

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10509...10654
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..23936
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3035. .13081
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4679. .15246
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8163. .18190
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1276. .11366
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7930. .18132
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Best Local Similarity 89.6
Matches 172; Conservative
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2380<u>6</u>.
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ACCESSION VERSION KEYWORDS SOURCE

RESULT 13 AC146127

ORGANISM

AUTHORS TITLE

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AUTHORS

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Pan troglodytes (chimpanzee)

Pan troglodytes

Pan troglodytes

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1 (bases 1 to 208066)

Trani,L., Cotton,M., Haglund,K. and Bielicki,L.

The sequence of Pan troglodytes BAC clone RP43-30K12

Unpublished (2001)

Suleron,J.E. and Wilson,R.

Sequencing of Pan troglodytes

Unpublished (2001)

Suleron,J.E. and Wilson,R.

Sequencing of Pan troglodytes

Unpublished (2001)

Suleron,R.K.
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The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA
was isolated from white blood cells obtained from a male chimpanzee
(Pan troglodytes, Cilnt,, Yerkes #C0471; birthdate: 6-6-80). The
clone and detailed information can be obtained from ResGen
(http://www.resgen.com) or Pieter de Jong and co-workers at
http://www.bacpac.chori.org.
              Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
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Pan troglodytes BAC clone RP43-30Kl2 from 7, complete sequence.
AC146483
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128996. .129012
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                                                                                                                                                                                                                                                                                                                                                             This sequence is the entire insert of the clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/chromosome="7"
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128925. .128976
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1. .190149
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    MAPPING INFORMATION:
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Matches 168; Conservative
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SOURCE
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                             CTGAGGCAGGAGAATCGCTTGAACCCAGGAGGTGGAGGTTGCAGTGAGCCGAGATCACGC 128950
                                                                                                                       128889 AAAGGCCGAGGCGGCGATCACGAGGTCAGGAGCAAGACCATCCTGGCTAACAT 128830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 190149)
1 (bases 1 to 190149)
1 The aguence of Pan troglodytes BAC clone RP43-23F10
Unpublished (2001)
2 (bases 1 to 190149)
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Submitted (01-MUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 190149)
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Louis, MO 63108, USA
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Pan troglodytes BAC clone RP43-23F10 from 7, complete sequence.
AC146127
CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
                                                                                              Genetics, Genome Sequencing Center,
Louis, MO 63108, USA
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On Jun 2, 2004 this sequence version replaced gi:46576149.
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Direct Submission
Submitted (27-APR-2004) Ger
Forest Park Parkway, St. L.
4 (bases 1 to 190149)
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Submitted (02-JUN-2004) Ge
Forest Park Parkway, St. L
5 (bases 1 to 190149)
Wilson, R. K.
Direct Submission
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Submitted (03-JAN-2004) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Dec 21, 2003 this sequence version replaced gi:33386957.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Pan.
1 (bases 1 to 211780)
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USA
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Submitted (01-MUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 211780)
                                                                                                                                                                                                                                                                                                                       AC146006 211780 bp DNA linear PRI 03-JAN-20
Pan troglodytes BAC clone RP43-165A19 from 7, complete sequence.
AC146006
CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
                                                                                        Center: Washington University Genome Sequencing Center
Center code: WUGSC
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The sequence of Pan troglodytes BAC clone RP43-165A19
Unpublished (2001)
2 (bases 1 to 211780)
Wilson, R.
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Direct Submission
Submitted (23-AUG-2003) Genetics, Genome S
Lorer Dark Parkway, St. Louis, MO 63108,
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Contact: submissions@watson.wustl.edu
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Pan troglodytes
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5 (bases 1 to 211780)
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3 (bases 1 to 211780)
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                                                                                                                                                                                                                                           Puriet Submission
Submitted (29-OCT-2003) Department of Genetics, Washington
Submitted (29-OCT-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Oct 4, 2003 this sequence version replaced gi:33859971.
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                          Direct Submission
Submitted (19-AUG-2003) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 208066)
                                                                                                                                              Submitted (04-OCT-2003) Genetics, Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA 5 (bases 1 to 208066)
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/clone lib="RPCI-43"
1. 349
/note="Sequence derived from one plasmid subclone."
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This sequence is the entire insert of the clone.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: submissions@watson.wustl.edu
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="7"
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Web site: http://genome.wustl.edu
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http://www.bacpac.chori.org.
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90.8%;
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Best Local Similarity
Matches 168; Conserv
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                              TITLE
JOURNAL
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                                                                                                                                                                                                                                  AUTHORS
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                                                                                                                      AUTHORS
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restriction digest.

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169993 AAAATACAAAATTAGCCCGGTGTGGTGGCCATGTGCCTGTAATCCCAGCTACTCGGGAGG 169934
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The RPCI-43 BAC Library has been constructed by Chung-Li Shu. DNA
was isolated from white blood cells obtained from a male chimpanzee
(Pan troglodytes, 'Clint', Yerkes #C0471; birthdate: 6-6-80). The
clone and detailed information can be obtained from ResGen
(http://www.resgen.com) or Pieter de Jong and co-workers at
http://www.bacpac.chori.org.
                  Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see http://genome.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="RP43-165A19"
/clone=lib="RPCI-43"
|11047...|11070
|note="Sequence derived from one plasmid subclone."
|11090...|1124
|note="Sequence derived from one plasmid subclone."
|1433&C...4340.
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                                                                                                                                                                                                                                                                                                          NEIGHBORING SEQUENCE INFORMATION:
This sequence is the entire insert of the clone. This clone is
overlapped by AC146236.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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/note="Sequence derived from one plasmid subclone."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52.6%; Score 157.8; DB 9; 90.8%; Pred. No. 5.7e-35; iive 0; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Pan troglodytes"
                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic_DNA"
/db_xref="taxon:9598"
/chromosome="7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      completed: August 4, 2005, 11:17:00 te : 1211.83 secs
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MAPPING INFORMATION:
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Best Local Similarity 90.8
Matches 168; Conservative
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This pool Blonk (Usolo)

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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OM nucleic - nucleic search, using sw model

August 3, 2005, 15:09:47 Run on:

; Search time 198.826 Seconds (without alignments) 8932.047 Million cell updates/sec

US-09-899-276C-6 Perfect score:

l aaaatataaaaattagccag....,...aatctaatagaagctactga 300 Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

N Geneseg 16Dec04:* Database

geneseqn1980s: *

geneseqn2003ds:* geneseqn2004as:* geneseqn2004bs:* geneseqn2003cs:* geneseqn2003as:*geneseqn2003bs:* geneseqn2001bs:*geneseqn2002as:* geneseqn2002bs:* geneseqn2001as:* genesedn1990s:* geneseqn2000s:* :01 11: 12: 13:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		مد				
Result No.	Score	Query	Query Match Length DB	DB	ID OI	Description
-	300	100.0	300	9	ADH13943	Adh13943 Human mon
7	300	100.0	11793	12	AD003803	Ado03803 Human Cc1
m	167.8	55.9	5926	9	ABL33652	Abl33652 Human imm
Ω	160.8	53.6	12026	4	AAK67211	Aak67211 Human imm
S	160.8	53.6	31926	13	ABD33528	Abd33528 Human can
9	156.4	52.1	5304	4	ABK42328	Abk42328 Genomic s
C 7	156.4	52.1	5304	4	ABK42327	Abk42327 Genomic B
υ υ	156.4	52.1	5304	0	ADB60483	Adb60483 Connectiv
6	156.4	52.1	5304	6	ADB60484	Adb60484 Connectiv
10	156.4	52.1	9426	9	ABK69846	Abk69846 Human sec
11	156.4	52.1	9426	8	ACC50861	Acc50861 Human sec
12	156.4	52.1	9426	œ	ABZ71483	Abz71483 Secreted
13	156.4	52.1	9796	6	ADB91839	Adb91839 Human sec
14	156.4	52.1	9196	10	ADC74614	Adc74614 Human sec
15	156.4	52.1	9196	10	ADD38134	Add38134 cDNA clon
16	156.4	52.1	9446	10	ADA57728	Ada57728 BAC fragm
17	156.4	52.1	20245	4	AAK72318	Aak72318 Human imm
18	156.4	52.1	20245	9	ABK69845	Abk69845 Human sec
19	156.4	52.1	20245	æ	ACC50860	Acc50860 Human sec
20	156.4	52.1	20245	œ	ABZ71482	Abz71482 Secreted

Adb91838 Human sec	Adc74613 Human sec	Add38133 cDNA clon	Ada57727 BAC fragm	Adq20606 Human sof	Abd32694 Human can	Aak81320 Human imm	Adc87623 Human GPC	Adc87010 Human GPC	Abz74262 Secreted	Ada98791 Human sec	Abz67828 Human sec	Acn44898 Human gen	Abd32581 Human can	Abn96931 Gene #342	Continuation (3 of	Abk83567 Human cDN	Aals4074 Human tra	Adq59422 Human can	Adp45592 Human MAP	Acn44958 Human gen	Adf77178 KALPA gen	Acn44298 Human gen	Aal02649 Human rep	Aba07691 Human ova
ADB91838	ADC74613	ADD38133	ADA57727	ADQ20606	ABD32694	AAK81320	ADC87623	ADC87010	ABZ74262	ADA98791	ABZ67828	ACN44898	ABD32581	ABN96931	ACH03408 2	ABK83567	AAL54074	ADQ59422	ADP45592	ACN44958	ADF77178	ACN44298	AAL02649	ABA07691
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52.1	52.1	52.1	52.1	51.9	51.8	51.5	51.3	51.3	51.2	51.2	51.2	51.0	50.9	50.9	50.9	50.9	50.6	50.5	50.5	50.5	50.4	50.4	50.3	50.3
156.4	156.4	156.4	156.4	155.8	155.4	154.6	153.8	153.8	153.6	153.6	153.6	153	152.8	152.8	152.8	152.8	151.8	151.6	151.4	151.4	151.2	151.2	151	151
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## ALIGNMENTS

RESULT 1

ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:6. ADH13943 standard; DNA; 300 BP. 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. 11-MAR-2004 (first entry) EP1170372-A1. Homo sapiens. 09-JAN-2002. ADH13943; 4DH13943 

(DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.

Poustka A; Delius H, Finzer P, Roesl F, Soto U, Coy J, Zur Hausen H, Patzelt A;

WPI; 2002-165895/22.

Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer.

Disclosure; SEQ ID NO 6; 30pp; English.

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention mas cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A

in particular Cc12-

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Best_Local Similarity 100.
Matches 300; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated macular degeneration (AMD). Specifically, it refers to
                                                                                                                                 9
   the treatment
                                                                                                                                                                                                                                                        AAAAATGCAGACTGTGATTCAGCAGGTCTGGGTTGAAGCCCCAGAACTCTCTGATAAATTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              age-related macular degeneration,
                                                                                                                                                                                                                                   AAAAATGCAGACTGTGATTCAGCAGGTCTGAGGTTGAAGCCCCAGAACTCTGTGATAAATTC
                                                                                                                                 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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                                                                                                                                                      CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGATAGTGC
                                                                                                                                                                                              Gaps
            e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                              human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen; lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Testing candidate drug for treating age-related macular degenera
administering drug to Cc12-deficient, Ccr2-deficient knockout mc
analyzing development or regression of drusen and/or lipofuscin
                                                                                           ;
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pharmaceutical composition of the invention is useful for the of diseases associated with dysregulation of MCP-1 expression, atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                       Length 300;
                                                                                           Indels
                                                     Sequence 300 BP; 95 A; 60 C; 76 G; 69 T; 0 U; 0 Other;
                                                                       ; Score 300; DB 6;
; Pred. No. 1.8e-77;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                             Human Cc12 gene and enhancer region DNA SeqID 4.
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                                                                                                                                                                                                                                                                                                                                                    DNA; 11793
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                                                                       100.0%;
ilarity 100.0%;
Conservative 0
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accumulation in eye.
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                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                   Best Local Similarity
Matches 300; Conserv
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administering a candidate drug to gene knockout mice, in particular Cc1 deficient, Ccr2-deficient and/ or a Cc12-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polymucleotide sequence is the human Cc12 gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTGGCACTTAACTACTTGGAGGTCATGGATGCCTTTGCTAATCTAATAGAAGCTACTGA
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                                                                                                                                                                                                                                                                                                          Sequence 11793 BP; 3209 A; 2913 C; 2559 G; 3112 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                      Length 11793;
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                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 300; DB 12;
100.0%; Pred. No. 7.3e-77;
ive 0; Mismatches 0;
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2000DE-01043826
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    The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                                                                                                                                                                                                                                                                                                                58 AGCTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAG 117
                                                                                                                                                                                                                                                                                                                                                                                                   240
                                                                                                                                                                                                                                                                                                                                 ATAAAAATGCAGACTGTGATTCAGCAGGTCTGGGTTGAAGCCCCAGAACTCTCTGATAAA 237
                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCAATGGCACTTAACTACTTGGAGGTCATGGATGCCTTTGCTAATCTAATAGAAGCTAC 297
                                                                                                                                                                                                                                                                                            Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                 including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurocibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                            Length 5926;
                                                                                                                                                                                                  Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                     Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                    47; Indels
                                                                                                                                                                                                                         Score 167.8; DB 6;
Pred. No. 2.2e-38;
0; Mismatches 47;
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ID AAK67211 standard; DNA; 12026 BP.
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2000US-018464P.
2000US-0189350P.
2000US-0198074P.
2000US-0190076P.
2000US-019123P.
2000US-0205515P.
2000US-0205467P.
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80.7%;
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Best Local Similarity 80.7
Matches 196; Conservative
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
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18-APR-2000;
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28-JUN-2000;
                           methylation.
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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acids encoding human immune/hematopoietic antigen polypeptides, for preventing, diagnosing and/or treating cancers and metastasis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 22023; 3071pp + Sequence Listing; English.
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01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0251930P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
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08-DEC-2000; 2000US-0251869P.
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08-DEC-2000; 2000US-0251869P.
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2000US-0246474P.
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The invention relates to cancer-associated proteins (CAP) and the cancer-associated (CA) nucleic acids encoding them. The invention also relates to a method for treating cancers involving administering to a patient an inhibitor of CAP, and a method of screening for anticancer activity in a potential drug involving providing a cell that expresses a CA gene, contacting a tissue sample derived from a cancer cell with an anticancer
                                                                                                                                                                                                                                                                                                                 4624
supplement the patients own production of (I). Additionally, (I) polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAW82169 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                          Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
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                                                                                                                                                                                                                                                                                                             4683 AAATACAAAAATTAGCCAGGCGTGGTGGCATGCGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                                                                                                                                                                                                  CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
                                                                                                                                                                                                                                                                               1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                            Sequence 12026 BP; 2791 A; 3406 C; 3411 G; 2418 T; 0 U; 0 Other;
                                                                                                                                                                                                           53.6%; Score 160.8; DB 4; Length 12026; 86.8%; Pred. No. 3.1e-36; ive 0; Mismatches 27; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cancer-associated (CA) gene HD07-104.
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Matches 177; Conserv
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14-AUG-2000;
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21-SEP-2000;
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29-SEP-2000;
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     17249 AAAATACAAAAATTAGCCAGGCGTGGTGGCATGCGCCTGTAGTCCCCAGCTACTCGGGAGG 17308
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drug candidate and monitoring the effect of the anticancer drug candidate on expression of the CA gene. The CAP proteins are useful for detecting cancer associated with expression of a CAP protein in a test call sample and for screening for a bioactive agent capable of modulating the activity of a CAP protein. The CA nucleic acids are useful for diagnosing cancer, involving determining the expression of a CA nucleic acid in a tissue. This sequence represents a human CA gene of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                             120
                                                                                                                                                                                                                                                                                                           Genomic sequence #227 encoding novel human connective tissue polypeptide
                                                                                                                                                                                                                                                           CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
                                                                                                                                                                                                              AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
                                                                                                                                                                                     0; Gaps
                                                                                                                                   Sequence 31926 BP; 6797 A; 9017 C; 8858 G; 7254 T; 0 U; 0 Other;
                                                                                                                                                             DB 13; Length 31926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; connective tissue related disorder; cancer; gene therapy cytostatic; gene; ds.
                                                                                                                                                                                     27; Indels
                                                                                                                                                          53.6%; Score 160.8; DB 1
86.8%; Pred. No. 4.5e-36;
tive 0; Mismatches 27
                                                                                                           ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                  GAAATGGCTAAGTGTGAGGCAGAA 17452
                                                                                                                                                                                                                                                                                                                                                           181 AAAAATGCAGACTGTGATTCAGCA 204
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                                                                                                                                                         Query Match 53.6
Best Local Similarity 86.8
Matches 177; Conservative
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04-FBB-2000;
24-FBB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
19-APR-2000;
19-APR-2000;
07-JUN-2000;
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30-JUN-2000;
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The present invention relates to the isolation of novel human connective tissue related polypeptides (AAU86435-AAU86923) and the polynucleotide (cDNA and genomic) sequences encoding them. The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with connective tissue(s), including cancer. The polynucleotide sequences of the invention are also useful in gene therapy. ABK42102-ABK43116 represent genomic sequences encoding the novel human connective tissue related polypeptides. Note: The sequence data for this patent did not form part of the printed specification, but the was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding novel connective tissue associated polypeptides, used in diagnosing, preventing, treating or ameliorating a disorder such as cancer or rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 1215; 673pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ruben SM
         2000US-0246478P.
2000US-0246523P.
2000US-0246524P.
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06-DEC-2000;
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CTGAGGCAGAAGAATCCCTTAAACCCGGGAGGCGGAGATTGCAGTGAGCTGAGATCATGC 3511
                                                                                                                                                      CTGAGGCAGCAGCAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 120
                                                                                                                                Genomic sequence #226 encoding novel human connective tissue polypeptide.
                                    9
                                 1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
           Gaps
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              Indels
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  Pred. No. 4.4e-35;
); Mismatches 41;
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16-MAR-2000; 2000US-0186350F.
18-APR-2000; 2000US-0189374F.
19-MAY-2000; 2000US-0198123F.
19-MAY-2000; 2000US-0205155F.
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14-JUC-2000; 2000US-0225266F.
14-JUC-2000; 2000US-0225266F.
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14-AUG-2000; 2000US-0225268P-
14-AUG-2000; 2000US-0225270P-
14-AUG-2000; 2000US-022547P-
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ID ABK42327 standard; DNA; 5304
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                  Conservative
Best Local Similarity
Matches 181; Conserv
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18-AUG-2000; 2
22-AUG-2000; 3
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17-NOV-2000;
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3630 AAACTATAAAAATTAGCTGGGGTGGCTGGCTGCCTGTAGTCCCCAGCTACTCGGGAGG 3571
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Pred. No. 4.4e-35;
0; Mismatches 41; Indels
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                    17.NOV-2000; 2000US-0249209F.
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0S-DEC-2000; 2000US-025186F.
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181 AAAAATGCAGACTGTGATTCAGCAGGTCTGGGGTTGAAGCCCA 222
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20-OCT-2000; 2000US-0241808P.
20-OCT-2000; 2000US-0241808P.
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20-OCT-2000; 2000US-0241826P.
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3570 CTGAGGCAGAAGAATCGCTTAAACCCGGGAGGCGGAGATTGCAGTGAGCTGAGATCATGC 3511

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The invention describes an isolated nucleic acid molecule (I), which comprises a sequence that is at least 95 % identical to a connective tissue-related polynucleotide encoding connective tissue antigens (CTA). The polypeptide or polynucleotide is useful for preventing, treating, or ameliorating medical conditions in a mammal. The connective tissue polypeptides, polynucleotides and antibodies are particularly useful for treating, preventing and/or prognosing disorders of connective tissues (e.g. rheumatoid arthritis, discoid and systemic lupus erythematosus, scleroderma, or Sjogram's syndrom,), cancer metastases and/or neoplasias (e.g. leukaemia), neurodegenerative disorders (e.g. Alzheimer's disease, or Parkinson's disease), cardiovascular diseases complications), autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.
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antiarteriosclerotic; immunosuppressive; antirhaumatic; darmathritic; antiarteriosclerotic; immunosuppressive; antirhaumatic; darmathritic; antiaflammatory; antiallargic; antiasthmatic; darmatological; antiaflammatory; antiallargic; antiasthmatic; darmatological; antiparasatic; demetorios; grace therapy; ds; connective tissues disorder; rheumatorid arthritis; sancer metastasis; neoplasia; leukaemia; neurodegenerative disorder; Malzheimer's disease; Parkinson's disease; cardiovascular disease; whatherosclerosis; myocarditis; cardiovancy bypass complication; antitis; ezema; inflammatory condition; Crohn's disease; rhintis; ezema; inflammatory condition; Crohn's disease; whithis is esema; inflammatory bowel disease; which immune system disorder; Bruton's disease; X-linked lymphoproliferative syndrome; Ms -call lymphoproliferative disorder; HIV, AIDS; infection; chromosome identification; chromosome mapping; connective tissue related polynucleotide; gene; ds.
                            121 CACTGCACTCCAGCCTGGGTGACAGAGTGAGACTCTGTCTCAAAAAATAAAAATA 180
                                                                                                                                                                                                                                                                           cytostatic; neuroprotective; nootropic; antiparkinsonian; cardiovascular;
                                                                                  3450 AAAGAAGAAGAAGAAGAAGGCTGTCTCTGGTCAAGGCCA 3409
                                                         181 AAAATGCAGACTGTGATTCAGCAGGTCTGGGGTTGAAGCCCA
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16-MAR-2000;
17-MAR-2000;
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Barash SC; (HUMA-) HUMAN GENOME SCI INC Rosen CA, Ruben SM, WPI; 2003-634869/60. P-PSDB; ADB59409.

New connective tissue-related polypeptides and polynucleotides, useful for treating, preventing and/or prognosing e.g. disorders of connective tissue, (e.g. rheumatoid arthritis), cancers, cancer metastases and/or neoplasias.

Disclosure, SEQ ID NO 1215; 248pp; English.

The invention describes an isolated nucleic acid molecule (I), which comprises a sequence that is at least 95 % identical to a connective tissue-related polymbroleotide encoding connective tissue antigens (CTA). The polymperide or polymbroleotide is useful for preventing, treating, or ameliorating medical conditions in a mammal. The connective tissue polymperides, polymucleotides and antibodies are particularly useful for preventing and/or prognosing disorders of connective tissues treating, preventing and/or prognosing disorders of connective tissues clear thritis, discoid and systemic lupus erythematosus, solaroderma, or Siogren's syndrome), cancers, cancer metastases and/or neoplassias (e.g. leukaemia), neurodegenerative disorders (e.g. Alzheimer's disease, or Parkinson's disease), cardiovascular diseases (e.g. atherosclerosis, myocarditis or cardiopulmonary bypass complications), autoimmune diseases (e.g. systemic lupus erythematosus, rheumatoid arthritis, or multiple sclerosis), allergic reactions (e.g.

ö 0; Gaps Query Match 52.1%; Score 156.4; DB 9; Length 5304; Best Local Similarity 81.5%; Pred. No. 4.4e-35; Matches 181; Conservative 0; Mismatches 41; Indels 0;

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WO200295010-A2.
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                                                                                                        3630 AAACTATAAAAATTAGCTGGGCGTGGTGCGTGCCTGTAGTCCCAGCTACTCGGGAGG 3571
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                                                                                                                                                                                                                                                                                                                           Human; ds; secreted protein; gene therapy; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; notropic; neuroprotective; antibacterial; virucide; fungicide; opthalmalogical; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cardiac arrest; cardiovascular disorder; cerebroul ischaemia; angiogenesis; nervous system disorder; Albeimer's disease; infection; coular disorder; corneal infection; wound healing; skin aging; epithelial cell proliferation; food additive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (or its fragment, homologue complement or allelic variant) encoding a human secreted protein (and its fragment, domain, epitope, variant, secreted form and species variant). Also included are a recombinant vector comprising the nucleic acid, a recombinant host cell comprising the vector that expresses the secreted protein and a method of identifying a binding partner of the secreted protein and a method of identifying a binding prevent, diagnose, treat or amelicate a medical condition in e.g. humans, mice, rabbits, goats, horses, cate, dogs, chickens or sheep for example autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel 71 isolated secreted polypeptides and polynucleotides encoding the polypeptides, useful for treating Huntington's disease, sepsis, meningitis, thrombocytopenia, hemolytic anemia, rheumatoid arthritis,
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                                                    CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAAGAGATAGTGC
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Soppet D
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Young PE,
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                                                                                                                                                                                                                                                                                                   Human secreted protein gene 22 genomic DNA fragment #7.
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Olsen H, Brewer LA, Florence KA,
Mucenski M, Ebner R;
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disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenssis, nervous system disorders e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. Many other diseases and disorders are listed in the specification. The polypeptides can also be used to aid wound healing an epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. The present sequence represents a ds DNA fragment of the gene for a novel human secreted protein of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel human secreted proteins, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating cardiovascular disorders such as arrhythmia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cardiant; antiarrhythmic; antiarteriosclerotic; vasotropic; cytostatic; vulnerary; antiinflammatory; nootropic; neuroprotective; antiparkinsonian; gene therapy; human; cardiovascular disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5808 AAAATACAGAAATTAGCTGGGTGTGATGGTGCGTGCCTGTAATCCCAGCTACTCGGGAGC
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es 31; Indels
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Pred. No. 5.5
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85.0%;
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19-JUL-2001; 2001US-0306171P.
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Matches 175; Conservative
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19-MAR-2002; 2002WO-US008276.

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The present invention tetates to nove induan secretes processing the ARR49145) and their coding sequences (ACC50344-ACC50856). The proteins and their coding sequences are useful for the preparation of a diagnostic or pharmaceutical composition for diagnosing or treating a cardiovascular disorder (e.g., arrhythmia, tachycardia, cardiac arrest, coronary carteriosclerosis and myocardial isordeers, reproductive disorders, immune system disorders, muscular disorders, pulmonary disorders, remained disorders, proliferative disorders and/or cancerous diseases and conditions, for conjustive disorders and/or cancerous diseases and conditions, for wound healing and epithelial cell proliferation, to treating or proliferation for treating thrombosis and arteriosclerosis, for treating or conference of the critical disorders or neurodegenerative conditions such as Alzheimer's disease and parkinson's neurodegenerative conditions such as Alzheimer's disease and parkinson's crimeurodegenerative or bone and periodontal regeneration and aid in tissue criminal are growth and differentiation of haematopoietic cells and bone are incombination with other cytokines, to maintain or gauss before transplantation or for supporting cell culture of primary cissues, to increase or decrease differentiation or proliferation of tissues, to increase or decrease differentiation or proliferation of cembryonic stem cells, and modulate mammalian characteristics or metabolism. The present sequence was used to illustrate the invention.

Compans before transplantation or for supporting cells and bone metabolism. The present sequence was used to illustrate the invention.
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                                                       invention relates to novel human secreted proteins (ABR47633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 9796 BP; 2064 A; 2679 C; 2566 G; 2487 T; 0 U; 0 Other;
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85.0%; Pred. No. 5.5e-35;
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Disclosure; SEQ ID NO 1041; 1881pp; English.
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tes 175;
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ABZ71190-ABZ71478 represent cDNAs corresponding to 178 human secreted protein genes, and ABP00011-ABP00299 represent the proteins they encode. protein genes, and ABP00011-ABP00299 represent the proteins they encode. ABZ71479-ABZ71540 represent human secreted protein genomic fragments. The invention also encompasses antibodies specific for the secreted proteins, the use of the secreted proteins in drug screening, and recombinant convectors and host cells comprising a nucleic acid of the invention. The secreted proteins, uncleic acids encoding them, antibodies or antibody cragments specific for the secreted proteins, and modulators of protein activity are useful for diagnosing, treating, ameliorating or preventing activity are useful for diagnosing, treating, ameliorating or preventing cosephagus, stomach, small intestine, large intestine, liver, biliary cosephagus, stomach, small intestine, large intestine, liver, biliary cract and pancreas, and include cancers of these organs and tissues. The reatment of immune disorders, inflammation, infection, cractment of immune disorders, and to promote wound healing. Nucleic acids of the invention may be used for chromosome indentification, chromosome compaping, in gene therapy, for identifying individuals from minute consideration and prosent and manner of immune sequence represents a human secreted protein genomic markers. The present sequence represents a human secreted protein genomic markers.
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                                                                                                                                                                                                                                       New human secreted proteins and nucleic acids, useful for detecting, preventing, diagnosing, prognosticating, treating and/or ameliorating e.g. gastrointestinal diseases and disorders, or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Secreted protein; gene therapy; antidiabetic; diabetes; human; ds.
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0
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                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 1143-1145; 1216pp; English.
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Best Local Similarity 85.0%;
Matches 175; Conservative (
                                 21-MAR-2001; 2001US-0277340P.
19-JUL-2001; 2001US-0306171P.
                                                         19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
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The invention relates to a novel human secreted polypeptide comprising a defined sequence given in the specification. The polypeptide, nucleic acid molecule, antibody, agonist or antibody, agonist or antibody, agonist or antibody, agonist or antibody, agonist or antibody, agonist or antibody, agonist or disposable of the invention may be useful for preparing a composition for disposable or treating a composition for disposable or treating a classification of disposable or shown as rheumatold arthritis, inflammation, Grave's disease, disposable or shown as rheumatold arthritis, inflammation, Grave's disease, classes, systemic lupus erythematosus or glomerulonephritis, neurodegenerative disorders including parkinson's disease and Alzheimer's disease, wounds and hyperproliferative disorders including arther since parasitic infections. The polypeptide may also be used during gene the polypeptide with a binding partner and determining whether the binding partner increases the activity of the polypeptide. The current sequence is that of the human secreted protein-related DNA of
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                                               antidiabetic; immunosuppressive; dermatological; nephrotropic; antidaktinsonian; neuroprotective; nootropic; antibacterial; virucide; fungicide; antiparasitic; antiarteriosclerotic; vulnerary; cytostatic; haematologic; anaemia; autoimmune disorder; rheumatoid arthritis; inflammation; Grave's disease; diabetes; systemic lupus arythematosus; glomerulonephritis; neurodegenerative; Parkinson's; Alzheimer's; wound; hyperproliferative; atherosclerosis; cancer; bacterial; viral; fungal; parasitic infection; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New human secreted polypeptide for diagnosing, preventing or treating hematopoietic or hematologic disorders (e.g. anemia), autoimmune disorders (e.g. diabetes) or hyperproliferative disorders (e.g. cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5868 CTGAGGCAGGGGAATCTCTTGAATCCGGGAGGCGCAGGGTTGCAGCGAGGTTGTAC
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Pred. No. 5.5e-35;
0; Mismatches 31; I
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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85.0%;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADB91448 and ADB91835-ADB91911 encoding human secreted proteins ADB91449.

ADB91834. Also disclosed is a recombinant vector comprising a polymerlectide of the invention, and a recombinant host cell comprising the recombinant vector. The polymeride of the invention is useful in identifying a binding partner. The polymeride of the invention is useful in identifying a binding partner by contacting the polymeride with a companient, and determining whether the binding partner increases or decreases activity of the polymeride. The polymeride, polymeride, antibody or its fragment, agonist or antagonist are useful for preparing antibody or its fragment, agonist or antagonist are useful for preparing conditions related to diabetes. The present sequence is that of the human immosplobulin Fc portion used to generate fusion proteins, increasing conditions the sequence data for this patent did not form part of the prince of the stability of the fused protein as compared to the secreted protein conly. Note: The sequence data for this patent did not form part of the prince of the prince of the patent of the patent of the patent of the prince of the prince of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of the patent of pate
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0; Mismatches
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19-JUL-2001; 2001US-0306171P.
13-NOV-2001; 2001US-0331287P.
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BP cDNA clone in ATCC deposit #28. ADD38134 standard; cDNA; 9796 21-MAR-2001; 2001US-0277340P. 19-JUL-2001; 2001US-0306171P. 13-NOV-2001; 2001US-0331287P. 19-MAR-2002; 2002WO-US008279 (HUMA-) HUMAN GENOME SCI INC. hypersensitivity disorders. (first entry) Rosen CA, Ruben SM; WPI; 2003-140218/13. Query Match Best Local Similarity from ATCC deposit. WO200290526-A2. Homo sapiens 14-NOV-2002 15-JAN-2004 ADD38134; RESULT 

The present invention relates to an isolated polypeptide or human secreted protein. The polypeptides, nucleic acid molecules, antibodies or their fragments, and agonists or antagonists that bind are useful for their fragments, and agonists or antagonists that bind are useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders. The polypeptide is also useful for identifying a binding partner by contacting the polypeptide with a contact partner increases or decreases the activity of the polypeptide. The polypeptide and nucleic acid molecules are also useful for detecting, preventing, diagnosing, contacting interaction, immune disorders, or ameliorating inflammatory disorders or prognosticating, treating or ameliorating inflammatory disorders infectious diseases, wound healing and disorders of epithelial cell proliferation, immune disorders, cardiovascular disorders, or gastrointestinal continuation in the nucleic acids are also useful for chromosome diseases, endocrime disorders, or mapping, as molecular weight markers, or as hybridization or diagnostic mapping, as molecular weight markers, or as hybridization or diagnostic mapping, as molecular weight markers, or as hybridization or diagnostic immunological probes for differential identification of the tissues immunological probes for differential identification of the tissues immunological probes in the present sequence represents a cDNA clone from the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the contact of the c New human secreted proteins and nucleic acid molecules, useful for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders, or related immediate human secreted protein; Antiallergic; Antiinflammatory; Antibacterial; Anti-HIV; Cytostatic; Immunosuppressive; Hemostatic; ss. Sequence 9796 BP; 2064 A; 2679 C; 2566 G; 2487 T; 0 U; 0 Other; Claim 1; SEQ ID NO 616; 1323pp; English

5808 AAATTACAGAAATTAGCTGGGTGTGATGGTGCGTGTAATCCCAGCTACTCGGGAGC 5867

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AQ749749 HS 5573 A
BF811137 CWG-ET012
CR556187 DKPZD459P
AQ313572 RPCI11-IO
BZ602060 WIABNO8ITR
AQ474644 CITBI-E1-
CF128365 UI-HF-ET0
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GenCore version 5.1.6
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1 (bases 1 to 344)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W.Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., Sarae, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.
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Fmax: +55-11-2707001
Fmax: +55-11-2707001
Fmax: seimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
fhtp://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM0&t2=CM0-ET0121-311000-658-f04&t3=2000-10-31&t4=1)
Seq primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            344 bp mRNA linear EST 17-JAN-2001
CMO-ET0121-311000-658-£04 ET0121 Homo sapiens cDNA, mRNA sequence.
BF871137
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shotgun sequencing of the human transcriptome with ORF expressed
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Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
                                                                                                                       Length 828;
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                                                                                                                     Query Match 51.6%; Score 154.8; DB 8; Best Local Similarity 73.1%; Pred. No. 8.9e-20; Matches 198; Conservative 0; Mismatches 73;
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/mol_type="mRNA"
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High quality sequence stop: 331.
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Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
Ingolstaedter Landstr.1, D-85764 Neuherberg, German,
This is the 5' sequence of the clone insert Clone from S. Wiemann,
This is the 5' sequence of the clone insert Clone from S. Wiemann,
This is the senome Analysis, German Cancer Research Center (DKFZ);
Email s.wiemann@dkfz-heidelberg.de; sequenced by BMFZ (Biomedical
Research Center at the Heinrich-Heine-University,
Duesseldorf/Germany) within the CDNA sequencing consortium of the
German Genome Project. This clone (DKFZP6459P1831) is available at
the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum,
Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email:
clonedzpd.de Further information about the clone and the
sequencing project is available at
http://mips.gsf.de/projects/cdna/.
/db_xref="taxon:9606"
/de_tagge="Adult"
/clone lib="ETO121"
/note="Organ: lung_tumor; Vector: puc18; Site_1: Sma1;
/note="Organ: lung_tumor; Vector: puc18; Site_1: Sma1;
/note="Organ: lung_tumor; Vector: puc18; Site_1: Sma1;
/note="Organ: lung_tumor; Vector: wade by cloning products
derived from ORESTES PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the PUC18 vector. Reverse transcription of
tissue mRNA and CDNA amplification were performed under
low stringency conditions.
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pcorl) Pongo pygmaeus cDNA clone
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1 (bases 1 to 526)
Koehrer,K., Beyer,A., Mewes,H.W., Weil,B., Amid,C., Osanger,A., Pobo,G., Han,M. and Wiemann,S.
Pongo pygmaeus mRNA (Koehrer,K., Beyer,A., Mewes,H.W., et al.)
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGAGGCAGGAGCACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 120
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                                                                                                                                                                                                                                                                                                                                                             Length 344;
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Pred. No. 5.6e-19;
0; Mismatches 35;
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/mol type="mRNA"
/db xref="taxon:9600"
/clone="DKPZp459P1831"
/tissue type="cortex"
/dev stage="adult"
/lab_host="DH108"
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DKFZp459P1831_5', mRNA sequence.
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Pongo pygmaeus
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ilarity 83.1%;
Conservative (
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AC111572 675 bp DNA linear GSS 04-MAY-1999 RPCI11-101F17.TV RPCI-11 Homo sapiens genomic clone RPCI-11-101F17, genomic survey sequence.
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1 (Dases 1 to 675)
Adams; M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J. C. Unpublished (1998)
Unpublished (1998)
Cohter_GSSS: RPCIII-101R17.
Cohter_CSSS: RPCIII-101R17.
Department of Eukaryotic Genomics
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Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library availability, please contact Pieter de Jong

(pieter@dejong med.buffalo.edu). Clones may be purchased from

BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genetics (info@resgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html

Class: BAC ends.
  and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at EcoRI sites"
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/cell type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3 6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                         CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGAGATAGTGC
                                                                                                                                                                                                                                                               59 AAAATACAAAATTAGCCAGGCGTGGGGGTGTGCCTGTAATCCCATCTACTCAGGAGG
                                                                                                                                                                                                                 1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCCAGCTACTCGGGAGG
                                                                                                                       Length 800;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                    Score 150.6; DB 8;
Pred. No. 5.7e-19;
0; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Homo sapiens"
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/db_xref="GDB:7538536"
/db_xref="taxon:9606"
/clone="RPCI-11-101F17"
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j. .675
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                                                                                                                       Query Match
Best Local Similarity 87.3%;
Matches 165; Conservative
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Homo sapiens
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AQ313572/c
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University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3687
Eax: (206) 616-3887
Email: jwallacedu.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, plasse contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1152 row: J column: 8
Seg primer: T7
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 800)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ750780 800 bp DNA linear GSS 19-JUL-1999 HS_5576_B2_E04_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1152 Col=8 Row=J, genomic survey sequence.
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                                                                                                                                                                                                                                                                                CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 120
                                                                                                                                                                                                                                                                                                                                 268
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/clone_lib="459 (synonym: pcor1)"
/note="Vector: pSport1_Sfi; Site_1: SfilA; Site_2: SfilB"
                                                                                                                                                                                           9
                                                                                                                                                                                         1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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                                                                                                                                             Gaps
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                                                                                               Length 526;
                                                                                                                                          Indels
                                                                                                                                             20;
                                                                                          Score 151; DB 7;
Pred. No. 5.2e-19;
0; Mismatches 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="Plate=1152 Col=8 Row=J"
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/mol type="genomic DNA"
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Location/Qualifiers
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AQ750780.1 GI:5537938
                                                                                            Query Match 50.3%;
Best Local Similarity 89.1%;
Matches 163; Conservative (
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CTGAGGCAGGAGCATCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAATAGTGC 120
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AQ474644/c
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1 (bases 1 to 757)
Volik, S., Zhao, S., Chin, K., Brebner, J.H., Herndon, D.R., Tao, Q., Volik, S., Zhao, S., Chin, K., Brebner, J.H., Harndon, D.R., Tao, Q., Gray, J.W. and Collins, C.
End-sequence profiling: Sequence-based analysis of aberrant genomes Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
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                                                                                                                                                                                                                                                                                                                                                                         BZ602060 757 bp DNA linear GSS 08-JUN-2003 WHABVG8TR Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_1-12K16, genomic survey sequence. BZ602060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="vector: pECBAC1; Site_1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 AAAATACAAAAATTAGCCAGGCATGGTGGTGTGCGCCTGTAGTCCCAGGTACTCAGGAGG 264
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                                                                                                                            61 CTGAGGCAGGAGAACTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 120
                                                                                                                                                                                            283 CTGAGGCAGGAGAATCACCTGAATCCAGGAGGGGGAGGTTGCAGTGAGCCAAGATCGTGC 224
                                                                                   /clone_lib="Human MCF7 breast cancer cell line library MCF7 1]"
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 Length 675;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             UCSF Comprehensive Cancer Center UCSF Bomprehensive Cancer Center UCSF 320 8089, San Francisco, CA 94143-0808, USA Tel: 415 502 7066 Fax: 415 502 5665
                                Indels
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This clone is available from Amplicon Express
http://www.genomex.com
   DB 8;
                    6.4e-19;
Query Match
50.1%; Score 150.4; Di
Best Local Similarity 88.6%; Pred. No. 6.4e~
Matches 163; Conservative 0; Mismatches
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1. .757
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="MCF7_1-12K16"
/sex="female"
                                                                                                                                                                                                                                                                                                                                                                                                                                               BZ602060.1 GI:31510522
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Volik SV
Colin Collins' lab
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Unpublished (1997)
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0200
Fax: 301 838 0208
Email: hbe@rigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seg primer: M13 Reverse
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukamalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 565)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.

Venter,J.C.

Wenter,J.C.

Wenter,J.C.

Wap Building
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                                                                                                                                                                                                                                                                                                         CITBI-E1-2584M11.TR CITBI-E1 Homo sapiens genomic clone 2584M11, agenomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /sex="male" /cell_type="sperm" /cell_type="sperm" /clone_lbb="CITBL-B1" /note="Vector: pBeloBAC11; Site_1: BcoR1; Site_2: BcoR1; CalTech Human BAC Library D"
                                                                  1 AAAATATAAAATTAGCCAGGGGTGATGTCATGTGCCTGTAGTCCCCAGCTACTCGGGAGG
Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="2584M11"
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/organism="Homo sapiens"
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/do xerf="texaon:9606"
/clone="IMAGE:3055903"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/tab host="DH10B (T1 phage resistant)"
/clone_lib="NH1 MGC_214"
/clone_lib="NH1 MGC_214"
/note="Organ: Lung; Vector: pXx-Asc; Site 1: EcoR I;
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pXX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
                                                                                                                                                                        CF128305
UI-HF-ETO-awf-o-16-0-UI.x1 NIH MGC_214 Homo sapiens cDNA clone
IMAGE:30555903 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quence located between the Not I site and the polyA tail GATAAGGCCA. Tissue was provided by Mary Hendrix."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: bento-goares@wiowa.edu
Tissue Procurement: Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genme.ulowa.edu/distribution/humanfl.html
HTP following repetitive elements were found in this CDNA
sequence: 579-751, >ALU (matched compliment)
Seq primer: pXx-5.
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              747 AAAATACAAAATNAGCTGCGTGTGGGGGGTGTGCCTGTAATCCCAGCTACTCAGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Iowa
Tys Newton Road , 4156 MEBRF, Iowa City, IA 52242,
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 6 (9), 791-806 (1996)
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Other GSSs RPGI-11-244E4 TJ

Other GSSs RPGI-11-244E4 TJ

Other GSSs RPGI-11-244E4 TJ

Other GSSs RPGI-11-244E4 TJ

Conted: Shaying Zhao, William Nierman, Mark Adams
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Tel: 301 838 0208
Email: hbe@tigr.org
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from Racearch Genet cs (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resegen.com). BAC end search page:
RLUB://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                           RPCI-11-244E4.TV RPCI-11 Homo Sapiens genomic clone RPCI-11-244E4, genomic survey sequence.
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Mammalia; Butheria; Primates; Catarrhini, Hominidae; Homo.
I (bases 1 to 657)
2hao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and
Venter, J.C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="Lymphocytes"
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RPCIII Human Male BAC Library"
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Pred. No. 7e-19;
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Appliance ST2 bp DNA linear GSS 27-APR-1999 RPCI11-73B12.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-73B12, genomic survey sequence.
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1 (bases 1 to 572)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mdddams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
New.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="Lymphocytes"
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RPCII1 Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AAAATATAAAAATTAGCCAGGGGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 49.9%; Score 149.6; DB 8; al Similarity 83.3%; Pred. No. 9.4e-19; 170; Conservative 0; Mismatches 34;
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GSS.
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Homo sapiens
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Best Local Similarity
Matches 170; Conserv
181 AAAAA 185
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/clone=IMAGE:296138#
/tissue type="thadomyosarcoma"
/tissue type="thadomyosarcoma"
/lab host="NHIOB (phage-resistant)"
/clone lib="NHI MGC_17"
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
/note="Organ: muscle; Vector: pOTB7; Site_1: EcoRI;
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/note="Organ: muscle; Vector: GCORIGO-dT priming.
Site_2: XhoI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the following S: adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATC
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing Center (NISC)
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
www-bio.llnl.gov/bbrp/image/image.html
Plate: LLCMS6 row: K column: 11
Seq primer: MAJRP1 reverse primer (ABI).
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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0
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Pred. No. 8.9e-19;
0; Mismatches 22; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
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Best Local Similarity 88.1%;
Matches 163; Conservative
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Homo sapiens
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Gaps ;

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Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoda, A., Taylor, T.D., Yada, T., Totoda, Y., Watanabe, H. and Sakaki, Y.
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (B-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the RkD process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AG160213 677 bp DNA linear GSS 09-JAN-2002 Pan troglodytes DNA, clone: RP43-025P15.T7, genomic survey sequence.
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Ban troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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                                                                                                     Puliyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49.8%; Score 149.4; DB 9; Length 642;
84.4%; Pred. No. 1e-18;
tive 0; Mismatches 31; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cell_type="lymphoblast"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .642
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/db xref="taxon:9598"
/clone="pTB-026M07.F"
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Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /sex="male"
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Matches 168; Conservative
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AG160213.1
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                                                                                                                                   AQ312235 638 bp DNA linear GSS 04-MAY-1999
RPCI1-103E16.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-103E16,
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Pan troglodytes DNA, clone: PTB-026M07.F, genomic survey sequence.
AG047289.1 GI:16584181
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/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site_l: EcoRI; Site_2: EcoRI;
RPCII1 Human Male BAC Library"
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83.3%; Pred. No. 9.2e-19;
iive 0; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="genomic_DNA"
/db_xref="GDB:7539279"
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/clone="RPCI-11-103E16"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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Best Local Similarity 83.3
Matches 170; Conservative
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1 (Dases I to 72)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
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                                                                                                                                                         Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (102-MUG-2001) Asao Pujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suchiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimposegasc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
end was generated during the R&D process and may have higher chance
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sapiens genomic clone Plate=3100 Col=21 Row=1, genomic survey
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/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
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84.4%; Pred. No. 9.9e-19;
iive 0; Mismatches 31;
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/organism="Pan troglodytes"
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/db_xref="taxon:9598"
/clone="RP43-025P15.T7"
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
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Matches 168; Conservative
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High Throughput Sequencing Center
University of Washington
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Seq primer: T7
Seg primer: T7
Seg primer: T6
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH108"
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Best Local Similarity 79.4%; Pred. No. 9.8e-19;
Matches 177; Conservative 0; Mismatches 46; Indels 0
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/db_xref="taxon:9606"
/clone="plate=3100 Col=21 Row=I"
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Location/Qualifiers
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6: /cgn2_6/ptodata/1/ina/pcTUS_COMB.seq:*
GenCore version 5.1.6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                 1202784 seqs, 818138359 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                       IDENTITY NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Issued Patents NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                  US-09-899-276C-6
300
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                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                 Searched:
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                                                                                                                                                    Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## Sequence 12366, A Sequence 80246, A Sequence 14046, A Sequence 78059, A Sequence 12216, A Sequence 14021, A Sequence 38743, A Sequence 143733, Sequence 177920, Sequence 15797, A 12577, A 17299, A 17533, A 204886, 204887, 143301, 143372, 14021, A 204885, Sequence 11823, A 12805, A Sequence 15787, Sequence 15788, Sequence 16264, Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence US-09-949-016-12366 US-09-949-016-12366 US-09-949-016-14046 US-09-949-016-14046 US-09-949-016-12216 US-09-949-016-12577 US-09-949-016-12577 US-09-949-016-17299 US-09-949-016-17299 US-09-949-016-17331 US-09-949-016-17331 US-09-949-016-143472 US-09-949-016-143472 US-09-949-016-14060 US-09-949-016-12805 US-09-949-016-12805 US-09-949-016-12805 US-09-949-016-15905 US-09-949-016-15905 US-09-949-016-15905 US-09-949-016-15905 SUMMARIES DB Query Match Length 30221 30222 128723 24496 24497 23155 601 601 36759 36760 421491 120727 120727 240157 601 68173 22539 40435 551.3 551.1 551.1 551.0 551.0 551.0 550.3 550.3 550.3 550.3 150.8 150.8 150.6 150.6 150.6 156.4 155.4 154.4 154.4 153.4 153.4 153.4 153.4 153.4 153.4 153.6 153.6 151.8 151.8 151.4 151.4 152 152 150.8 Result Š. 00000

US-09-949-016-17792

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## ALIGNMENTS

RESULT 1 US-09-949-016-11823

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JAPLICANT: VENTALLY,

JAPLICANT: VENTALLY,

JAPLICANT: VENTALLY,

JITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRALSEQ for Windows Version 4.0

LENGTH: 24496
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Sequence 11823, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
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US-09-949-016-14253
; Sequence 14253, Application US/09949016
; Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 85.0°
Matches 175; Conservative
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US-09-949-016-11823
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Gaps

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Indels

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Matches 179; Conservative
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US-09-949-016-80246
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| Sequence 12366, Application US/09949016
| Patent No. 6812339
| GENERAL INFORMATION:
| THERE OF INVENTION: OLYMORPHISMS IN KNOWN GENES ASSOCIATED
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WIMBER: US/09/949,016
| CURRENT FILING DATE: 2000-04-14
| PRIOR APPLICATION NUMBER: 60/241,755
| PRIOR FILING DATE: 2000-10-20
| PRIOR FILING DATE: 2000-10-03
| PRIOR PILING DATE: 2000-09-08
| NUMBER OF SEQ ID NOS: 207012
| SOFTWARE: PRESENCE OF WINDOWS VETSION 4.0
| SEQ ID NO 12366
| LENGTH: 23155
                      JAPPLICATT: VENTER, J. Craig et al.

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOO1307

CURRENT APPLICATION NUMBER: G0/241,755

PRIOR PELING DATE: 2000-04-14

PRIOR PELING DATE: 2000-10-20

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 14253
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Pred. No. 2.1e-38;
0; Mismatches 31
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LCCATION: (1)...(23155)
COTHER INFORMATION: n = A,T,C or G
US-09-949-016-12366
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81.4%;
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85.0%;
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Matches 175; Conservative
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US-09-949-016-12366
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US-09-949-016-14253
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Best Local Similarity

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RESULT 4

US-09-949-016-80246/c

US-09-949-016-80246, Application US/09949016

Satent No. 681233

GENERAL INFORMATION:

TITLE OF INVENITON: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENITON: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENITON: WINDER: US/09/949,016

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR PILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFUTHARE PASELSEQ for Windows Version 4.0

LENGTH: 601
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; Sequence 14046, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.;
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
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Best Local Similarity 81.77
Matches 178; Conservative
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14 AAAATAGAAAAATTAGCCGGGCATGGTGGCATGCACCTGTAGTCCCAGCTACTTGGGAGG 73
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US-09-949-016-12216/c
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US-09-949-016-12216
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REFERENCE: CLOO1307
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REFERENCE: CLOO1307
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REFERENCE: CLOO1307
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR PRIOR DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-08
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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Pred. No. 3e-38;
0; Mismatches 31;
            CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PELLING DATE: 2000-04-175
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
SOFTWARE: PASCE ID NOS: 207012
SOFTWARE: PASCES FOR WINDOWS VERSION 4.0
SEQ ID NO 14046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 78059, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
LOCATION: (1)...(68173)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 84.7%;
Matches 172; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 81.7
Matches 178; Conservative
FILE REFERENCE: CL001307
                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Human
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US-09-949-016-78059
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LENGTH: 601
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Sequence 12216, Application US/09949016

Sequence 12216, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRASESQ for Windows Version 4.0

SEQ ID NO 12216
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| Sequence 14021, Application US/09949016
| Sequence 14021, Application US/09949016
| Patent No. 6812339 |
| GENERAL INFORMATION: Craig et al. |
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF |
| TITLE REPRESENCE: CL001307 |
| CURRENT APPLICATION NUMBER: 02/99/949,016 |
| CURRENT FILING DATE: 2000-04-14 |
| PRIOR APPLICATION NUMBER: 60/241,755
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                                           379 AAAAA 375
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US-09-949-016-12577
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                                                                                                                                                       Score 153.4; DB 4;
Pred. No. 2.3e-37;
0; Mismatches 31;
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PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FEASTER FOR Windows Version 4.0
SERIGING: 36760
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ilarity 84.7%;
Conservative
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Best Local Similarity 89.2
Matches 165; Conservative
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Matches 172; Conserv
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US-09-949-016-204885/c
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US-09-949-016-204885
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US-09-949-016-14021
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                                                                                                             TYPE: DNA
                                                                                                                                                            Query Match
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Sequence 17299, Application US/09949016

Sequence 17299, Application US/09949016

Patent No. 6812339

GENERAL INTORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION OF THE OF THE 2000-04-14

PRIOR REPLICATION NUMBER: 60/241, 755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

PRIOR PILING DATE: 2000-10-03

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SPRIOR FILING DATE: 2000-10-03

SPRIOR FILING DATE: 2000-10-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241, 755
PRIOR APPLICATION NUMBER: 60/241, 755
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR APPLICATION NUMBER: 60/237, 768
PRIOR APPLICATION NUMBER: 60/231, 498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
PRIOR SEQ ID NOS: 207012
SOFTWARE: FRASESEQ for Windows Version 4.0
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Best Local Similarity 81.8%; Pred. No. 2.7e-37;
Matches 189; Conservative 0; Mismatches 40
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| APPLICANT: VENTER, J. Craig et al. |
| APPLICANT: VENTER, J. Craig et al. |
| APPLICANT: VENTER, J. Craig et al. |
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
| FILE REFERENCE: CLOO1307 |
| CURRENT APPLICATION NUMBER: 06/241,755 |
| PRIOR APPLICATION NUMBER: 60/241,756 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-10-03 |
| PRIOR FILING DATE: 2000-09-08 |
| NUMBER OF SEQ ID NOS: 207012 |
| SSOFING APPLICATION WINDER: 40/231,498 |
| NUMBER OF SEQ ID NOS: 207012 |
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                                                                                                                                                                                                                                                            2;
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Pred. No. 5.6e-37;
0; Mismatches 20; Indels 0;
                                                                                                                                                                               Score 153; DB 4; Length 30222;
Pred. No. 2.7e-37;
0; Mismatches 40; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 12
US-09-949-016-17533/c
Sequence 17533, Application US/09949016
; Petent No. 6812339
                                                                                                                                                                               51.0%;
81.8%;
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Best Local Similarity 89.2%;
Matches 165; Conservative
                                                                                                                                                                        Query Match
Best Local Similarity 81.8°
Matches 189; Conservative
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                                      ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17299
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LENGTH: 30222
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Sequence 204887, Application US/09949016

patent No. 681239

GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHIGNS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENT APPLICATION NUMBER: US/09/949,016
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT PILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-03
PRIOR PELING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-0-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PRESEEQ for Windows Version 4.0
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Pred. No. 5.4e-38;
1; Mismatches 20;
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Pred. No. 5.4e-38;
1; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                      50.9%;
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Best Local Similarity 88.6
Matches 164; Conservative
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Best Local Similarity 88.6
Matches 164; Conservative
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US-09-949-016-204887/c
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                                                                                                                                                                                                                                                                                                                     ORGANISM: Human
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208 AAAATATAAAAATTAGCTGGGGGGGGGGCGCTGTAGTCCCAGCTACTCGGGAGG 267
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                                                                    61 CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC 120
                                           266 CTGAGGCATGAGAATCACTTGAACCCAGGAGGCGGAGGTTGCAGTGAGCCGAGATCGAGC 207
1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG 60
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Job time : 64.8219 secs
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US-09-949-016-143301
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us-09-899-276c-6.rnpb

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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(without alignments)
3633.986 Million cell updates/sec l aaaatataaaaattagccag......aatctaatagaagctactga 300 August 4, 2005, 08:04:16 ; Search time 535.142 Seconds 7297361 seqs, 3241162794 residues OM nucleic - nucleic search, using sw model IDENTITY NUC Gapop 10.0 , Gapext 1.0 US-09-899-276C-6 300 Title: Perfect score: Scoring table: Sequence: Searched: Run on:

Total number of hits satisfying chosen parameters: Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

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/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO0_PUBCOMB.seq:* Published Applications NA:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

## Sequence 4, Appli Sequence 1625, Ap Sequence 712, App Sequence 128663, Sequence 128663, Sequence 1214, Ap Sequence 6, Appli Description 19 US-10-685-705-4 15 US-10-311-455-1625 19 US-10-322-281-712 13 US-10-027-632-128663 17 US-10-027-622-128663 9 US-09-764-847-1214 US-09-899-276-6 Query Match Length DB 11793 5926 31926 Score 167.8 160.8 156.6 156.6

Sequence 1215, Ap	121	12866				128		135	135	equence 13537	13537	25783	257		157	e 50,	3428,	e 176			æ	m	Sequence 3, Appli	m	Ñ	H			1666,	676,	2650,	248,	98423	Sequence 98424, A	98423	Sequence 98424, A
US-09-764-847-1215	US-10-092-154-121	-10-027-632-128	7 US-10-027-632-128	٥	3 US-10-027-632-128	US-10-027-632-1	US-1	3 US-10-027-632-135370	US-10-027-632	US-10-027-632	US-10-027-632-1	US-10-027-632-2	US-10-027-632-257	US-10-292-798-146	3 US-10-087-192-1576	9 US-10-367-094-50	₽		US-09-844-653-5	US-10-027-632	US-10-027-632-882	US-10-917-647	US-09-822-246-	0 US-10	US-10-322-696-58	US-10-027-632-116	7 US-10	1 US-10-741-600	US-10-087-192-166	3 US-10-087-192-676	ns-0	US-1	US-1	-10-027-632-984	7 US-10-027-632-98423	7 US-10-027-632-98424
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52.1	52.1	51.9	51.9	51.9	51.8	51.8	51.8	51.5	51.5	51.5	51.5	51.4	51.4	51.3	51.0	50.9	50.9	50.9	50.9	50.8	50.8							50.5	50.5	50.4	50.3	50.3	50.3	50.3	50.3	50.3
99	156.4	155.8	155.8	155.8	155.4	155.4	155.4	154.4	154.4	154.4	154.4	154.2	154.2		153	152.8	152.8	152.8	152.8	152.4	152.4	152.2	151.8	151.8	151.6	151.4	151.4	151.4	151.4	151.2	151	151	151	151	151	151
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## ALIGNMENTS

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APPLICANT: Soci, Ubaldo
APPLICANT: Soci, Ubaldo
APPLICANT: Soci, Ubaldo
APPLICANT: Soci, Ubaldo
APPLICANT: Coy, Johannes
APPLICANT: Poiste, Hajo
APPLICANT: Poiste, Annemarie
APPLICANT: Poiste, Annemarie
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APPLICANT: Poiste, Annemarie
APPLICANT: Poiste, Annemarie
APPLICANT: Description NUMBER: US/09/899,276
CURRENT APPLICATION NUMBER: US/09/899,276
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: EP 00 114 560.6
PRIOR APPLICATION NUMBER: EP 00 114 560.6
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 300; DB 9; 100.0%; Pred. No. 8.4e-82; tive 0; Mismatches 0;
                          Sequence 6, Application US/09899276
Patent No. US20020106355A1
GENERAL INFORMATION:
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Best Local Similarity 100.
Matches 300; Conservative
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US-09-899-276-6
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Gaps

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Length 300; Indels

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; Sequence 4, Application US/10685705
; Publication No. US20040177387A1
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; APPLICANT: UNiversity of Methods And Animal Model For Analyzing Age-Related Macular
; TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular
; TITLE OF INVENTION: Degeneration
; TITLE OF INVENTION: Degeneration
; TITLE OF ILING DATE: 2002-9-0415
; CURRENT PILING DATE: 2003-10-16
; PRIOR FILING DATE: 2003-10-16
; PRIOR FILING DATE: 2002-10-30
; SOFTWARE: PatentIN version 3.2
; SEQ ID NO 4
; LANGETH: 11793
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                  1 AAAATATAAAAATTAGCCAGCGGGATGTCATGTGCCTGTAGTCCCAGCTACTCGGAGG
                                                                             181 AAAAATGCAGACTGTGATTCAGCAGGTCTGGGGTTGAAGCCCCAGAACTCTCTGATAAATTC
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1 AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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100.0%; Score 300; DB 19;
Best Local Similarity 100.0%; Pred. No. 4.1e-81;
Matches 300; Conservative 0; Mismatches 0;
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US-10-311-455-1625
; Sequence 1625, Application US/10311455
; Publication No. US20030143606A1
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US-10-685-705-4
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APPLICANT: OLEK, Alexander
APPLICANT: OLEK, Alexander
APPLICANT: DEFERBNECK, Christian
APPLICANT: DEFERBNECK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Ortoine methylation
TITLE OF INVENTION: Ortoine methylation
FILE REFERENCE: 5013.1014
CURRENT APPLICATION NUMBER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR PELICATION NUMBER: DE 10032529.7
PRIOR PELICATION NUMBER: DE 10033529.7
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
PRIOR FILING DATE: 2000-09-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 712, Application US/10322281

Sequence 712, Application US/10322281

Sequence 712, Application US/10322281

GENERAL INFORMATION:

APPLICANT: David W. Morris

APPLICANT: Marc S. Malandro

TILLE OF INVENTION: Novel Compositions and Methods in Cancer

TILLE OF INVENTION: Novel Compositions and Methods in Cancer

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 712.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 167.8; DB 1.
Pred. No. 1.3e-40;
0; Mismatches 47
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Best Local Similarity 80.7%;
Matches 196; Conservative 0
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Best Local Similarity 86.8
Matches 177; Conservative
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US-10-322-281-712
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378 AAAATACAAAATTAGCCAGGCATGGTGGCATGTGCCTGTAGTCCCAGCTACTCGGGAGG 319
                                                   GENERAL INCOMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Delymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT PAPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR PALICATION NUMBER: US 60/198,676
PRIOR PALICATION NUMBER: US 60/198,676
PRIOR PLING DATE: 2000-04-20
PRIOR PAPLICATION NUMBER: US 60/193,483
PRIOR PLING DATE: 2000-04-20
PRIOR PLING DATE: 2000-03-24
PRIOR PLING DATE: 1090-01-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-11-23
PRIOR PLING DATE: 1999-10-24
PRIOR PLING DATE: 1999-09-28
PRIOR PLING DATE: 1999-09-28
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Patent No. US20020132767A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENITION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC09
CURRENT APPLICATION NUMBER: US/09/764,847
CURRENT FILING DATE: 2001-01-17
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Pred. No. 1.2e-37;
0; Mismatches 19;
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Pred. No. 3.8e-37;
0; Mismatches 41;
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81.5%;
           US20030204075A9
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Best Local Similarity 89.8%;
Matches 168; Conservative
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Best Local Similarity 81.5
Matches 181; Conservative
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US-09-764-847-1214/C
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US-10-027-632-128663
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US-09-764-847-1214
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LENGTH: 5304
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APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
ITILE OF INVENTION: Identification and Mapping of Single Nuclectide
ITILE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US 60/218,006

FRIOR PELING DATE: 2002-04-30

FRIOR PELING DATE: 2000-07-20

FRIOR PELING DATE: 2000-04-20

FRIOR PELING DATE: 2000-04-20

FRIOR PELING DATE: 2000-03-24

FRIOR PELING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-11-23

FRIOR FILING DATE: 1999-09-28

FRIOR FILING DATE: 1999-09-28

FRIOR FILING DATE: 1999-09-28

FRIOR FILING DATE: 1999-09-08

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FRIOR FILING D
                                                                                                          CTGAGGCAGGAGAACCTCTTGAATCCAGGAGGCGCAGGTTGCAGTGAGCAGAGATAGTGC
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0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 128663, Application US/10027632; Publication No. US20020198371A1; GENERAL INFORMATION:
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US-10-027-632-128663/c
; Sequence 128663, Application US/10027632
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Matches 168; Conservative
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US-10-027-632-128663/C
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Sequence 11215, Application US/09764847

Patent No. US20020132767A1

GENERAL INFORMATION:

APPLICATION:

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION: Number: US/09/764,847

CURRENT FILING DATE: 2001-01-17

CURRENT FILING DATE: 2001-01-17

FILOR APPLICATION ACE REMOVED: FOR SEQ ID NOS: 2003

SOFTWARE: PatentIN Ver. 2.0

SEQ ID NO 1215

LINGTH: 5304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 1214, Application US/10092154
; Publication No. US20030054375A1
; Publication No. US20030054375A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; TURRENT APPLICATION NUMBER: US/10/092,154
; CURRENT FILING DATE: 2002-07
; NUMBER OF SEQ ID NOS: 2003
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIN Ver. 2.0
; SGO ID NO 1214
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CORGANISM: Homo sapiens
US-09-764-847-1215
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US-10-092-154-1214/c
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Publication No. US20020198371A1;
GENERAL INFORMATION:
APPLICANT: WANG, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide;
TITLE OF INVENTION: Polymorphisms in the Human Genome
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Pred. No. 3.8e-37;
0; Mismatches 41; Indels 0;
                                                        DB 14; Length 5304;
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Sequence 1215, Application US/10092154

Bublication No. US20030054375A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

FILE REFERENCE: PC009C1

CURRENT FILING DATE: 2002-03-07

NUMBER OF SEQ ID NOS: 2003

PRIOR Application removed - See File Wrapper or Palm

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1215

LENGTH: 5304
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                                                        Query Match 52.1%; Score 156.4; DB 14; Best Local Similarity 81.5%; Pred. No. 3.8e-37; Matches 181; Conservative 0; Mismatches 41;
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Best Local Similarity 81.5%;
Matches 181; Conservative <sup>0</sup>
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US-10-092-154-1215
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-092-154-1214
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                                                                                                                           Score 155.8; DB 17; Length 556;
Pred. No. 2.2e-37;
0; Mismatches 17; Indels 0;
                                                                                                                                                                                                                    AAAATATAAAAATTAGCCAGGCGTGATGTCATGTGCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3426, Application US/10723860
Publication No. US20040253606A1
GENERAL INFORMATION
APPLICANT: Aziz, Natasha
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Ginsburg, Wendy M.
APPLICANT: Glothik, Albert
ITLE OF INVENTION: Methods of Diagnosis of So;
ITLE OF INVENTION: Methods for Screening for TILE REFERENCE: 05882.0193, NPUSO1
CURRENT APPLICATION NUMBER: US/10/723,860
CURRENT FILING DATE: 2003-11-26
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR APPLICATION NUMBER: 60/429,739
PRIOR FILING DATE: 2002-11-26
NUMBER OF SEQ ID NOS: 8939;
SOFTWARE: PatentIn version 3.2
                                                                                                                             51.9%;
                                                                                                                         Query Match
Best Local Similarity 90.7
Matches 166; Conservative
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ORGANISM: Homo sapiens
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US-10-027-632-128664/c
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US-10-723-860-3426/c
                                                                                  US-10-027-632-128662
                                      TYPE: DNA
ORGANISM: Human
SEQ ID NO 128662
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Pred. No. 2.2e-37;
0; Mismatches 17;
         CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/19,676
PRIOR PELING DATE: 2000-04-20
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 2000-03-29
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-11-23
PRIOR PELING DATE: 1999-10-28
PRIOR PELING DATE: 1999-10-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-28
PRIOR PELING DATE: 1999-09-09
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
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CURRENT FILING DATE: 2002-04-30
PRIOR PLING DATE: 2002-04-30
PRIOR PLLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-07-12
PRIOR PLING DATE: 2000-03-29
PRIOR PLING DATE: 2000-03-29
PRIOR PPLING DATE: 2000-03-29
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PRIOR PLING DATE: 3090-11-23
PRIOR PLING DATE: 3090-11-23
PRIOR PLING DATE: 1999-109-28
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PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASESEQ FOR WINDÓWS VERSION 4.0
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Publication No. US20030204075A9
GENERAL INFORMATION:
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Best Local Similarity 90.7%;
Matches 166; Conservative
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ORGANISM: Human
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LENGTH: 556
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Query Match 51.8%;
Best Local Similarity 90.2%;
Matches 165; Conservative
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; ORGANISM: Human
US-10-027-632-128664
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y Sequence 128664, Application No. US20030204075A9
y Publication No. US20030204075A9
y GENERAL INFORMATION:
APPLICANTY WANG, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE REFERENCE: 108827.12.9
CURRENT APPLICATION NUMBER: US 60/218,006
PRIOR PILING DATE: 2002-04-30
PRIOR FILING DATE: 2000-07-22
PRIOR PELICATION NUMBER: US 60/198,676
PRIOR PELICATION NUMBER: US 60/199,483
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-24
PRIOR FILING DATE: 1999-11-23
                                      1 AAAATATAAAAATTAAGCCAGGCGTGATGTCATGTGCCTGTAGTCCCAGCTACTCGGGAGG
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Sequence 128664, Application US/10027632
Publication No. US20020198371A1
GENERAL INFORMATION:
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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    .650
    /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Sequence 7 from Patent EP1170372.
                AC114440
MMU238892
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ACCESSION
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KEYWORDS
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
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Maximum DB seq length: 200000000
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/db_xref="a(31:992947"

/translation="MKVSAALICLILIAATFIPQGLAQP"

3148. ->327

/number=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3227;
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             Atsunisa Ueda
First Department of Internal Medicine
Yokohama City University School of Medicine
3-9 Pukuwra, Kanazawa-ku
Yokohama 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 650; DB 9;
100.0%; Pred. No. 5e-190;
ative 0; Mismatches 0;
Submitted (06-Dec-1993) to DDBJ by:
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Location/Qualifiers
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3012. .3147
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Ueda,A., Okuda,K., Ohno,S., Shirai,A., Igarashi,T., Matsunaga,K.,
Ueda,A., Okuda,K., Ohno,S., Ishigatsubo,Y. and Okubo,T.
Fukushima,J., Kawamoto,S., Ishigatsubo,Y. and Okubo,T.
NF-kappa B and Spi reale transcription of the human monocyte
chemoattractant protein-1 gene
J. Immunol. 153 (5), 2052-2063 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (06-DEC-1993) Atsuhisa Ueda, Yokohama City University School of Medicine, First Department of Internal Medicine; 3-9 Fukuura, Kanazawa-ku, Yokohama 236, Japan (Tel:045-787-2630, Fax:045-786-3444)
                                                                                                                                                                                  CCATGGGCTAATTGGTCTCCTTCTGGGATTGTGGCTTATCAGATAAAAACAAGTGAGTC
                                                                                                                                                                                                                                      241 CCAGAAGACTTTCTTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATAT
                                                                                                        CCAACACTCAGAAGCCTATGTGAACACTCAGCCAGCAAAGCTGGAAGTTTTTCTCTGTGA
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Rollins,B.J., Stier,P., Ernst,T. and Wong,G.G.
The human homolog of the JE gene encodes a monocyte secretory
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Human gene for monocyte chemoattractant protein-1, 5'-genome
region.
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MCP-1; monocyte chemoattractant protein-1.
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9174 bp DNA linear PRI 09-JUL-2002
Homo sapiens small inducible cytokine A2 (monocyte chemotactic
protein 1) (SCYA2) gene, complete cds.
AFS19531
AFS19531.1 GI:21435976
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To cite this work please use: SeattleSNP8. NHLBI HL66682 Program
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1 (bases 1 to 9174)

Rieder,M.J., Armel,T.Z., Carrington,D.P., Ozuna,M., Kuldanek,S.A., Rajkumar,N., Toth,E.J., Yi,Q. and Nickerson,D.A.
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                                                                                                 Length 11793;
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                                                                                             Query Match 94.9%; Score 616.6; DB 9; Best Local Similarity 97.7%; Pred. No. 1.2e-179; Matches 636; Conservative 0; Mismatches 14;
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Location/Qualifiers
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1. 11793
/ organism="Homo sapiens"
/ mol type="genomic DNA"
/ mol type="genomic DNA"
/ db xref="taxon:9606"
/ chromosome="17"
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ancer / gene="MCP-1"
ancer / 935. 4944
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Differential transcriptional regulation of the monocyte-chemoattractant protein-1 (MCP-1) gene in tumorigenic and non-tumorigenic HPV 18 positive cells: the role of the chromatin
802 CTAAGCCAGGAGACTTATTTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGAA 861
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join(<7550. .7685,8468. .8585,8968. .>9073)
/gene="MCP-1"
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/gene="MCP-1"
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join(7610. .7685,8468. .8585,8968. .9073)
/gene="MCP-1"
/codon_erart=1
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/gene="MCP-1"
/number=2
8586. .8967
/gene="MCP-1"
/number=2
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Roesl, F.
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United Summission

Submitted (12-AUG-1998) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

18 (Bases 1 to 1474[6]

18 Sirren, B., Fasman, K., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Barker, J., Bardwin, N., Barckerly, R., Benn, J., Boutwell, C., Brown, A., Castle, A., Cerny, J., Colangelo, M., Bovon, K., Dewar, K., Donelan, L., Ferreira, P., Fitzhugh, W., Porrest, C., Funke, R., Gage, D., Gardyna, S., Geraigery, K., Grant, G., Hagoes, B., Haedrod, A., Herena, L., Horton, L., Howland, J. C., Jacotot, L., Jones, C., Kaml, L., Karatas, A., Lehoczky, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Malta, M., Morris, W., Morrow, J., Mychaleckyj, J., Nolla, M., Morris, W., Morrow, J., Wychaleckyj, J., Stange-Thomann, N., Stilwell, J., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Tichovolsky, N., Torruella-Miller, I., Vas, H., Vo, A., Wagner, A., Wheeler, J., Wuw, Y., Wyman, D., Ye, W. J., Zhao, J., and Zody, M., Wheeler, J., Wuw, Y., Wyman, D., Ye, W. J., Labo, J., and Zody, M., Wheeler, J., Wuw, Y., Wyman, D., Ye, W. J., Labo, J., and Zody, M., Wheeler, J., Wuw, Y., Wyman, D., Ye, W. J., Labo, J., Labo, J., Labo, J., Labo, J., Labo, J., Labo, J., Labo, J., Labo, J., Labo, J., Whan, D., W., Ye, W. J., Wyman, D., Ye, W. J., Labo, J., Labo, J., Labo, J., Whan, D., W., Ye, W. J., Wyman, D., Ye, W. J., Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, Labo, La
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Homo sapiens chromosome 17, clone hRPK.215_B_13, complete sequence.
AC005549
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1 (bases 1 to 147416)

Birren, B., Linton, L., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 17, clone hRPK.215_B_13
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Submitted (12-SRP-1998) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
4 (bases 1 to 147416)
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AC005549/c
LOCUS
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ACCESSION
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SOURCE
ORGANISM
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1297<u>9</u>.
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Licet Submission

Submitted (22-SEP-1998) Whitehead Institute/MIT Center for Genome Submitted (22-SEP-1998) Whitehead Institute (3141, USA On Sep 13, 1998 this sequence version replaced gi:3581743.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, J. P. (1996-1997).
                                                                                                                                                                                                                                                                                                                                                                   Only the first 147416 bases of this clone are being submitted. Bases 145417-155040 overlap accession number AC004147 (WICGR project L228). The first 2Kb of the overlapping region are submitted to confirm overlap.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                       http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N., Birren, B., Linton, L., Nusbaum, C., Lander, E., Beda, F., Baldwin, J., Barna, N., Beckerly, R., Beda, F., Coske, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Choepel, Y., Eptzhugh, M., Collins, S., Collymore, A., Cooke, P., Gardyna, S., Firzhugh, M., Doyle, M., Doyle, M., Doyle, M., Corlon, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Karates, A., Klein, J., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., Morman, C.H., O'Comnor, T., O'Donnell, P., Olivar, T. M., Peterson, K., Pisani, C., Pollara, V., Raymond, C., Riley, R., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N., Subramannian, A., Talamas, J., Wux, K., Wyman, D., Ye, W.J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Tirrell, A., Vassillev, H., Viel, R., Vo, A., Wu, X., Wyman, D., Ye, W.J., Theopats were identified using RepeatMasker:

Smit, A.F. A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker:html
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Homo sapiens chromosome 17 clone RP11-329H16 map 17, LOW-PASS
SOCIENCE SAMPLING.
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1 (bases 1 to 73806)
1 Elran, Ballan, Linton, L., Nusbaum, C. and Lander, E. Homo sapiens chromosome 17, clone RP11-329H16
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Contact: sequence submissions@genome.wi.mit.edu
------ Project Information
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Query Match

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J.N.U. Campus, New Delhi 110 067,
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Mammalia; Butheria; Primates; Platyrrhini; Callitrichidae;
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Submitted (21-MAR-2002) Virology
Immunology, Aruna Asag Ali Marg,
India
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3684 CITATACCGAAATATTCCCAACACACACCCCATATAAAAACTCCCTAACTCCGAACCCAAT 3625
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/organism="synthetic construct"
/mol.type="unasigned DNA"
/db xref="texon:32630"
/note="chemically treated genomic DNA (Homo sapiens)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGCTTGTGCCCGAGTTCTCCCAGCCACAGCCCCATGTGAGAGCTCCCTGGCTCCGGGGCCCA
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                                                                3624 AICTABABATACABACTCCAACCABATACATTCTCTTCTACGABATCTABABACTTCCABA
                                                                                                                                                       243 AGAAGACTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATAT
                                                                                                                                                                                                                                                                                                                                                                                           ATCTGGAATGCAGGCTCCAGCCAAATGCATTCTTCTTACGGGATCTGGGAACTTCCAAA
                                                                                                                                   GCTGCCTCCTCAGAGTGGGAATTTCCACTCACTTCTCTCACGCCAGGCACTGACCTCCCAG
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Diagnosis of diseases associated with the immune system
Patent: WO 0200928-A 1625 03-JAN-2002;
Epigenomics AG (DE)
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llarity 73.6%; Pred. No. 1.1e-101;
Conservative 0; Mismatches 171;
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synthetic construct
other sequences; artificial sequences.
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AF493700 312 bp DNA linear PRI 12-MAY-2002
Macaca radiata monocyte chemoattractant protein 1 (MCP1) gene,
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Homo sapiens isolate 1 monocyte chemoattractant protein 1 (MCP1)
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                                                                                                                                                                        Macaca radiata

Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Bumanlai, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.

1 (bases 1 to 312)
Shanmugasundaram, G.K., Chakraborti, S., Sankaranarayanan, K. and
                                                                                                                                                                                                                                                                                             Banerjea, A.C.
Direct Submission
Submitted (21-MAR-2002) Virology II, National Institute of
Immunology, Aruna Asag Ali Marg, J.N.U. Campus, New Delhi 110 067,
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Direct Submission
Submitted (21-MAR-2002) Virology II, National Institute of
Immunology, Aruna Asag Ali Marg, J.N.U. Campus, New Delhi 110 067,
India
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Shanmugasundaram, G.K., Chakraborti, S., Sankaranarayanan, K. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 ATGACAACTCCTTCCTGAAGTAGAGACATGCTTCCAACACTCAGAAGCCTATGTGAACAC
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21.4%; Score 139; DB 9; Length 312;
Best Local Similarity 86.3%; Pred. No. 1.6e-31;
Matches 177; Conservative 0; Mismatches 25; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MCP1"
/note="monocyte chemoattractant protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                             1. .312
/organism="Macaca radiata"
/mol_type="genomic DNA"
/db_xref="taxon:9548"
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                                                                                                                                                        Macaca radiata (bonnet macaque)
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AF493697
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/gene="MCP1"
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Homo sapiens
                                                                                promoter region.
AF493700
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AF493697
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Homo sapiens isolate 2 monocyte chemoattractant protein 1 (MCP1)
                                                                                387
                                                                                                                  171
                                                                                                                                                          445
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                                                                                                                                                                                                                                                     232 TGGATTGTGGCTTTATCAGATAAAAAAGAGGTGGTCATGCCACAGGATGTCTATAAGCCCA 291
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328 ATGACAACTCCTTCCTGAAGTAGAGACATGCTTCCAACACTCAGAAGCCTATGTGAACAC 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGATTGTGGC-TTATCAGATAAAACAAGTGAGTCATGCCACAGGATGTCTATAAGCCCA 505
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Submitted (21-MAR-2002) Virology II, National Institute of
Immunology, Aruna Asag Ali Marg, J.N.U. Campus, New Delhi 110 067,
India
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Shanmugasundaram,G.K., Sankaranarayanan,K. and Banerjea,A.C.
                                                                                                                                                    112 ACGCCAGCACTGACCTCCCAGCGAGACATGCTTCCAACACTCCAGAAGCCTATGTGAACAC
                                                                                                                                                                                                                               TGGATTGTGGCTTATCAGATAAAACAAGTGAGTCATGCCACAGGATGTCTATAAGCCCA
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7
      Length 316;
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                                                                            328 ATGACAACTCCTTCCTGAAGTAGAGACATGCTTCCAACACTCAGAAGCC
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<1. .>307
/gene="MCP1"
/note="monocyte chemoattractant protein 1"
                                          Indels
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    Score 147.8; DB 9;
Pred. No. 2.9e-34;
0; Mismatches 27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.8%; Score 141.4; DB 9; Best Local Similarity 90.2%; Pred. No. 2.8e-32; Matches 185; Conservative 0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .307
/organism="Homo sapiens"
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/isolate="2"
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/gene="MCP1"
Query Match 22.7%;
Best Local Similarity 85.9%;
Matches 176; Conservative
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Homo sapiens
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184 GGGGGAGGGATCTTTCTTGACAGAGCTGGGAGGGGAGCAGCAGCTGTCACTTTCCA 243
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Rollins, B.J., Morrison, B.D. and Stiles, C.D.
Rollins and expression of JE, a gene inducible by platelet-derived growth factor and whose product has cytokine-like properties proc. Natl. Acad. Sci. U.S.A. 85 (11), 3738-3742 (1988)
530
                                                                                         312
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Alberta,J.A., Irminger,J. and Stiles,C.D.
Macrophage chemoattractant protein-1 (mcp-1) 5' flanking region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jackses 1 to 2788)

Abberta, J.A.

Direct Submission
Submitted (20-JUL-1994) John A. Alberta, Cellular and Molecular
Biology, Dana Farber Cancer Institute and Harvard Medical School,
44 Binney St., Boston, MA 02115, USA
Location/Qualifiers
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                                                              471 CAAGTGAGTCATGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGAT
                                                                            253 AGAAGTGGCCATGCGACAGGATGTCTGTAAGCCCATTGATTCTGGAATTCGATGAGTGAT
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/gene="mcp-1"
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                                                                                                                                                                                                                                             chemokine; mcp-1; macrophage chemoattractant protein-1
Mus musculus (house mouse)
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/clone="JUJCI-50"
                                                                                                                                                                        2788 bp
                                                                                                                                                                                        Mus musculus Balb/c macrophage gene, 5' flanking region.
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2788. .>2788
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Matches 204; Conserv
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J.N.U. Campus, New Delhi 110 067,
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Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
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Shanmugasundaram, G.K., Chakraborti, S., Sankaranarayanan, K. and
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Pred. No. 1.3e-27;
0; Mismatches 26; Indels
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                                                                                             <1. \ . > 310
/gene="MCPI"
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Papio hamadryas
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Submitted (21-MAR-2002) Virology
Immunology, Aruna Asag Ali Marg,
India
                                   sapiens"
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Matches 153; Conservative (
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/gene="MCP1"
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Matches 161; Conserv
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	**************************************	AGIII 3244 HUMAII MOII	Ado03803 Human Cc1	Adn12120 MCP1 gene	Ado03802 Human Cc1	Acf64397 Human MCP	Abl33653 Human imm	Abl33652 Human imm	Ada71938 Rice gene	Abl33000 Human imm	Adb31378 Testoster	Acn37240 Human per	Acn44200 Mouse gen	Adq97331 Human can	Aai91704 Human pol	Acn44066 Human gen	Abd32866 Mouse can	Abl70575 Chemicall	Aas61258 Human gen	Abz12660 Arabidops	Abl33011 Human imm
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de	Query Match I	000	7001	94.9	93.6	93.6	79.0	61.8	56.2	9.9	5.9	9.6	5.5	5.5	5.4 1	5.4	5.4	5.4 1	5.3	5.3	5.3	5.3
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AAF65257 AAF65185 ADM01616 ABM01835 ABM1938 ABM32738 ABM32738 ABM170179 AASM170179	AAS46692 ABZ13218 ABD33027 ABD70604 AAA96366	ADL1254 ADL12148 ADB52913 ADB52913 AAV21209 AAV21209 ABO91330 ABO97661 ABX33717 ⁰ ADB81391 ⁰	ALIGNMENTS	BP.		tractant-protein-1 therapy; atheroscl				SZENIKUM. Finzer P, Delius	encoding monocyte-c treating atheroscle	Opp; English. novel nucleic activities of MCP-1. A cytostatic, and action may have a is useful in the osclerosis or can
402 682 2243 2243 2000 22 2000 22 6759 22 15923 22 15923	24259 24259 22 16509 22 24792 23 34548 250000	5.1 1759 12 5.1 10757 4 5.1 110007 4 5.1 110000 6 5.1 110000 6 5.1 110000 6 5.1 110000 8		lard; DNA; 650	(-2004 (first entry) monocyte-chemoattractant-protein-1	cyte-chemoat rotic; gene oma.		2000EP-00114560	2000EP-00114560	KEBSFORSCHUNG U, Coy J, Patzelt A;	195/22. acid molecule	relates to a novel nucling monocyte-chemoatrx ological activity of MCI vention has cytostatic, I of the invention may be invention is useful:
1.5 £ 4 2.0 5 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	0 1 2 2 4 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	64 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	r1 E+	944 ADH13944 standard; ADH13944;	11-MAR-2004 ( Human monocyte	ds; human; monocyt antiarteriosclerot cervical carcinoma Homo sabiens,	_ EP1170372-A1.	09-JAN-2002. 06-JUL-2000; 2	L-2000;	(DEKK-) DEUT K Roesl F, Soto Zur Hausen H,	WPI; 2002-1658 Novel nucleic a	Disclosure, SEQ II The invention relisequence encoding having the biolog acid of the inven A nucleic acid of compound of the ii
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accumulation in eye.
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 WO2004041160-A2
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                                                   30-OCT-2002;
                  21-MAY-2004
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pharmaceutical composition of the invention is useful for the of diseases associated with dysregulation of MCP-1 expression, atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 650;
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4.7e-215;
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                                             Seguence 650 BP; 167 A; 165 C; 147 G; 171 T; 0
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                                                              Query Match
Best Local Similarity 100.0%;
Matches 650; Conservative 0;
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This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated mecular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular Ccl2-deficient, Ccr2-deficient and/ or a Ccl2-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polynucleotide sequence is the human Ccl2 gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                                     Testing candidate drug for treating age-related macular degeneration, by administering drug to Cc12-deficient, Ccr2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
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Pred. No. 1.1e-202;
0; Mismatches 14; Indels 1; C
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                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 4; 64pp; English.
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2003WO-US032933
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ACTAAGCCAGGAGACTTATTTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGA
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iive 0; Mismatches 14;
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Matches
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ò 셤 ઠે (first entry)

13-OCT-2003

ACF64397;

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                                                                           This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated metaliar degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular Ccl2-deficient, Ccr2-deficient and/ or a Ccl2-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or regression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polynucleotide sequence is the human Ccl2 promoter region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AATGCAGGCTCCAACCAAATGCATTCTCTACGGGATCTGGGAACTTCCAAAGCTGCC 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              241 CTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATATGCAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                        TCCTCAGAGTGGGAATTTCCACTCACTCTCACGCCAGCACTGACCTCCCAGCGGGG
                                                                                                                                                                                                                                                                                                                                                                                                   CCGAGATGTTCCCAGCACACATGTGAGAGCTCCCTGGCTCCGGGCCCAGTATCTGG
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                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                  Query Match
93.6%; Score 608.6; DB 12; Length 3221;
Best Local Similarity 97.7%; Pred. No. 3.2e-200;
Matches 628; Conservative 0; Mismatches 14; Indels 1;
analyzing development or regression of drusen and/or lipofuscin accumulation in eye.
                                                                                                                                                                                                                                                                                                    Sequence 3221 BP; 859 A; 793 C; 727 G; 842 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCATGACTGGATTATAAAGGGAAATTGAATGCGGTCCACCAA 650
                                                      Disclosure; SEQ ID NO 3; 64pp; English.
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ACF64397 standard; DNA; 599

ACF64397 ID ACF6 XX RESULT

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The present invention describes an isolated polynucleotide (PN) comprising: (a) a sequence comprising at least 15 contiguous nucleotides of a sequence comprising variant sequences (A) from Table 4 given in the specification; or (b) a sequence that is complementary to (A). Also described: (1) an array of (PN)s comprising two or more of the isolated (PN)s; (2) detecting a (PN) in an individual; (3) a computer-readable storage medium, where each record has a field identifying a base occupying a (PN) site and a location of the polymorphic site; and (4) a signal carrying data for access by an application program having executed associated with multiple sclerosis. Refedois to Acred 424 represent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; detection; computer-readable storage medium; polymorphic site; signal carrying data; data processing system; multiple sclerosis; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAGAAGACITTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATAT
                                                                                                                                                                                                                                                                                                                                                                                                       New polynucleotide, useful for detecting loci associated with multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               41 GGCTTGTGCCGAGATGTTCCCAGCACCCCATGTGAGAGCTCCCTGGCTCCGGGCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 GTATCTGGAATGCAGGCTCCAGCCAAATGCATTCTCTTCTACGGGATCTGGGAACTTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 AAGCTGCCTCCTCAGAGTGGGAATTTCCACTCACTTCTCTCACGCCAGCACTGACCTCC
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                                                                                                                                                                                                                                                                                                                                               Natsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 599 BP; 145 A; 160 C; 139 G; 154 T; 0 U; 1 Other;
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                                                                                                                                                                                                                                                                                                                                                Jones HB, Xu H, White R, Rienhoff HY,
                                                        Human MCP1 nucleotide sequence >MCP1_pro.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 74; 93pp; English.
                                                                                                                                                                                                                                                                       07-AUG-2001; 2001US-0310741P.
24-SEP-2001; 2001US-0324790P.
                                                                                                                                                                                                                                            07-AUG-2002; 2002WO-US025268
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Best Local Similarity 97.0
Matches 543; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fragment of chemically modified gene, useful for of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AlDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                             CCAACACTCCAGAAGCCTATGTGAACACTCAGCCAGCAAAGCTGGGAAGTTTTTCTCTGTG
                                                                                                                                                                               CATGCCACAGGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATG
CATGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATG
                                                                                                                                                    ACCATGGCTAATTGGTCTCCTTCTCGGATTGTGGCTTATCAGATAAAAACAAGTGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antiarteriosclerotic; antianaemic; cytostatic; nootropic; neuroprotective; anti-HIV; anticonvulsant; ophthalmological; antirheumatic; antiarthritic; antidabetic; antipsortatic; antiarthritic; antidabetic; antipsortatic; anticlammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 5926 BP; 1554 A; 55 C; 1492 G; 2825 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 1626; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 1626.
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ABL33653/C

ABL33653,C

ABL33653;

ABL33653;

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ABL33653;

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ABL33653;

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ABL33653;

Z6-MAR-2002 (first entry)

XX

Human; immune system disease; c; antianaemi

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Human; immune system disease; c; antianthritic; antianthritic; antianthritic; antianthritic; antianthritic; antinflammatory; cancer; eye disease, emuly findlammatory; cancer; eye disease, emuly findlammatory; cancer; eye disease, emuly findlammatory; cancer; eye disease, emuly findlammatory; cancer; eye disease, emuly findlammatory; cancer; eye disease, emuly findlammatory; cancer; eye disease, emuly findlammatory; cancer; eye disease, emuly findlammatory; cancer; eye disease, emuly findlammatory; cancer; eye disease, emuly findlammatory; condessed emuly findlammatory; condessed emuly findlammatory; conditioned by diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as including eye diseases such as experiments.
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Length 5926;

DB 6;

61.8%; Score 401.8;

Query Match

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    3684 CTTATACCGAAATATTCCCAACACACCCCATATAAAAACTCCCTAACTCCGAACCCAAT
                                                                                                                                                                                                                                                                                                                               3624 ATCTAAAATACAAACTCCAACCAAATACATTCTCTTCTACGAAATCTAAAAACTTCCAAA
                                                                                                                                                                                                                                                                           123 GCTGCCTCCTCAGAGTGGGAATTTCCACTCACTTCTCTCACGCCAGCACTGACCTCCCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGAAGACTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3444 AAAAAACTITCTITCTTATICCTACCCTICCCCTACCCTATATITACTATCTAATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATCTGGAATGCAGGCTCCAGCCAAATGCATTCTCTTCTACGGGATCTTGGGAACTTCCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                              3384 ACAAAAACCAAATCACTTTCCAAAATAACAACTCCTTCCTAAAATAAAACATACTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AACACTCAGAAGCCTATGTGAACACTCAGCCAGCAAAGCT-GGAAGTTTTTCTCTGTGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGCCACAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                542 TAAGCCAGGAGACTTATTTAAAGATCTCCAGCATCTTTCAGCTTGTTAACCTAGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CATGGGCTAATTGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; immune system disease; cytosine methylation; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3084 ACCCGAAACATAAATTATAAAAAAATTAAATAAGATCCACCAA 3036
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The present invention relates to a method (M1) for identifying genes involved in plant resistance or response to pathogenic infection. M1 comprises identifying a gene whose expression is significantly altered in the incompatible interaction of plant gene expression relative to expression of the gene in an uninfected plant, in a mutant plant that does not express a gene associated with response to pathogenic infection, or in a corresponding incompatible or compatible interaction. (M1) is useful for conferring resistance to resistance or tolerance to a plant to bacterial, fungal or yiral infection. The present sequence was used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAGAAGCCTATGTGAACACTCAGCCAGGAAAGCTGGAAGTTTTTCTCTGTGACCATGG-G 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAATTGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAACAAGTGAGTCATGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           309 GCCAAGTCACTTTCCAGAGATGACACTCCTTCCTGAAGTAGAGACATGCTTCCAACACT
                                                                                                                                                                                                                  bacterial infection; fungal infection; viral infection; rice;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying at least one gene involved in plant resistance or respathogenic infection for conferring resistance or tolerance to a bacterial, fungal or viral infection by determining or detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              involved in plant resistance or
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2000 BP; 336 A; 265 C; 284 G; 363 T; 0 U; 752 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 2000;
Hon
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Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6.6%; Score 43.2; DB 8;
1.2%; Pred. No. 0.002;
ve 154; Mismatches 122;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 , J,
Xie 'n
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glazebrook
Whitham S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 27; SEQ ID NO 5263; 899pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          (SYGN ) SYNGENTA PARTICIPATIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 Similarity 11.2%; Pr. 35; Conservative 154;
                                                                                                  BP
                                                                                                                                                                                                                                                                                                                                                               22-JUN-2001; 2001WO-IB001105.
                                                                                                                                                                                                                                                                                                                                                                                             22-JUN-2001; 2001WO-IB001105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cooper E
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bacterial, fungal or viral
illustrate the invention.
                                                                                                                                                                (first entry)
                                                                                                                                                                                             Rice gene, SEQ ID 5263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quan S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-175290/17.
                                                                                                    standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene expression
                                                                                                                                                                                                                                                                                                     WO2003000898-A1
                                                                                                                                                                                                                                                                         Oryza sativa.
                                                                                                                                                                                                                                                                                                                                    03-JAN-2003
                                                                                                                                                                20-NOV-2003
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Katagiri 1
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Best Local 8
                                                                                                      ADA71938
                                                                                                                                    ADA71938;
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                           2841
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       360
                                                                                                                                                                                                                                                                      The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAGCTGCCTCCTCAGAGTGGGAATTTCCACTCACTTCTCTCACGCCAGCACTGACCTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGCGGGGAGGCATCTTTCTTGACAGAGCAGAAGTGGGAGGCAGACAGCTGTCACTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2241 GGTTTGTGTCGAGATGTTTTAGTATAGTTTTATGTGAGAGTTTTTTGGTTTTGGTTTA
                                                                                                                                                                                  fragment of chemically modified gene, useful i of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 AAACCCGAAGCATGACTGGATTATAAAGGGAAATTGAATGCGGTCCACCAA 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 5926;
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 5926 BP; 1562 A; 55 C; 1318 G; 2991 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 1625; 32pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4; DB 6;
2.3e-115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 365.4;
Pred. No. 2.3
                                                                                                                            Berlin K;
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                    56.2%;
73.6%;
                 02-JUL-2001; 2001WO-EP007537
                                                  30-JUN-2000; 2000DE-01032529
01-SEP-2000; 2000DE-01043826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                        Nucleic acid comprising diagnosis and treatment
                                                                                                                            Piepenbrock C,
                                                                                              (EPIG-) EPIGENOMICS AG.
                                                                                                                                                           WPI; 2002-130909/17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
tes 479; Conserv
                                                                01-SEP-2000;
                                                                                                                                                                                                                          methylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    420
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The invention discloses a method for determining whether a compound can be used to treat prostate cancer and comprises measuring the expression level of a nucleic acid in prostate cancer cell sample in the presence and absence of the compound. Determining whether a compound can be used to treat prostate cancer reatment when the expression level of the nucleic acid in the presence of the compound is less than the expression level of the nucleic acid in the absence of the compound. Prostate cancer is usually cretated by androgen withdrawal, by castration or through the use of an anti-androgenic drug. Bicalutamide (casodex) is one such anti-androgenic compound or testosterone, can be used to treat the prostate cancer can be made on a patient by patient basis. The sequence presented is an expressed sequence tag (EST) which is more highly expressed in testosterone treated prostate cancer cells than the untreated cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Determination of whether compound is useful for prostate cancer treatment comprises measuring expression level of specific nucleic acid sequence in prostate cancer cell sample in the presence and absence of compound.
399 GTGGATATTTGTAATTTTTAGTTATTTTGGAAGTTTAGGTAGGAGAATCGTTTGAGTTTGG 458
                                            547 CAGGAGACTTATTTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTTAGAGAAAACCCG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACAGCCCCATGTGAGAGCTCCCTGGCTCCGGGCCCAGTATCTGGAATGCAGGCTCCAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; 88; prostate cancer; cancer; androgen; castration; anti-androgenic drug; bicalutamide; casodex; testosterone; EST; expressed sequence tag.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10; Length 1497;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1497 BP; 397 A; 284 C; 247 G; 387 T; 0 U; 182 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36.6; DB 10;
Pred. No. 0.34;
90; Mismatches 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Testosterone regulated prostate cancer gene #49.
                                                                                                                                          607 AAGCATGACTGGATTATAAAGGGAAATTGAA 637
                                                                                                                                                                                       519 GAGATTTTTTTAAAAATAAAAAAAA 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                                                                                                                                                           BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 1; Col 253-256; 194pp;
                                                                                                                                                                                                                                                                                                           ADB31378 standard; cDNA; 1497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-00220132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97US-0068821P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98US-0079303P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   5.68;
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                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-595981/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
es 48; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US6506607-B1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                    04-DEC-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JAN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shyjan AW;
                                                                                                                                                                                                                                                                                                                                                          ADB31378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25
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                                                                                                                                                                                                                                                            RESULT 10
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                                                                                                                                          8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders,
                                                 YRYSMKWYTWCTMWGYWWYWRTYMKMYKCTKTYWYWSATYWTGTWAAWMAKTKM 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTAATTGGTCTCCCTTCTCTGGATTGTGGCTTATCAGATAAAACAAGTGAGTCATGCCA 486
                      AGGAGAGACTTATTAAAGATCTCAGCATCTTTCAGCTTGTTAACCTAGAGAAACCCGA 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      339 Grinainichaingrinnichinnarachaaaanahahahahachachahang 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       487 CAGGATGTCTATAAGCCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGC 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antinflammatory; cancer; eye disease; arteriosclerosis; anaemia; acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy; neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel diseases. The present sequence is a gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiasthmatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 38.2; DB 6; Length 6557;
Pred. No. 0.23;
0; Mismatches 108; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; immune system disease; cytosine methylation; antiasthm
antiarteriosclerotic; antianaemic; cytostatic; nootropic;
neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 973; 32pp + Sequence Listing; German
                                                                                                                                                                                                                                                                                                                                                                                                                             Human immune system associated gene SEQ ID NO: 973.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                                                                                                                                                                                                                                  BP.
                                                                                                                                                                                                                                                                                ABL33000 standard; DNA; 6557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-JUL-2001; 2001WO-EP007537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JUN-2000; 2000DE-01032529.
01-SEP-2000; 2000DE-01043826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 5.9%;
Best Local Similarity 48.8%;
Matches 103; Conservative (
                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                 619
                                                                                                                                                              844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG.
                                                                                                               608 AGCATGACTGGA
                                                                                                                                                           833 RMGMTGAKTRGR
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/*tag= ab
/standard_name= "Single nucleotide polymorphism"
/note= "Variable nucleotide C,G"
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/note= "Variable nuclectide G,A"
32397
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/standard_name= "Single nucleotide polymorphism"
/note= "Variable nucleotide C,T"
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/etandard_name= "Single nucleotide polymorphism"
/note= "Variable nucleotide deletion,CT"
30580
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/etandard_name= "Single nucleotide polymorphism"
/note= "Variable nucleotide G,T"
11500
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/note= "Variable nucleotide C,T"
24796
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standard name= "Single nucleotide polymorphism"
note= "Variable nucleotide C,T"
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/standard_name= "Single nucleotide polymorphism"
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29877
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standard_name= "Single nucleotide polymorphism"
note= "Variable nucleotide C,G"
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standard_name= "Single nucleotide polymorphism"
'note= "Variable nucleotide A,G"
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standard_name= "Single nucleotide polymorphism"
lote= "Variable nucleotide C,G"
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standard_name= "Single nucleotide polymorphism"
note= "Variable nucleotide A,G"
294
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standard name= "Single nucleotide polymorphism"
'note= "Variable nucleotide A,G"
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/*tag= m.Single nucleotide polymorphism"
//note= "Vāriable nucleotide A,G"
12746
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/standard_name= "Single nucleotide polymorphism"
/note= "Variable nucleotide A,G"
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frandard_name= "Single nucleotide polymorphism"
forte= "Variable nucleotide C,T"
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standard_name= "Single nucleotide polymorphism"
note= "Variable nucleotide C.T"
?746
                                              standard name= "Single nucleotide polymorphism"
/note= "Variable nucleotide G,T"
note= "Variable nucleotide A,G"
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/standard
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       AAAIGCAIICICIICIACGGGAICIGGGAACIICCAAAGCIGCCICCICAGAGIGGGAAI 144
                                               ||:::::||::||:|::||:339 AAWYCMWKGKTTTYMAAAWKGRAMYKGRAAARRGSMWTYCCRSMMMWYTWWWAMMMWAW 398
                                                                                               *tag= b
fatandard_name= "Single nucleotide polymorphism"
note= "Variable nucleotide T,C"
103
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standard_name= "Single nucleotide polymorphism"
note= "Variable nucleotide G,A"
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note= "Variable nucleotide C,G"
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note= "Variable nucleotide T,C"
3328
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ktandard_name= "Single nucleotide polymorphism"
note= "Variable nucleotide A,G"
455
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'standard_name= "Single nucleotide polymorphism"
'note= "Variable nucleotide A,G"
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'grandard name= "Single nucleotide polymorphism"
'note= "Variable nucleotide T.C"
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standard name= "Single nucleotide polymorphism"
note= "Variable nucleotide A,G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human periodontal disease related gene PLOD SEQ ID NO:150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      periodontal disease; polymorphism; ds; human; gene; SNP; single nucleotide polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                              ACN37240 standard; DNA; 34796 BP.
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'standard_)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-NOV-2004 (first entry)
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519 TTYYYK 525
                                                                                                                                                                                                                                                     265 ATACCCT 271
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                    ACN37240;
                                                                                                                                                                                                                                                                                                                                               RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                      HERETER TREETE
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18-NOV-2004 (first entry)

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16482 CCAGCGCCGCTATTTATTGGCTGTGTGACCTTGGGCACATTACTCAACCTCTCTGTGCT 16541
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a novel method for examination of periodontal disease in which genetic polymorphisms are detected in one or more of 51 genes. The method is useful for examination, diagnosis and assessment of periodontal disease or risk of periodontal disease and the risk of its progression to severe, aggressive and chronic periodontal disease. The present sequence represents a polymorphic gene of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Single nucleotide polymorphisms associated with periodontal disease for examination and assessment of susceptibility to periodontal disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGGCTTATCAGATAAAACAAGTGAGTCATGCCACAGGATGTCTATAAGCCCATTGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGCAAAGCTGGAAGTTTTTCTCTGTGACCATGGGCTAATTGGTCTCCTTCTGGATT
                           standard_name= "Single nucleotide polymorphism"
note= "Variable nucleotide C,G"
                                                                                    polymorphism
                                                                                                                                           'standard_name= "Single nucleotide polymorphism"
'note= "Variable nucleotide C,T"
                                                                                                                                                                                                   "rd_name= "Single nucleotide polymorphism"
"Variable nucleotide G,T"
                                                                                                                                                                                                                                                            name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 34796 BP; 7631 A; 9152 C; 9368 G; 8645 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 34796;
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                                                                                   "rd_name= "Single nucleotide
"Variable nucleotide C,G"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Muramatsu M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                          note= "Variable nucleotide A,C"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.5%; Score 35.8; D
54.1%; Pred. No. 4.3;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ji G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 9; SEQ ID NO 150; Opp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Numabe Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCAGCACTTTGGGAG 16616
                                                                                                                                                                                                                                                                                                                                                               22-OCT-2003; 2003WO-IB004669
                                                                                                                                                                                                                                                                                                                                                                                          23-OCT-2002; 2002JP-00308634
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CTGGGATTCTATGAG 526
                                                                       ad
                                                                                                                             /*tag= ae
/standard_
               /*tag= ac
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                                                                       /*tag= ad
/standard
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(KAMO/) KAMOI K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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33127
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                                                        3004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-400678/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 73; Conserv
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misc_feature
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                                                        misc_feature
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ACN44200 standard; DNA; 211257 BP.

ACN44200

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57794 CGGTGGTGATGGGCTCCTAGAGACAGCAGGCATGGGAATCAGCTCACTCCCACTT 57853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (1) for screening of bioactive agent capable of binding to Carcinoma Associated Protein (GAP); (iii) for screening of bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma augus; (v) for diagnosing carcinoma; (vi) for inhibiting the activity of CAP; (iv) for carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and including CAP; (viii) for the carcinoma associated (CA) gene copy number. In addition, the CAP genes are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent useful for which no sequence data was published
                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 211257 BP; 55148 A; 47354 C; 46616 G; 57484 T; 0 U; 4655 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180 CAGCGGGGGAGGCATCTTTTCTTGACAGAGCAGAAGTGGGAGGCAGACAGCTGTCACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 11; Length 211257;
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                                                                       Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35.8; DB Pred. No. 13; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        57854 TAGAGGAGAGTGTCTTCTCAGCTTCCT 57880
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510000
523643
BP.
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210000
310000
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 529; Opp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACD97331 0/c
WP Sequence split into 6 fragments LA
WP Fragment Name Begin EN
WP AD097331 0 100001 2:
WP AD097331 2 200001 3:
WP AD097331 2 200001 4:
WP AD097331 5 500001 4:
WP AD097331 5 500001 4:
WP AD097331 5 500001 4:
WP AD097331 5 500001 5:
WP AD097331 5 500001 5:
WP AD097331 5 500001 5:
WP AD097331 5 500001 5:
WP AD097331 5 500001 5:
WP AD097331 5 500001 5:
WP AD097331;
XX XX
                                    Mouse genomic sequence mCG15870.
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milarity 63.2%; 1
Conservative 0;
                                                                                                                                                                                                                     28-FEB-2003; 2003WO-US006235
                                                                                                                                                                                                                                                        01-MAR-2002; 2002US-00087192
                                                                                                                                                                                                                                                                                            (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-328604/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
tes 55; Conserv
                                                                                                                                              WO2003073826-A2
                                                                                                           Mus musculus.
                                                                                                                                                                                 12-SEP-2003
                                                                                                                                                                                                                                                                                                                                 Morris DW;
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201 AATGGCAAAAATGGGCTTTGTTTAACGACAAATGAACTTTAATGCATGTATTTAAGAAAC 142
                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids and polypeptides, useful for preventing diagnosing and treating e.g. leukemia, inflammation and immune disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to human polymucleotides (AAI79941-AAI93841) and the encoded proteins (AA000010-AA013910) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polymetides and polymetides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, peptide therapy. The polypeptides have various cytokine-like activities, c.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           261 CITICCAGGATTCCTTTTTTTTTTTTTTAAAAGCCCCTTTTTCCTAAATTTAGGGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      237 CITICCAGAAGACTITCTITTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID NO 11764; 1399pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 294;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cytostatic; carcinoma; lymphoma; cancer; human; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
5.4%; Score 35.2; DB 4; Length 2
Best Local Similarity 47.7%; Pred. No. 0.39;
Matches 103; Conservative 0; Mismatches 113; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 294 BP; 100 A; 54 C; 63 G; 77 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      417 GIGACCAIGGGCIAAIIGGICICCTICTCIGGAIIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACN44066 standard; DNA; 99886
                                                                                                                                                                                                                                  Drmanac RT;
                                                                                                                         28-FEB-2000; 2000US-00515126.
18-MAY-2000; 2000US-00577409.
                                                                                  26-FEB-2001; 2001WO-US004927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                               WPI; 2001-514838/56.
                                                                                                                                                                                           (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                    Liu C,
                                                                                                                                                                                                                                                                                                      P-PSDB; AAO11773.
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WO200164835-A2
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                                      07-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84222 crichgicacricicariani partratrati de centra cantra en 163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTGTGACCATGGGCTAATTGGTCTCCTTCTGGATTGTGGCTTATCAGATAAAAAAA 473
                                                                                                                                                                                                                                                                                                                                                                                                                                    New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 523643 BP; 156586 A; 96986 C; 101753 G; 168278 T; 0 U; 40 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory, cancer; leukaemia; nervous system disorders; arthritis; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to cancer associated sequences (ADQ97025-ADQ98004). The sequences are useful for the diagnosis, prevention and/or treatment of cancer, such as leukemia and lymphoma. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic formate directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84162 readaracadedededecredecretorededededereraderaceredararaciere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 110000;
                                             dв.
                                           Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35.4; DB 12;
Pred. No. 12;
0; Mismatches 106;
    Human cancer associated sequence HD08-032,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84042 TCTAATCACACACATGAATTCAAT 84018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 308; 199pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         474 GTGAGTCATGCCACAGGATGTCTAT 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human polynucleotide SEQ ID NO 11764.
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AAI91704 standard; cDNA; 294
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                                                                                                                                                                                                                           22-DEC-2003; 2003WO-US041389
                                                                                                                                                                                                                                                                    27-DEC-2002; 2002US-00330773
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                                                                                                                                                                                                                                                                                                                                                         Malandro MS;
                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-543781/52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                      WO2004060304-A2
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                                                                                             Homo sapiens
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AAI91704/ RESULT

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12-SEP-2003.

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The present invention relates to novel DNA and protein sequences which are associated with carcinomas. The sequences are useful for: (i) for screening drug candidates; (ii) for secreening of bioactive agent capable of binding to Carcinoma secret Protein (CAP); (iii) for screening of a bioactive agent capable of modulating the activity of CAP; (iv) for evaluating the effect of a candidate carcinoma drug; (v) for diagnosing carcinoma; (vii) for inhibiting the effect of CAP; (ix) for treating carcinoma; (vii) for neutralizing the effect of CAP; (ix) as a biochip; (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for determining Carcinoma are propensity to carcinoma; and (xi) for determining Carcinoma Associated (CA) gene copy number. In addition, the CAP enses are useful as DNA vaccines and the CAP are useful as markers of carcinoma including lymphoma. The present sequence is one such CA coding sequence. Note: This patent is an equivalent to basic patent capables of the capable of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Recombinant nucleic acid useful for diagnosis and treatment of carcinoma comprises a nucleotide sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 328; Opp; English.
                                                                                                                   28-FEB-2003; 2003WO-US006235.
                                                                                                                                                                                                    01-MAR-2002; 2002US-00087192.
                                                                                                                                                                                                                                                                                 (SAGR-) SAGRES DISCOVERY
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-328604/31.
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Sequence 99886 BP; 25734 A; 17089 C; 18193 G; 27127 T; 0 U; 11743 Other; 0; Gaps Query Match 5.4%; Score 34.8; DB 11; Length 99886; Best Local Similarity 54.8%; Pred. No. 18; Matches 69; Conservative 0; Mismatches 57; Indels 0;

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completed: August 4, 2005, 08:31:29 Search co

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AL521194 BX687092 AQ222496 BG118574 BF389719 AK0471811 BB002636

UI-R-FS1-UI-R-DO1-

Mus muscu BB002636 QV0-BT084 Mus muscu 602459329

UI-R-DO0-BS2900015

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BZ278233 834 bp DNA linear GSS 15-OCT-2002 CH230-343L19.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone CH230-343L19, genomic survey sequence.
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Department of Eukaryotic Genomics
The Institute for Genomic Research
The Institute for Genomic Research
Trel: 301 838 0206
Fax: 301 838 0206
Eax: 301 838 0206
Eax: 101 838 0206
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
clones may be purchased from BACPAC Resources
Clones may be purchased from BACPAC Resources
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html plate: a43 row: L column: 19 Seq primer: TOW: L column: Column: 
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/cell_type="Brain"
/clone_lib="CHORI-230 Segment 2"
/note="Vector: pTARBAC1.3; Site_1: MboI; Site_2: MboI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao, S., Shetty, J., Shatsman, S., Tsegaye, G., Geer, K., Shvartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 Mbol segment Unpublished (1999)
Other_GSSs: CH230-343119.TJ
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/clone="CH230-343L19"
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AV315743 AV315743

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CK453423 00115 MA

CK453429 UI-R-DZI-

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CR314130 Medicago
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                                                                                                                                                                                                                                                                                                                                                                      ggcttgtgccgagatgttcc.....aattgaatgcggtccaccaa 650
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                           GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34239544 segs, 19032134700 residues
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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650
1 ggcttgtgccqaqat
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gb_htc::*;
gb_est4::*;
gb_est4::*;
gb_est6::*;
gb_gs81::*;
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Match Length
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Chen, D.,

us-09-899-276c-7.rst

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GSS 02-NOV-2001
                                                                                                                             AGU53846 673 bp DNA linear GSS 02-NOV-200:
Pan troglodytes DNA, clone: PTB-038B14.R, genomic survey sequence.
AG053846
                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                   Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 673;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Indels
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Pred. No. 0.66;
0; Mismatches
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-038B14.R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
                                                                                                                                                                                                                                           Pan troglodytes (chimpanzee)
Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CE213266.1 GI:35368935
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                                                                                                                                                                                                           AG053846.1 GI:16591289
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Best Local Similarity 90.0%;
Matches 45; Conservative
                  547 CAGGAGAGACTT 558
                                                    322 ACAGTGTGÁTŤŤ 311
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AG053846/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                CG856718 845 bp DNA linear GSS 19-NOV-2003
ZMMBBC0260N04f ZMMBBC (ECORI) Zea mays genomic clone ZMMBBC0260N04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae; PACCAD calde; Panicoideae, Andropogoneae; Zea.

(Dases 1 to 845)

Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C., Schovetz, V., Fuks, G., Yu, Y., Wing, R. and Messing, J.

Sequencing of the maize genome at PGIR (2003c)
                                                                                                                                                                                                                                 517 ATTCTATGAGGGATGATGATGAGTAAGCCAGGAGAGACTTATTTAAAGATCTCAGCAT 576
                                                                                                                                                                                            523 TCATTATAGAATATTCTTCATTCATGCCAGAATAATTACATAAGGTGTATTAATTGTGGA 464
                                                                                                                                                                                                                                                           /drarate="taxon:4577"
/clone="ZMMBBC0260N04"
/lab hosts="R. coll DH10B"
/clone lib="ZMMBBC (ECORI)"
/note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     427 GCTAATTGGTCTCCTTCTCTGGATTGTGGCTTATCAGATAAAAAAAGTGAGTCATGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                        457 TTATCAGATAAAACAAGTGAGTCATGCCACAGGATGTCTATAAGCCCATTGATTCTGGG
CHORI-230 Rat (BN/SBNHsd/MCW) BAC library produced by Pieter de Jong"
                                                                                                                     0; Gaps
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Pred. No. 0.54;
0; Mismatches 56; Indels
                                                                               Query Match 6.6%; Score 42.8; DB 8; Length 834; Best Local Similarity 54.4%; Pred. No. 0.41; Matches 86; Conservative 0; Mismatches 72; Indels
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190 Frelinghuygen Road, Piscataway, NJ 08854, USA
                                                                                                                                                                                                                                                                                                                577 CTTTCAGCTTGTTAACCTAGAGAAACCCGAAGCATGA 614
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High quality sequence start: 445.
Location/Qualifiers
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/cultivar="B73"
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CG856718
CG856718.1 GI:38429431
GSS.
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Best Local Similarity 57.6%;
Matches 76; Conservative
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Fax: 732 445
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SOURCE
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CG856718/c
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JOURNAL
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LL11266
tigr-gas-dog-17000372782879 Dog Library Canis familiaris genomic,
genomic survey sequence.
2 (bases I to 673)
2 (bases I to 673)
3 (bases I to 673)
4 (bases I to 673)
5 (bases I to 673)
7 (cotoki, Y., Watanabe, H. and Sakaki, Y.
7 (cotoki, Y., Watanabe, H. and Sakaki, Y.
7 (cotoki, Y., Watanabe, H. and Sakaki, Y.
8 (cotoki, Y., Watanabe, H. and Sakaki, Y.
8 (cotoki, Y., Watanabe, H. and Saka, Y. A. (cotoki, Y. Cotoki, Sciences Center (GSC);
8 (cotoki, Tellin, Cariston, Tourumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbesagac.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tell:81-45-503-9111, Fax:81-45-503-9170)
7 (clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
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Canis familiaris
Bukaryota: Metazos, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 764)
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/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGCTTGTGCCGAGATGTTCCCAGGCACAGCCCCATGTGAGAGCTCCCTGGC
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Query Match
Best Local Similarity 50.5
Matches 95; Conservative
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AV215743
LOCUS
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                                                                                                                                                                                                                                                                     The Institute for Genomic Research
Department of Bukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .764
/organism="Canis familiaris"
/organism="Canis familiaris"
/mol type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone lib="hog Library"
/note="Site l: BstXI; Libraries were prepared from peripheral blood"
                                                                                                      The dog genome: survey sequencing and comparative analysis
Science 301 (5641), 1898-1903 (2003)
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Loftus, B., Shetty, J., Knudson, D. and Severson, D. BAC end sequencing of Aedes aegypti
Unpublished (2003)
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Library was provided by David Severson
Seq primer: 17
Class: BAC ends.
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Tel: 301-838-3543
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/mol_type="genomic DNA"
/strain="Liverpool"
/db_xref="taxon:7159"
/clone="NDL.94D3"
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Department of Eukaryotic Genomics
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                                                                                                                                                                                                                                                                                                                                                                Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                     Contact: Kirkness EF
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AUTHORS
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Mammalia; Butheria; Rodentia; Sciurognath; Muridae; Mutinae; Musmalia; Butheria; Rodentia; Sciurognath; Muridae; Mutinae; Mus. 1 (bases 1 to 306)

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuon, Y., Makamura, M., Oda, H., Okazaki, Y., Shibata, Y., Shibata, K., Shibata, Y., Shibata, K., Shibata, Y., Shibata, K., Shibata, Y., Suzuki, H., Takahabi, F., Tateno, M., Tominaga, N., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTS (Konno, H., et al. 1999)

L. Contact: Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse Este (Sonio, H., et al. 1999)

L. Contact: Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Phe Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9216

Fax: 81-45-503-9216
/clone_lib="Notre Dame Liverpool"
/note="Vector: pECBAC1; Site_1: Hind III; The library was
prepared from whole body tissue of newly hatched L1 larvae
by David Severson at the University of Notre Dame and
Hongbin Zhang"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 TITITATICIATGGAGGCTACATACAACAAAAATAATTIGGGICCAGGCATICAATAAA 204
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sasaki,v., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
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                                                                                                                                                                                                                                                                                                Score 39.2; DB 8; Length 454; Pred. No. 3.9; O; Mismatches 93; Indels
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Mus musculus
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AV215743.1 GI:6156588
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FEATURES

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Enkaryota, Alveolata; Apicomplexa; Coccidia; Eimeriida;

Barcocystidae; Toxoplasma.

Sarcocystidae; Toxoplasma.

E I (bases 1 to 569)

S Tang, K., Cole, R., Fogarty, S., Sibley, L.D., Ajioka, J.A., White, M.,

Clifton, S., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M.,

Clifton, S., Raguire, J., Martin, S., Wylie, T., Dante, M., Marra, M.,

Ritter, E., Maguire, L., Waterston, R. and Wilson, R., Ronko, I.,

Kennedy, S., Maguire, L., Waterston, R. and Wilson, R., Ronko, I.,

Connedy, S., Coloret: Clifton, S.

Connect: Clifton, S.

Concact: Clifton, S.

Concact: Clifton, S.

Toxoplasma EST Project

Washington University School of Medicine
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TGSTzy123e02.yl TgMAS Tachyzoite CDNA Library Toxoplasma gondii CDNA clone TGSSTzy123e02.yl 5', mRNA sequence.
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Contact David Sibley (toxoest@borcim.wustl.edu) for further
information relating to organism, libraries, or clone availability.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        509 AGCAGAAGGGGGGGGGGGGGGGACAACAACTTTCTCACAACATTGCCTTTGTGTTTCAGCAC 450
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Tel: 314 286 1800
Fax: 314 286 1810
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55.2%; Pred. No. 7.1;
tive 0; Mismatches 60; Indels (
found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: NDAM1163 row: a column: 22 High quality sequence start: 3 High quality sequence stop: 361.
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Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                  High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rml0A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mary Hendrix
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6.0%; Score 38.8; DB 1; Length 306; 31.1%; Pred. No. 4.5; ve 0; Mismatches 87; Indels 0
                                                                                                                                                                                                      organism="Mus musculus"
                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="2410152G06"
/cell_type="ES_cells"
/lab_host="SOLR"
                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                            /mol_type="mRNA"
/strain="C57BL/6J"
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CO247511.1 GI:49113790
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Conservative
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Best Local Similarity
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CO247511/c
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// Ab xref="taxon:966"
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// Ab made by oligo-dr priming. Directionally cloned into EcoRI; cDNA made by oligo-dr priming. Directionally cloned into EcoRI/Abot sites using the following 5' adaptor:
// Abb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley)
using ZAP-CDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
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                                                                                                                                                                                                                                                                   444 TCTGGATTGTGGCTTATCAGATAAAACAAGTGAGTCATGCCACAGGATGTCTATAAGCC 503
                                                                                                                                                                                                                                                                                                                              200 rericcargrataraaargcaaaargcarreccaaccaaagcaraagargraccaargca 259
                                                                                                                                                                                                                                                                                                                                                                                             504 CATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGCCAGGAGAGACTTATTTA 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                        260 cacadadregesecregradeargardacaagadearcccaascaseseseserer 319
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.W.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.b column: 12.
Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
NIH-MGC http://mgc.nci.nih.gov/.
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-romail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                        Gaps
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"
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                                                                                                                                      Length 636;
                                                                                                                                                                                                     99; Indels
                                                                                                                                      Query Match 5.8%; Score 37.6; DB 9;
Best Local Similarity 49.5%; Pred. No. 13;
Matches 97; Conservative 0; Mismatches 99;
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Pred. No. 18;
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BF128374.1 GI:10967414
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The Institute for Genomic Research
Department of Enkaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246 AGACTITCTITICTGAITCAFACCCTTCACCTTCCCTGTGTTACTGTCTGAIATATGCA 305
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.

1 (bases 1 to 636)

Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Science 301 (5641), 1898-1903 (2003)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.8%; Score 37.8; DB 6; Length 569; 60.0%; Pred. No. 11; ive 0; Mismatches 42; Indels
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/organism="Toxoplasma gondii"
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/strain="Standard Poodle"
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/clone_lib="Dog Library"
                -40RP from Gibco
                                              Location/Qualifiers
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Matches 63; Conservative
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                   Sed primer:
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                                              FEATURES
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Location/Qualifiers
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Mus musculus
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Local Similarity 54.8%;
Les 74; Conservative 0
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Piao, Y., Ko, N.T., Lim, M.K. and Ko, M.S.H.
Construction of long-transcript enriched cDNA libraries from submicrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                        CF895308 637 bp mRNA linear EST 04-NOV-2003 A0146D02-5 NIA Mouse Undifferentiated ES Cell cDNA Library (Long 1) Mus musculus CDNA clone NIA:A0146D02 IMAGE:30728005 5', mRNA
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                                                    188 GAGGGCATCTTTCTTGACAGAGGAGGAGGCAGAGACAGCTGTCACTTTCCAGAAG 247
     Gaps
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National Institutes of Health
National Institute on Aging/National Institutes of Health
National Institute on Aging/National Institutes of Health
Bmail: cana@lgsun.grc.nia.nih.gov
Plater A0146 row: D column: 02
Seq primer: M13 Reverse
High quality sequence stop: 637
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     39; Indels
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/note="Vector: pcMv-SPORT6 (Invitrogen); Site 1: SalI; Site 2: Not1; Mouse cDNA project by the Laboratory of GeneTics, National Institute on Aging (NIA), Intramural Research Program, NIH (http://lgam.grc.nia.nih.gov/cDNA). This is a long-transcript enriched cDNA library (Ref. Genome Res. 11: 1553-1558 (2001). [PMID: 11544199]). Total RNAS were obtained from Dr. Kenneth R. Boheler (National
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukamalia; Eutheria, Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 640) Piao, Y. Ko, N.T.; Lim, M.K. and Ko, M.S.H. Construction of long-transcript enriched cDNA libraries from submigrogram amounts of total RNAs by a universal PCR amplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CF895446 64-NOV-2003 A0147H12-5 NIA Mouse Undifferentiated ES Cell CDNA Library (Long 1) Mus musculus cDNA clone NIA:A0147H12 IMAGE:30728159 5', mRNA
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and cloned into Sall/NotI site of pCMV-SPORT6 plasmid vector. The DH10B E. coli host was transformed with the ligation mixture by the standard chemical method. The average insert size is about 2.4 kb. The library was constructed by Yulan Piao."
                                                                                                                                                                                                                                                                                                                                                                  225 AGACAGCTGTCACTTTCCAGAAGACTTTTTTTTTCATACCCTTCACCTTCCCTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // Organism="Mus musculus"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/mol type="mRNA"
/db xref="niaEST:A0147H12-5"
/db xref="maxon:10090"
/clone="NRA:A0147H12 IMAGE:30728159"
/dev grage="R1 ES cells"
/dev grage="R1 ES cells"
/dev grage="R1 ES cells"
/clone llb="NA Mouse Undifferentiated ES Cell CDNA Library" (Long 1)
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Laboratory of Genetics
Mational Institutes of Health
National Institute on Aging/National Institutes of Health
National Institute, Suite 4000, Baltimore, MD 21224-6820, U
Email: cdna@lgsun.grc.nia.nih.gov
Blate: Al3 Reverse
High quality sequence stop: 640
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0
                                                                                                                                                                                                                        Score 37.4; DB 7; Length 637;
Pred. No. 15;
0; Mismatches 61; Indels (
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clone_lib="CSEQCHN23"
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Mus musculus (house mouse)

Mus musculus

Bukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Musmanalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

E 1 (bases 1 to 644)

S Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S.,

Akinret, B., Levins, M., Mcgann, S., Tsegaye, G., Geer, K., Krol, M., de
Jong, P. and Fraser, C.M.

Mouse BAC End Sequences from Library RPCI-23

Other GSSs: RPCI-23-93C11.TV

Contact: Shaying Zhao

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AZ248574 15-JUN-2000 644 bp DNA linear GSS 15-JUN-2000 RPCI-23-93C11, TJ RPCI-23 Mus musculus genomic clone RPCI-23-93C11,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       225 AGACAGCTGTCACTTTCCAGAAGACTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGT 284
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Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library RPCI-23. For BAC
Clones are derived from the mouse BAC library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac ends/mouse/bac_end_intro.html
Plate: 93 rows. C column: 11
Seg primer: SP6
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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/dlonellb="RPGI-23"
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1:
FcoRI; Site_2: BcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACe3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BU224166 655 bp mRNA linear EST 26-NOV-2002
603799875F1 CSEQCHN23 Gallus gallus cDNA clone ChEST769£20 5', mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             225 AGACAGCTGTCACTTTCCAGAAGACTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGT 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       426 AGAGAATTGTAAATTGAAGGAATAATTCTGCTTTTTCTCTTTCTCTTCTTCGTTCCATAC 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                486 AGTICTIGITIGCIACATGCACACCACAATCATICTACCAAGATGTCTCCTTTATCAAT 545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
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Gallus gallus
Gallus gallus
Gallus gallus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.

1 (bases 1 to 655)
Boardman, P.B., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, I. Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J. A Comprehensive Collection of Chicken cDNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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University of Manchester Institute of Science and Technology
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/strain="White Leghorn, Hisex"
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'organism="Mus musculus"
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Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers
                            /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                      /db_xref="taxon:10090"
/clone="RPCI-23-93C11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO Box 88, Manchester, M60 1QD,
Tel: 01612008930
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                                                                                                                                               /sex="Female"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 AAGTAGAGACATGCT 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      546 AGTTACAGTCCTGGT 560
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ECORI; Site_2: Not1: This normalized library was constructed from 1 million independent clones. CDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with ECORI, size-selected, and cloned into the NotI and ECORI compatible sites of a custom medified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soarse et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            End-sequence profiling: Sequence-based analysis of aberrant genomes
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
22709111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PECUBEU4 THE HUMAN MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_1-7111, genomic survey sequence.
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'note="Organ: heads; Vector: pBluescript II KS(+); Site_1:
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Volik,S., Zhao,S., Chin,K., Brebner,J.H., Herndon,D.R., Tao,Q., Kowbel,D., Huang,G., Lapuk,A., Kuo,W.-L., Magrane,G., de Jong,P., Gray,J.W. and Collins,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Contact: Volik SV
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 S02 766
Fax: 415 S02 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.
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'note="Vector: pECBAC1; Site_1: HindIII; This library was
constructed from MCF7 breast cancer cell line by Amplicon
Express (http://www.genomex.com) using their standard
procedure."
                                                                                                                                                                                                                              634
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                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Human MCF7 breast cancer cell line library (WCF7 ])"
                                                                                                                                                                                                                                                                                                                         492 IGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGCCAGGA
                                                                                                                                                                                                                            432 TIGGICICCTICTCIGGALTGIGGCTIATCAGALAAAACAAGIGAGICAIGCACAGGA
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                                                                                                                                    Length 725;
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Sequence 273, App
Sequence 1, Appli
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Sequence 154, App
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Sequence 15851, A
Sequence 15852, A
Sequence 12387, A
Sequence 12724, A
Sequence 12724, A
Sequence 17724, A
Sequence 17490, A
Sequence 16539, A
Sequence 106, App
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Sequence 834, App
Sequence 2294, Ap
Sequence 17434, A
Sequence 13915, A
Sequence 14, Appl
Sequence 160628,
Sequence 10265, A
Sequence 2476, Ap
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1788, Ap
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-09-107-433-1788
US-09-949-016-16240
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Sequence 94, Application US/09220132
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; GENERAL INFORMATION:
; APPLICANT: Shyjan, Andrew W.
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; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANC:
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; TITLE OF INVENTION: OF PROSTATE CANCER THERAPIES AND THE DIAGNOSIS OF PROSTATE CANC:
; CURRENT FILING DATE: 1999-12-23
; PRIOR FILING DATE: 1996-13-25
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 191
; SEQ ID NOS: 191
; SEQ ID NO 94
; FEATHARE: FEATERED for Windows Version 4.0
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Sequence 2813, Ap
Sequence 2813, Ap
Sequence 663, App
Sequence 15238, A
Sequence 15238, A
Sequence 17504, A
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Sequence 13909, A
Sequence 13118, A
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Sequence 13118, A
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Sequence 13118, A
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Sequence 11809, A
Sequence 154033,
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19.4%; Pred. No. 0.085;
live 90; Mismatches 109;
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; OTHER INFORMATION: n = A,T,C or
US-09-220-132-94
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nes 48; Conservative
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1200
143644
187848
16404
276237
44789
10786
  298336
385136
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ORGANISM: Homo sapiens
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NAME/KEY: misc_feature
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; LOCATION: (1) ... (205044)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15852
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US-09-949-016-12387/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 205044
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Sequence 15852, Application US/09949016

Sequence 15852, Application US/09949016

Sequence 15852, Application US/09949016

Sequence 15852, Application US/09949016

GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERRACE: CL001307

CURRENT FILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-04-16

PRIOR PLILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SEQ ID NO 15852

LENGTH: 205044
                                                                                        US-US-1949-ULC-15851, Application US/09949016

; Sequence 15851, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; FILE REFERENCE: CLOAD1307;
; CURRENT APPLICATION NUMBER: 60/241,755
; CURRENT FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 15851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32749 TATCTGCTGGCGCTGAAATTCTCTCAGGACAGCTCAGCCCTGCTTTCCAGAAGATGAGAG 32690
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S.6%; Score 36.2; DB 4; Length 205044;
Best Local Similarity 53.1%; Pred. No. 2.6;
Matches 77; Conservative 0; Mismatches 68; Indels 0;
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US-09-949-016-15851
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ORGANISM: Human
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ORGANISM: Human
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US-09-949-016-15853/C

| Sequence 15853, Application US/09949016
| Sequence 15853, Application US/09949016
| Sequence 15853, Application US/09949016
| GENERAL INFORMATION:
| APPLICANT: VENTER, J. Craig et al.
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
| PRIOR APPLICATION NUMBER: 60/241,755 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PELING DATE: 2000-10-03 |
| PRIOR PILING DATE: 2000-00-09-08 |
| PRIOR PILING DATE: 2000-00-09-08 |
| WIMBER OF SEQ ID NOS: 207012 |
| SOFTHARE: RESELECT FOR WINDOWS VERSION 4.0
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                                                                                                               99 CTACGGGATCTGGGAACTTCCAAAGCTGCCTCCTCAGAGTGGGAATTTCCACTTCT
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                                                             68;
Query Match
5.6%; Score 36.2; DB 4;
Best Local Similarity 53.1%; Pred. No. 2.6;
Matches 77; Conservative 0; Mismatches 68;
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5.6%; Score 36.2; DE
Best Local Similarity 53.1%; Pred. No. 2.6;
Matches 77; Conservative 0; Mismatches
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; LOCATION: (1)...(205044)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15853
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Sequence 12725, Application US/09949016

Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLOOL307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT RILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-00-08
PRIOR FILING DATE: 2000-00-08
NUMBER OF SEQ ID NOS: 207012
SOFFWARE: PRESEEQ for Windows Version 4.0
                                                                                                                                                                                                   3176 TATCTGCTGGCGCTGAAATTCTCTCAGGACAGCTCAGCCCTGCTTTCCAGAAGATGAGAG 3117
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                                                                                  3236 ccandedeccededadegreecaacanadenecareadadededeacreececececereca 3177
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Batent No. 6639063

GENERAL INFORMATION:

APPLICANT: Johns Milne Edwards, J.B.

APPLICANT: Johert, S.

APPLICANT: Johert, S.

TILLE OF INVENTION: ESTS and Encoded Human Proteins.

FILE REFERENCE: GENSET.054PR2

CURRENT APPLICATION NUMBER: US/09/621,976

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm
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; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12725
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US-09-949-016-12725/c
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US-09-621-976-15639
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 223471
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1S-Gquence 12724, Application US/09949016

1S-Gquence 12724, Application US/09949016

1S-Gquence 12724, Application US/09949016

1S-Gquence 12724, Application US/0949016

1S-GGREAL INFORMATION: WITH HOWN GENES ASSOCIATED

1TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

1S-GGREAT TOWN NUMBER: 06/241,755

1PRIOR FILING DATE: 2000-04-03

1PRIOR PELICATION NUMBER: 60/231,768

1PRIOR PELING DATE: 2000-10-03

1PRIOR APPLICATION NUMBER: 60/231,498

1PRIOR PILING DATE: 2000-09-08

1PRIOR PILING DATE: 2000-09-08

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2PRIOR PILING DATE: 2000-09-08

2PRIOR PILIN
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
CURRENT APPLICATION WUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR PPLICATION NUMBER: 60/241,755
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR PPLICATION NUMBER: 60/237,768
PRIOR PLING DATE: 2000-10-03
PRIOR PLING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR PILNG DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: PSECSE OF WINDOWS VERSION 4.0
SEQ ID NO 12387
LENGTH: 223471
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5.6%; Score 36.2; DE
Best Local Similarity 53.1%; Pred. No. 2.8;
Matches 77; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ) NAME/KEY: misc_feature

) LOCATION: (1)...(224471)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12387
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| LOCATION: (1)...(223471)
| OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: FOLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/231,768
PRIOR PILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASESEQ FOR WINDOWS VERSION 4.0
SEQ ID NO 17490
                                                                                                                                                                                                                                                                                                                                                                     204 GACAGAGCAGAAGTGGG-----AGGCAGACAGCTGTCACTTTCCAGAAGACTTTCTTTC 258
                                                                                                                                                                                                                                                                                                                                                                                                                                        TGATICATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATATGCAAAGGCCAAGTCAC 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITCCAGAGATGACAACTCCTTCCTGAAGTAGAGACATGCTTCCAACACTCAGAAGCCTA 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                302 YAMMSMWCARMMCAMAGMRSAWWKCSRAKYMYMAKSCMYCAKWSCSARSAKCGRSCCTT 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TGTGAACACTCAGCCAGCAAAGCTGTTTTTCTCTGTGACCATGGGCTAATTGGTCT 438
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 CAAATGCATTCTTCTACGGGATCTGGGAACTTCCAAAGCTGCCTCCTCAGAGTGGGAA 143
                                                                                                                                                                                                                                                                                                  122 KMYYYRMKCYSCASYSYSYRRCKKYTGWTRGWYGCKKRWCKSSTRYMTRYTRYWKWTGAC 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                            242 CTYKKSYYTCRKSYYTYRISTSKKGMGTKKSRWSYTWSNKSYTWGCSKKWRRMYWSAGAW 301
                                                                                                                                                                                               61
                                                                                                                                                                                                                                                     182 YGSKGMSCKGSRSKYYGSMKMYYGKYTMCTSKYKSSKMSYKKSSMCYTYMMCYYTYWWCT
                                                                                                                                                              24 CACAGCCCCATGTGAGAGCTCCCTGGTCCGGGCCCCAGTATCTGGAATGCAGGCTCCAGC
                                                                                                                                                                                    Gaps
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                                                                                                                                .,
                                                                                            Query Match 5.5%; Score 35.6; DB 4; Length 505; Best Local Similarity 14.3%; Pred. No. 0.096; Matches 65; Conservative 181; Mismatches 205; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                439 CCTTCTCTGGATTGTGGCTTATCAGATAAAACAAG 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    422 KOMYNWITCTCWIWIWYGITRAITGAGRRGIARRAG 457
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.2%; Score 33.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 17490, Application US/09949016
Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17490
                                TYPE: DNA
CORGANISM: Homo sapiens
US-09-621-976-15639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Human
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SEQ ID NO 15639
LENGTH: 505
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APPLICANT: Purness, Michael
APPLICANT: Purness, Michael
APPLICANT: Purness, Michael
APPLICANT: Buchbinder, Jenny
TILE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
CURRENT APPLICATION NUMBER: 10/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR PILING DATE: 2000-10-12
                                                                                                                                                                                                                                                                                                                                         17605 ATTAGGTCAAGATGTGTAAGACCTGTATACTGAGAACTATGATATATTGCTCAGAGAAAT 17664
                                                                                                                       17485 İCİCİTİRAİGİRĞITİRİRĞİCİTGİRAĞCİĞTCAACTIĞİRARIĞATĞÜĞGTIĞĞARAİT 17544
                                                                                                                                                                                                                                17545 GAAAIGTAAATAACATTACATTTATAATAGCATCAAAAATATGAAATATTAGGAATAA 17604
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       256 ITCTGALTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATATGCAAAGGCCAAGT 315
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APPLICANT: Wright, David A.
APPLICANT: Woytas, Daniel F.
TITLE OF INVENTION: PLANT RETROELEMENTS AND METHODS RELATED THERETO
FILE REPERENCE: P-1065A
CURRENT APPLICATION NUMBER: US/09/586,106D
CURRENT FILING DATE: 2003-02-07
FRIOR PELLON NUMBER: 60/087,125
FRIOR PELLON NUMBER: 09/322,478
FRIOR PILING DATE: 1998-05-28
FRIOR PILING DATE: 1999-05-28
NUMBER OF SEQ ID NOS: 1100
SOFTWARE: FastSEQ for Windows Version 4.0
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                         436 TCTCCTTCTTGGGATTGTGGCTTATCAGATAAAAACAAGTGAGTCATGCCACAGGATGTC
                                                                                                                                                                               TATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGCCAGGAGAGA
                                                                                                                                                                                                                                                                                        556 CITATITAAAGAICTCAGCATCTTTCAGCTTGTTAACCTAGAGAAAACCCGAAGCATGAC
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Pred. No. 14;
0; Mismatches
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; Patent No. 6720479
; GENERAL INFORMATION:
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Patent No. 6673549
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Best Local Similarity 52.9%;
Matches 72; Conservative (
     Local Similarity 48.7%;
les 92; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Solanum tuberosum
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TION: (657081)..(657081)
INFORMATION: n equals a, t,
                                                                                                                                                                                               MANEATION: (148948).
COCATION: (148948).
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (163385). (163385).
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (191989). (191989).
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (191995). (191995).
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (231980). (231980).
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (231980). (231980).
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OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (234814)...(234814)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (30939)...(30939)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (309418)...(309418)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (312837)...(312837)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
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LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t,
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LOCATION: (600992). (600992)
OTHER INFORMATION: n equals a,
NAMEKEY: misc_feature
LOCATION: (622708). (622708)
    LOCATION: (98266)..(98266)
OTHER INFORMATION: n equals a,
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LOCATION: (234187) ..(234187)
OTHER INFORMATION: n equals a,
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LOCATION: (312993)..(312993)
THER INFORMATION: n equals a,
                                                                       LOCATION: (98343)..(98343)
OTHER INFORMATION: n equals a,
                                                                                                                NAME/KEY: misc feature
LOCATION: (103998) .. (103998)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
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LOCATION: (319226)..(319226)
OTHER INFORMATION: n equals a,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a,
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LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
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LOCATION: (713652)..(713652)
                                                NAME/KEY: misc feature COCATION: (98343)..(98
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APPLICANT: Bult et al.
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ TITLE OF INVENTION: jannaschij
TITLE OF INVENTION: jannaschij
TITLE OF INVENTION: jannaschij
TURERENT APPLICATION NUMBER: US/08/916,421B
CURRENT APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 3
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                       1275 TCCTCTTCCTTTTTTTTTTCCCCTTCCCTGATAGCGAAGGAGTGTTTTCTTTACCC 1334
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CTHER INFORMATION: Incyte ID No. 6673549 404601.11

NAME/KEX: unsure

LOCATION: 1731, 1736, 1739, 1742-1743, 1747, 1749, 1751-1752, 1754, 1756

US-09-976-594-273
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                                                                                                                                                                                                                                                                                                             Query Match
5.1%; Score 33.4; DB 4; Length 1759;
Best Local Similarity 55.7%; Pred. No. 1.2;
Matches 64; Conservative 0; Mismatches 51; Indels 0
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NAME/KEY: misc_feature
LOCATION: (28222)
CTHER INFORMATION: n equals a, t, c, or
NAME/KEY: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a, t, c, or
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LOCATION: (98239). (98239)
OTHER INFORMATION: n equals a, t, c,
NAME/KEY: misc_feature
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
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LOCATION: (84773)...(84773)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (84808)...(84808)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (84812)...(84812)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (88120)...(98120)
OTHER INPORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (98120)...(98120)
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL Program
SEQ ID NO 273
LENGTH: 1759
                                                                                         TYPE: DNA
ORGANISM: Homo sapiens
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LENGTH: 1664976
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RESULT 13
US-09-692-570-1/c
i Sequence 1, Application US/09692570
j Patent No. 6797466
j GENERAL INFORMATION:
j Patent No. 6797466
j GENERAL INFORMATION:
j TITLE OF INVENTION: dannaschii
j TITLE OF INVENTION: jannaschii
j TITLE OF INVENTION: jannaschii
j TITLE OF INVENTION: 2003-01-14
j FILE REPRENCE: PB275C1
cURRENT APPLICATION NUMBER: US/09/692,570
j CURRENT PILING DATE: 1996-08-22
j PRIOR FILING DATE: 1996-08-22
j PRIOR FILING DATE: 1996-08-22
j PRIOR FILING DATE: 1997-08-22
j PRIOR FILING DATE: 1997-08-22
j PRIOR FILING DATE: 1997-08-22
j RIGHENT APPLICATION NUMBER: US 08/916,421
j SEQ ID NOS: 20
j SOFTWARE: PatentIn version 3.1
j SEQ ID NO 1
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NAME/KEY: misc_feature
LOCATION: (148948)..(148948)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98120)..(98120)
OTHER INFORMATION: n equals a, t,
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LOCATION: (98159)..(98159)
OTHER INFORMATION: n equals a, t,
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LOCATION: (103998)..(103998)
OTHER INFORMATION: n equals a,
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LOCATION: (28222)...(28222)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc_feature
LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a,
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NAME/KEX: misc_feature
LOCATION: (84773)..(84773)
OTHER INFORMATION: n equals a,
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LOCATION: (84812)..(84812)
OTHER INFORMATION: n equals a,
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LOCATION: (84808)..(84808)
OTHER INFORMATION: n equals a,
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LOCATION: (163385)..(163385)
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LOCATION: (98343)..(98343)
JTHER INFORMATION: n equals
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LOCATION: (98239)..(98239)
OTHER INFORMATION: n equals
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OTHER INFORMATION: n equals
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LOCATION: (98266)..(982
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; OTHER INFORMATION: n equals a, t, c, or g
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LOCATION: (871619)..(871619)
OTHER INFORMATION: n equals a, t, C,
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a, t,
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OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
LOCATION: (1313224)...(1313224)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1349491)..(1349491)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1470091)..(1470091)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1084830)...(1084830)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc_feature
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LOCATION: (1130881). (1130881)
OTHER INFORMATION: n equals a, t,
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INFORMATION: n equals a, t,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a, t,
NAME/KEX: misc_feature
LOCATION: (779676)..(779676)
OTHER INFORMATION: n equals a, t,
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LOCATION: (1602912)..(1602912)
OTHER INFORMATION: n equals a,
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LOCATION: (1637998)..(1637998)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (1349473)..(1349473)
OTHER INFORMATION: n equals a,
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                                    NAME/KEY: misc_feature_
LOCATION: (741684)..(741684)
OTHER INFORMATION: n equals a,
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LOCATION: (1569020)..(1569020)
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LOCATION: (674435)..(674435)
OTHER INFORMATION: n equals a, t, c, or g
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NAME/KEY: misc_feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t, c,
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LOCATION: (312993)..(312993)
JTHER INFORMATION: n equals a, t, c,
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LOCATION: (234814)..(234814)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCHTION: (191995). (191995)
OTHER INFORMATION: n equals a, t,
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LOCATION: (234187)..(234187)
OTHER INFORMATION: n equals a, t,
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LOCATION: (309418)..(309418)
OTHER INFORMATION: n equals a, t,
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LOCATION: (559241)..(559241)
OTHER INFORMATION: n equals a, t,
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LOCATION: (657203)..(657203)
OTHER INFORMATION: n equals a, t,
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OCATION: (312837)..(312837)
OTHER INFORMATION: n equals a, t,
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LOCATION: (191989)..(191989)
OTHER INFORMATION: n equals a,
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LOCATION: (234220)..(234220)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
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OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (600592)..(600992)
OTHER INFORMATION: n equals a,
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LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
OTHER INFORMATION: n equals a,
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LOCATION: (309398) ..(309398)
OTHER INFORMATION: n equals a,
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LOCATION: (559167)..(559167)
OTHER INFORMATION: n equals a,
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LOCATION: (622708)..(622708)
OTHER INFORMATION: n equals a,
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57.0%; Pred. No. 91;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: misc_feature
LOCATION: (1349473).(1349473)
OTHER INFORMATION: n equals a, t, c, or g
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US-09-640-211A-154
; Sequence 154, Application US/09640211A
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NAME/KEY: misc_feature
LOCATION: (1313224).
OTHER INFORMATION: n equals a, t,
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LOCATION: (1310988)..(1310988)
OTHER INFORMATION: n equals a, t,
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NAME/KEY: misc_feature
LOCATION: (1096846)..(1096846)
OTHER INFORMATION: n equals a,
NAME/KEY: misc feature
LOCATION: (682442)..(682442)
OTHER INFORMATION: n equals a,
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LOCATION: (855539)..(855539)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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LOCATION: (779455)..(779455)
OTHER INFORMATION: n equals a,
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LOCATION: (1130881)..(1130881)
OTHER INFORMATION: n equals a,
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LOCATION: (871519)..(871619)
OTHER INFORMATION: n equals a,
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LOCATION: (1119881)..(1119881)
OTHER INFORMATION: n equals a,
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NAME/KEY: misc_feature
LOCATION: (741684)...(741684)
OTHER INFORMATION: n equals
                                                                      NAME/KEY: misc feature
LOCATION: (713552)..(713652)
OTHER INFORMATION: n equals
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LOCATION: (779576)..(779676)
OTHER INFORMATION: n equals
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Best Local Similarity 57.0°
Matches 61; Conservative
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Sequence 16944, Application US/09949016

Sequence 16944, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT'S USWIER,

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT APPLICATION NUMBER: 06/241,755

PRIOR PELLING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOTUMBE: PRIOR SEQ ID NOS: 207012
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Pred. No. 21;
0; Mismatches 108; Indels 0;
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0
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Best Local Similarity 55.1%; Pred. No. 1.1;
Matches 65; Conservative 0; Mismatches 53; Indels 0
                        GENERAL INFORMATION:
APPLICANT: Wood, Marion
APPLICANT: Shenk, Michael A.
APPLICANT: Scath, Annette
APPLICANT: Glenn, Matthew
ITITLE OF INVENTION: Compositions and Methods for the
ITITLE OF INVENTION: Modification of Gene Transcription
FILE REFERENCE: 11000.1021C1U
FILE REPERENCE: 11000.1021C1U
CURRENT APPLICATION NUMBER: US/09/640,211A
CURRENT APPLICATION NUMBER: 2000-08-16
NUMBER OF SEQ ID NOS: 2368
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 154
LENGTH: 1144
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Best Local Similarity 47.6%;
Matches 98; Conservative (
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CRGANISM: Eucalyptus grandis
US-09-640-211A-154
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; ORGANISM: Human
US-09-949-016-16944
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US-09-949-016-16944
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LENGTH: 121384
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QY 614 ACTGGATTATAAAGGGAAATTGAATG 639
Db 114410 CCAACATTAGAAACTGAATTTCAATG 114435
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Search completed: August 4, 2005, 14:41:07 Job time : 142.947 secs

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August 4, 2005, 08:04:16; Search time 1159.47 Seconds (without alignments) 3633.986 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

			Description	Sequence 7. Appli	Sequence 4. Appli	Sequence 3, Appli	Sequence 1626, Ap	Sequence 1625, Ap	Sequence 973, App	Sequence 94, Appl
SUMMARIES			ID	9 US-09-899-276-7	US-10-685-705-4	US-10-685-705-3	US-10-311-455-1626	US-10-311-455-1625	US-10-311-455-973	US-10-831-704-94
			DB	6	13	13	15	15	15	71
			re Match Length DB ID	650	11793	3221				
	ф	Query	Match	100.0	94.9	93.6	61.8	56.2	5.9	5.6
			Score	650	616.6	608.6	401.8	365.4	38.2	36.6
		Result	No.	1	8	m	Ω	S	9	7

Sequence 254387, Sequence 254388,	2543	equence 25439	25438	25438	25438	25439	ഗ	26490		Sequence 105632,								15(	326	95,	146	219	4	465	984	30	474	71	89	416	10	100	102	e 103	e 129	Sequence 191, App
US-10-027-632-254387 US-10-027-632-254388	7	ᅼ	-	US-10-027-632-254388	_	-	US-10-087-192-529	US-10-027-632-264907	US-10-027-632-264907	US-10-027-632-105632	- 1	US-10-027-632-17506			US-10-027-632-16668	US-10-027-632-16668	US-10-027-632-150617	US-10-027-632-150617	US-10-087-192-328	US-10-461-862-95	US-10-767-701-14649	ģ	US-09-938-842A-465	US-09-938-842A-465	10-311	10-108-260A-	-09-876-143-4	2	-10-221-613-	-10-221	US-10-395-607-106	US-10-799-870-106	938-842A-102	-09-938-842A-1	-311-455-1	US-10-388-934-191
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## ALIGNMENTS

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APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Coto, Ubaldo
APPLICANT: Coto, Ubaldo
APPLICANT: Delius, Hajo
APPLICANT: Delius, Annemarie
APPLICANT: Delius, Annemarie
APPLICANT: Zur Hausen, Harald
APPLICANT: Zur Hausen, Harald
APPLICANT: Patzelt, Andrea
TITLE OF INVENTION: No. US20020106355A1e1 Regulatory Sequences of the MCP-1 Gene
TITLE OF INVENTION: No. US20020106355A1e1
CURRENT PAPLICATION NUMBER: US/09/899,276
CURRENT FILING DATE: 2001-07-06
PRIOR APPLICATION NUMBER: ED 00 114 560.6
PRIOR PILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
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100.0%; Score 650; DB 9; Length 650;
Best Local Similarity 100.0%; Pred. No. 1e-209;
Matches 650; Conservative 0; Mismatches 0; Indels
                          ; Sequence 7, Application US/09899276; Patent No. US20020106355A1; GENERAL INFORMATION:
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US-09-899-276-7
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| Sequence 4, Application US/10685705
| Publication No. US20040177387A1
| GENERAL INFORMATION:
| APPLICANT: University of Kentucky Research Foundation
| APPLICANT: University of Methods And Animal Model For Analyzing Age-Related Macular
| TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular
| TITLE OF INVENTION: Degeneration
| TITLE OF INVENTION: Degeneration
| TITLE OF INVENTION: Degeneration
| TITLE OF INVENTION: Degeneration
| TITLE OF INVENTION NUMBER: US/10/685,705
| CURRENT APPLICATION NUMBER: 60/422,096
| PRIOR FILING DATE: 2002-10-30
| NUMBER OF SEQ ID NOS: 10
| SEQ ID NO 4
| LENGTH: 11793
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                                       GGCTTGTGCCGAGATGTTCCCAGCACAGCCCCATGTGAGAGCTCCCTGGCTCCGGGCCCCA
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                                                                             AGCGGGGAAGGCATCTTTTTTTTGACAGAGCAGAAGTGGGAAGGCAAGACAGCTTTT
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                                                                                                                                                                                                                                                   AAGCTGCCTCCTCAGAGTGGGAATTTCCACTCACTTCTCTCACGCCAGCACTGACCTCCC
                                                                                                                      Score 616.6; DB 19; Length 11793; Pred. No. 1.2e-197; 0; Mismatches 14; Indels 1;
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al Similarity 97.7%;
636; Conservative
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CORGANISM: Homo sapiens
US-10-685-705-4
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Best Local S
Matches 636
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sequence 3, Application US/10685705
; Sequence 3, Application US/10685705
; Publication No. US2004017738741
; Publication No. US2004017738741
; APPLICANT: University of Kentucky Research Foundation
APPLICANT: UNIVERSITY, Ambati
TITLE OF INVENTION: Methods And Animal Model For Analyzing Age-Related Macular
TITLE OF INVENTION: Degeneration
FILE REFERENCE: 050229-0415
; CURRENT APPLICATION NUMBER: US/10/685,705
; CURRENT FILING DATE: 2003-10-16
; PRIOR APPLICATION NUMBER: 60/422,096
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3.2
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                                                                                                                                                                                                                                                                                                                                         CCAACACTCAGAAGCCTATGTGAACACTCAGCCAGCAAAGCT-GGAAGTTTTTCTCTGTG
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                                                          4857 GTATCTGGAATGCAGGCTCCAGCCAAATGCATTCTCTTCTACGGAATCTGGGAACTTCCA
                                                                                                      AAGCTGCTCCTCAGAGGGGAATTTCCACTCACTTCTCACGCCAGCACTGACCTCCC
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Pred. No. 3e-195;
0; Mismatches 14; Indels 1;
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Best Local Similarity 97.7%;
Matches 628; Conservative
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US-10-685-705-3
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                                  3684 CITATACCGAAATATTCCCAACACCCCATATAAAAACTCCCTAACTCCGAAT
                                                                                                                    3624 ATCTAAAATACAAACTCCAACCAAATACATTCTCTTCTACGAAATCTAAAAACTTCCAAA
                                                                                                                                                                                 123 GCTGCCTCCTCAGAGTGGGAATTTCCACTCACTTCTCTCACGCCAGCACTGACCTCCCAG
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; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-311-455-1625
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ORGANISM: Artificial Sequence
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Publication No. US20030143606A1

GENERAL INFORMATION:

APPLICANT: OLEK, Alexander

APPLICANT: PIERENBROCK, Christian

APPLICANT: BERLIN, Kurt

TITLE OF INVENTION: Cytosine methylation

TITLE OF INVENTION: Cytosine methylation

FILE REFERENCE: 5013.1014

CURRENT APPLICATION NUMBER: US/10/311,455

CURRENT FILING DATE: 2002-12-16

PRIOR PILING DATE: 2001-07-02

PRIOR APPLICATION NUMBER: DE 10032529.7

PRIOR PILING DATE: 2000-06-30

PRIOR PILING DATE: 2000-09-01

NUMBER: 2000-09-01

PRIOR FILING DATE: 2000-09-01

SEQ ID NO 1626

LENGTH: 5926
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                         AGGCCATCTTTTCTTGACAGAGCAGAGGGAGGCAGACAGCTGTCACTTTCCAGAAGA
                                                                                                                                                                                                                                                                  CTTTCTTTTCTGATTCATACCCTTCACCTTCCCTGTGTTTACTGTCTGATATATGCAAAG
                                                                                                                      121 TCCTCAGAGTGGGAATTTCCACTCCCTCTCAGCCAGCACTGACCTCCCAGCGGGG
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Pred. No. 8.8e-125;
0; Mismatches 147; Indels 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (Homo sapiens)
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; OTHER INFORMATION: chemically treated genomic DNA
US-10-311-455-1626
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Best Local Similarity 77.2%;
Matches 501; Conservative
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US-10-311-455-1626/c
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US-10-831-/U4-94

| Sequence 94, Application US/10831704
| Sequence 94, Application US/2085100931A1
| GENERAL INFORMATION:
| Publication No. US20050100931A1
| GENERAL INFORMATION:
| APPLICATION: METHODS AND COMPOSITONS FOR THE IDENTIFICATION AND TITLE OF INVENTION: ASSESSMENT
| TITLE OF INVENTION: ASSESSMENT
| TITLE OF INVENTION: ASSESSMENT
| TITLE OF INVENTION: ASSESSMENT
| TITLE OF INVENTION: ASSESSMENT
| TITLE OF INVENTION: ASSESSMENT
| TITLE OF INVENTION: US/10/001
| CURRENT APPLICATION NUMBER: US/10/155,653
| PRIOR PILING DATE: 1998-12-23
| PRIOR PILING DATE: 1998-12-23
| PRIOR PILING DATE: 1998-03-25
| PRIOR PILING DATE: 1998-03-25
| PRIOR PILING DATE: 1997-12-24
| NUMBER OF SEQ ID NOS: 191
| SEQ ID NOS: 191
| SEQ ID NOS: 191
| SEQ ID NOS: 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  547 CAGGAGACTTATTTAAAGAICTCAGCATCTTTCAGCTTGTTAACCTAGAGAAAACCG 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  459 galdindengothahanggaldinganarnaharharitarahanggangang 518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     487 CAGGATGTCTATAAGCCCATTGATTCTGGGATTCTATGAGTGATGCTGATATGACTAAGC
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FEATURE:
NAME/KEY:
LOCATION: 5.004
OTHER INFORMATION: n is a or g or c or t
US-10-311-455-973
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                                                                                                                                                                                                                                                                            Length 6557;
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; Pred. No. 0.59;
90; Mismatches 109; Indels
                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                               Score 38.2; DB 15;
Pred. No. 0.39;
                                                                                                                                                                                                                                                                                                                                            0; Mismatches 108;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: (1)...(1497)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity 19.4%;
Matches 48; Conservative 9
                                                                                                                                                                                                                                                                                         Query Match 5.9%;
Best Local Similarity 48.8%;
Matches 103; Conservative
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Sequence 973, Application WS/10311455
Publication No. US20030143606A1
Sequence 973, Application No. US20030143606A1
SERNERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
APPLICANT: PIEPENBROCK, Christian
FILE OF INVENTION: UNMER: US/10/311,455
CURRENT FILING DATE: 2002-12-16
PRIOR PILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 2424
SEQ ID NO 973
LENGTH: 6557
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTAAGTTAGGAGAATTTAATTTAAAGATTTTTAGTATTTTAGTTTTGTTAATTTTAGAGA 2840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2480
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                                                                                                                                                                                                                                                                                                         GTATCTGGAATGCAGGCTCCAGCCAAATGCATTCTCTTCTACGGGATCTGGGAACTTCCA 120
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                                                                   Length 5926;
                                                                                                                               1;
                                                                                                                            Indels
                                                                      Score 365.4; DB 15;
Pred. No. 2.1e-112;
0; Mismatches 171;
                                                                         Query Match 56.2%;
Best Local Similarity 73.6%;
Matches 479; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
US-10-311-455-973
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RESULT 10
US-10-027-632-254389
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; ORGANISM: Human
US-10-027-632-254389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Human
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                                                     TICCACTICACTICICICACGCCAGCACTIGACCTCCCAGCGGGGGGGCGCATCTTTTCTTG 204
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TITLE OF INVENTION: I David G.

TITLE OF INVENTION: I Definition and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108927.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2000-04.30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-03-24

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 1099-11.23

PRIOR PILING DATE: 1999-11.23

PRIOR PILING DATE: 1999-11.23

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

PRIOR FILING DATE: 1999-09-28

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PRIOR FILING DATE: 1999-09-28
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Sequence 254389, Application US/10027632

Publication No. US20020198371A1

GENERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: POLYMATION:
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 254387
LENGTH: 1266
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Publication No. US20020198371A1
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT FILING DATE: 2002-04-30
FRIOR FILING DATE: 2000-07-12
PRIOR PAPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 12000-02-24
PRIOR FILING DATE: 1999-09-11-23
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-08-09
PRIOR FILING DATE: 1999-08-09
SOFTWARE: FASTEED FOR Windows Version 4.0
SEQ ID NO S54389
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Pred. No. 0.73;
0; Mismatches
PRIOR PELLING DATE: 2002-04-50
PRIOR PELLING DATE: 2000-07-12
PRIOR PELLING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/196,676
PRIOR FILING DATE: 2000-04-20
PRIOR PELLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR FILING DATE: 1999-01-23
PRIOR APPLICATION NUMBER: US 60/165,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/156,358
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
PRIOR FILING DATE: 1999-09-28
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PRIOR FILING DATE: 1999-09-09
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Best Local Similarity 53.1%;
Matches 77; Conservative
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US-10-027-632-254388
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US-10-027-632-254387
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                                                                                                                              99 CTACGGGATCTGGGAACTTCCAAAGGTGCTCCTCAGAGTGGGAATTTCCACTCTTCT
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CURRENT APPLICATION NUMBER: 05/04.30

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-04-20

PRIOR PELING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR PELING DATE: 2000-03-29

PRIOR PELING DATE: 1900-00-224

PRIOR PELING DATE: 1900-00-224

PRIOR PELING DATE: 1990-11-23

PRIOR PELING DATE: 1990-11-23

PRIOR PELING DATE: 1990-11-23

PRIOR PELING DATE: 1990-02-28

PRIOR PELING DATE: 1990-02-28

PRIOR PELING DATE: 1990-08-09

NUMBER OF SEQ ID NOS: 325720

NUMBER OF SEQ ID NOS: 325720
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                                                  Gaps
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5.6%; Score 36.2; DB 13; Length 1266;
Best Local Similarity 53.1%; Pred. No. 0.73;
Matches 77; Conservative 0; Mismatches 68; Indels 0;
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ch 5.6%; Score 36.2; DB 13; Length 1266; I Similarity 53.1%; Pred. No. 0.73; 77; Conservative 0; Mismatches 68; Indels 0;
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US-10-027-632-254387
; Sequence 254387, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
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US-10-027-632-254390
; Sequence 254390, Application US/10027632
; Publication No. US20020198371A1
         Query Match
Best Local Similarity
Matches 77; Conserv
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US-10-02/-632-254388

Sequence 254388, Application US/10027632

publication No. US20030204075A9

GENERAL INFORMATION:

APPLICANT: Wang, David G

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

TITLE OF INVENTION: 108827.129

CURRENT PLICATION NUMBER: US 60/218,006

PRIOR APPLICATION NUMBER: US 60/128,006

PRIOR APPLICATION NUMBER: US 60/199,676

PRIOR FILING DATE: 2000-03-22

PRIOR PLING DATE: 2000-04-20

PRIOR FILING DATE: 2000-04-20

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 2000-03-24

PRIOR PLING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-10-28

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PRIOR FILING DATE: 1999-00-28

PRIOR FILING DATE: 1999-00-28

PRIOR FILING DATE: 1999-00-28
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 10827.129
CURRENT PILING DATE: 2002-04-30
CURRENT FILING DATE: 2002-04-30
PRIOR PELICATION NUMBER: US 60/218,006
PRIOR PELING DATE: 2000-07-12
PRIOR PELING DATE: 2000-07-20
PRIOR PILING DATE: 2000-03-20
PRIOR PILING DATE: 2000-03-29
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 254388
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Publication No. US20030204075A9

Publication No. US20030204075A9

FURDERAL INFORMATION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: Identification and Mapping of Single Nucleotide

FILE OF INVENTION: DATE: 2002-04-30

FRIOR PELING DATE: 2000-07-12

PRIOR FILING DATE: 2000-07-12

PRIOR FILING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR PLING DATE: 2000-03-29

PRIOR FILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-23

PRIOR FILING DATE: 1999-11-23

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0; Mismatches 68; Indels 0;
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Best Local Similarity 53.1%;
Matches 77; Conservative
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Best Local Similarity 53.1<sup>5</sup>
Matches 77, Conservative
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US-10-027-632-254388
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US-10-027-632-254389
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AC096195 Rattus no
AX343337 Sequence
AX34338 Sequence
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AC137407 Rattus no
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Mus musculus chromosome 12, clone RP23-36H21, complete sequence.
AC121286
AC121286.7 GI:45237272
HTG.
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AL928696 MOUSE DNA
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                 GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Birren, B., Lintcon, L., Musbaum, C., Lander, E., Ali, A., Allen, N., Allen, N., Anderson, S., Barna, N., Bastien, V., Elong, Y., Boudalavdiy, L., Anderson, S., Barna, N., Bastien, V., Calmagua, Candogalar, Choepel, C., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Choepel, P., Erzelfano, K., Colangan, J., Garad, Pierare, N., Garade, D., Garad, S., Gardyna, S., Ginde, S., Gord, S., Goyche, M., Male, C., Inlaw, I., Johnson, R., Jones, C., Kamat, A., Karates, A., Kalls, C., Marquis, N., Matthews, C., Kamat, A., Karates, A., Kalls, C., Marchan, J., Garad, Pierare, N., Garade, A., Kartews, R., Landerson, R., Landerson, R., Macchan, J., Garad, Pierare, N., Garade, A., Kartews, M., Margay, J., Levine, R., Lindblad-Toh, K., Liu, G., Macchan, J., Mardia, N., Matthews, C., Macchan, M., Menga, V., Lenter, R., Majoren, R., Majoren, C., Norana, C.H., Connor, T., Majore, J., Mardia, N., Matthews, C., McCarthy, M., McGarthy, M., McGarthy, M., McGarthy, M., Margay, T., Naylor, T., Naylor, T., Naylor, C., Norana, C.H., Connor, T., Orlonnell, P., O'Neil, D., Norby, C., Norana, C.H., Connor, T., Peterson, M., Stolanovic, N., Stenan, S., Severy, P., Sponcer, B., Stange-Thomann, N., Stolanovic, N., Stonann, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Schauer, S., Lander, E., Lander, E., Ander, B., Wu, X., Wyman, D., Ye, W., J., Young, G., Doley, R., Dorris, D., Bestien, V., Boogialavity, V., Bodis, S., Corling, S., Anderson, W., Azachehi, H. M., Barra, M., Bestien, V., Bloom, T., Boguslavity, V., Boukhgalevity, C., Boukhgalevity, C., Boukhgalevity, C., Boukhgalevity, C., Boukhgalevity, C., Manning, J., Manning, J., Marthews, C., McCard, P., Manning, J., Manning, J., Manning, J., Mence, J., Manning, J., Mence, J., Manning, J., Raymond, J., Raymo Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Camara, J., Chang, J., Choepel, Y., Collymore, A., Cook, P., Corum, B., DeArellano, K., Collymore, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farco, S., Ferreira, P., Fitzgerre, M., Hafez, N., Hagopian, J., Gardyna, S., Graham, L., Grand-Pierre, M., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamæft, A., Karactas, A., Karactas, A., Karactas, A., Karactas, A., Karactas, A., Maratas, A., M Submitted (22-JAN-2004) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, NA 02141, USA (bases 1 to 227648) Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus. 1 (bases 1 to 227648) Birren, B., Nusbaum, C. and Lander, E. Mus musculus chromosome 12, clone RP23-36H21 (bases 1 to 227648)

Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovitc, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Direct Submission Street, Cambridge, MA 02141, USA Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 6, 2004 this sequence version replaced gi:41058341.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html Contact: sequence gubmissions@genome.wi.mit.edu ------ Project Information Center project nome: 1.22843 Center clone name: 36_H_21 clone lib="RPCI-23 Female Mouse BAC" 1. .2223 Center code: WIBR Web site: http://www-seg.wi.mit.edu /note="wgs_end_extension clone_end:SP6" /rpt family="(CA)n"
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Buckfasiler, B., Chospel, Y., Colangelo, M., Campopiano, A., Chang, J., Chagaro, B., Chospel, Y., Colangelo, M., Collins, S., Collymore, A., Chacaro, B., Chocke, P., DeArellano, K., Dewar K., Diaz, J. S., Dodge, S., Farciara, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Grade, D., Galagan, J., Gardyna, S., Gangels, B., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Karls, C., LaRocque, K., Landbiad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Martune, R., Lindbiad-Toh, K., Liu, G., MacCarhy, M., McBwan, P., McKernan, K., Meldrim, J., Meneus, L., Minova, T., Manga, V., Murphy, T., Naylor, J., Nauthews, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Stantos, R., Schauer, S., Schupback, R., Stantos, S., Severy, P., Spencer, B., Stanger, Themann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Millon, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Simbek, L., Zimmer, A. and Zody, M., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M., Salices, Submission, C., Simmer, A., and Zody, M., Salices, Submission, C., Simmer, A., and Zody, M., Salices, Submission, C., Simmer, A., and Zody, M., Salices, Submission, C., Simmer, A., and Zody, M., Salices, Submission, C., Simmer, A., and Zody, M., Salices, Submission, Simmer, A., and Zody, M., Salices, Submission, Simmer, A., and Zody, M., Salices, Submission, Simmer, A., and Zody, M., Subraman, S., Severy, P., Simmer, A., and Zody, M., Subraman, S., Simmer, A., and Zody, M., Subraman, S., Severy, B., Simmer, A., and Zody, M., Subraman, S., Simmer, A., and Zody, M., Subraman, S., Simmer, A., and Zody, M., Subraman, S., Simmer, A., and Zody
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Submitted (12-SEP-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

E (bases 1 to 234354)

E (bases 1 to 234354)

Sirren, B., Nusbauum, C., Lander, B., Abouelleil, A., Allen, N., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Anderson, M., Arachchi, H.M., Cook, P., Corum, B., DeArellano, K., Collymore, A., Cook, A., Cook, P., Corum, B., DeArellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Farros, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Gardyna, S., Garham, L., Grand-Pierre, N., Hagos, D., Galagan, J., Gardyna, S., Garham, L., Grand-Pierre, N., Halse, V., Jude, J., Manden, R., Lindblad-Toh, K., Liu, G., Lui, X., Mabbitt, R., MacLean, C., McCarthy, M., Macdonald, P., Major, J., Manthews, C., McCarthy, M., Major, J., Manning, J., Matthews, C., McCarthy, M., Maddrim, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., O'Neil, D., Oliver, J., Peterson, Radhud, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (02-AUG-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
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JOURNAL
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AUTHORS
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Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 234554)
Birren,B., Nusbaum,C. and Lander,E.
Mus musculus chromosome 3, clone RP23-427K12
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DEFINITION ACCESSION VERSION KEYWORDS SOURCE

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AUTHORS TITLE REFERENCE

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168. .4224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_family="MER5A"
391. .5414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rpt_family=" (TC) n"
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AC104259
Homo sapiens chromosome 15, clone CTD-252514, complete sequence.
AC104259
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 155753)

Birren, B., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 15, clone CTD-252514

Unpublished

Unpublished

2 (bases 1 to 15575)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, N., Bastien, V., Boguslavkiy, L., BoukMalter, B., Anderson, S., Barra, J., Campopiano, A., Chang, J., Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S.,
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                                                                                                                                                                                                                                                                                                                                                              /rpt family="PB1D9"
complement[1997, .20155]
/rpt family="B3"
20579. .2067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   92.0%; Score 18.4; D
95.0%; Pred. No. 44;
:ive 0; Mismatches
                                                      12731. 12760

/rpt family="(TTTTA)n"

complement (12848. 13133)

/rpt family="B4A"

13261. 13403

/rpt family="MER5A"

complement (13906. 14971)

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/rpt family="LX8"
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17055. 17241
17056. 18294
17513. 18294
17513. 18294
17pt family="MER34B-int"
18411. 18709
18751. 18901
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/rpt_family="(TG)n"
complement(20716. .21003)
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complement (22294. .22371)
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family="(TTTA)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   family="AT_rich"
12220
                                                                                                                                                                                                                                                                                                                                                      family=" (TAGA) n"
                                                                                                                                                                                                                                                                                                                  /rpt_family="RSINE1"
8920. .19075
                                       /rpt_family="T-rich"
12731. .12760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . .21957
family="(TA)n"
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TITLE
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REFERENCE
AUTHORS
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Ferreira, P., FitzHugh, W., Gage, D.,

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Ginde, S., Gord, S., Goyette, M., Graham, L., Garand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacGonald, P., Major, J., Marquis, N., Matthews, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., MacGonald, P., Major, J., Marquis, N., Matthews, C., Morbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Nell, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Schauer, S., Schupback, Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupback, Senann, S., Severy, P., Spencer, B., Stanger-Thomann, N., Schyanovic, N., Strauss, N., Subramannan, A., Talamas, J., Tesfaye, S., Theodore, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., L., Zimmer, A. and Zody, M., Young, G., Shansel, M., Simmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer, A. and Zody, M., Subrassiok, L., Zimmer
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Direct Submassion

Direct Submassion

Research, 320 Charles Street, Cambridge, MA 02141, USA

1 (Dases I to 155753)

Salren, Nusbaun, C., Lander, E., Ali, A., Allen, N., Anderson, S.,
Barna, N., Bastien, V., Bloom, T., Boguslavkiy, L., Boukhgalter, B.,
Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collymore, A.,
Cook, A., Cooke, P., Pearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Faro, S., Ferreira, P., P. Hizcerald, M., Gage, D., Galagan, J.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R.,
Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J.,
Matthwas, C., McCarthy, M., Maldrim, J., Mahova, T.,
Matthwas, C., McCarthy, M., Maldrim, J., Mahova, L.,
Mhorda, V., Murphy, T., Naylor, J., Naylow, C., Nicol, R., Norbu, C.,
Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J.,
Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N.,
Stojanovic, N., Talamas, J., Tagay, S., Trbedore, J., Topham, K.,
Travers, M., Voussiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., and Zody, M.
Direct Submission

L. Shart H. A., Mitchand, Therthin, A.M.T. Canter, For Connell, Submith, C., Sencer, B., Stanger, S., and Zody, M.
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (21-NOV-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA (bases 1 to 155753)
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Only the first 155.8 kilobases of this clone are being submitted.
The remainder overlaps accession number AC013489 [WICGR project
Contact: sequence_submissions@genome.wi.mit.edu
------------- Project Information
Center project name: L22081
Center clone name: 2525_I_4
                                                                                                                                                                                                                                        /clone="CTD-252514"
/clone_lib="CITD2 Human BAC"
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complement (1166. 1215)
/rpt_family="MER5A"
1219. 1872
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complement (2383. 2504)

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/rpt family="MERSA"

/rpt family="L2"

/rpt family="L2"
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4472. .5119
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5160. .5397
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1906. .2031
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2032. .2056
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6229. .6747
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10922. .10965
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. .11114
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repeat_region

COMMENT

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Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassiliev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.

Direct Submission

Submitted (G5-SEP-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, 320 Charles Street, Cambridge, MA 02141, USA

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Research, 320 Charles Street, Cambridge, MA 02141, USA

Research, Chang, J., Chazaro, B., Chopel, Y., Collymore, A.,
Cook, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S.,
Farch, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J.,
Rarctas, A., Kells, C., Lander, F., Grand-Pletre, N., Hagos, B.,
Horton, L., Hulme, W., Iliev, I., Johnson, R., Lindblad-Toh, K.,
Karatas, A., Kells, C., Lander, F., Levine, R., Lindblad-Toh, K.,
Liu, G., MacLean, C., Macdonald, P., Major, J., Marchews, C.,
Inu, G., MacLean, C., Macdonald, P., Minou, T., Norbu, C., Norman, C.,
Phunkhang, P., Pierre, N., Raymon, C., Nicol, R., Norbu, C., Norman, C.,
Phunkhang, P., Pierre, N., Raymon, C., Stojanovic, N., Talamas, J.,
Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J.,
Submitted (22-Ann-2002) Whitehead Instinta/MIT Center for Cannon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission

AL Submitted (22-AuG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

ES Barren, 320 Charles Street, Cambridge, MA 02141, USA

Tesearch, 320 Charles Street, Cambridge, MA 02141, USA

ES Birren, M., Nastien, V., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, M., Bloom, T., Boguslavkiy, L., Boukhgalter, B., Cooke, P., DeArellano, K., Dewell, Y., Collymore, A., Gooke, P., DeArellano, K., Deard, Y., Callymore, A., FitzGerald, M., Gage, D., Galagan, J., Farceira, P., FitzGerald, M., Gage, D., Galagan, J., Farceira, P., FitzGerald, M., Gage, D., Margus, S., Gord, S., Graham, L., Ghnson, R., Jones, C., Kamat, A., Kartas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., MacLean, C., Macdonald, P., Major, J., Mathews, C., Marthews, C., Levine, R., Liu, G., MacLean, C., Macdonald, P., Majoor, J., Meneus, J., Micol, R., Morbu, C., Norman, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., O'Connor, T., O'Donnell, P., Mayod, R., Seaman, S., Schupback, R., Seaman, S., Sepencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Venkel, L., Zimmer, A. and Zody, M.

Direct Submission
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All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washingcon.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 We are submitting the first 164.4 kilobasesof hte project at this time. The remainder overlaps AC091495 [WICGR project L12630]. Location/Qualifiers
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Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
Center: project Information
Center project name: 12244
Center clone name: 19_F_9
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Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

I (bases 1 to 164359)

Sirren, B., Nusbaum, C. and Lander, E.

Homo sapiens chromosome 18, clone RP11-19F9

Unpublished

Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baker, J., Baldwin, J., Barna, N., Beckerly, R., Benn, J., Brown, A., Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Castle, A., Cerry, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DaArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, M., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Gilbert, D., Grant, G., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Medraim, J., Molla, M., Morriow, J., Mychaleckyj, J., Naylor, J., Nolleff, M., O'Connor, T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P.,
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Bukheria; Primates; Catarrhini; Hominidae; Homo.

I (bases 1 to 177456)

I Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Hong sapiens 177,456 genomic DNA of 18q12

L. Published Only in DataBase (2000)

E. Chases 1 to 177456

Is Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

E. Chases 1 to 177456

Is Hattori,M., Ishii,K., Toyoda,A., Taylor,T.D., Hong-Seog,P., Fujlyama,A., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Direct Submission

L. Submitted (06-MAR-2000) Masshira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

I-15-1 Kitasato, Sagamihara, Kanagawa 228-8555, Japan (E-mail:hattori@gsc.riken.go.jp,, Tel:81-42-778-9924)

On Jul 15, 2000 this sequence version replaced gi:8117270.

Center: RIKEN Genomic Sciences Center (GSC)

Center: RIKEN Genomic Sciences Center (GSC)

Center: RIKEN Genomic Sciences Center (GSC)
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Homo sapiens chromosome 18 clone RP11-776M20 map 18q12, WORKING
DRAFT SEQUENCE, 8 unordered pieces.
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Contact: hattori@gsc.riken.go.jp
------- project Information
Center project name: Humbrafil8
Center clone name: RP11-776M20
/rpt_family="MLTIH"
23443. .23487
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complement(22513. .23779)
/rpt_family="L2"
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'rpt_family="(TTCA)n"
27773. .27812
                                                                                                                                                                            /rpt_family="(TGAA)n"
28640. .28671
/rpt_family="(CAAAA)n"
29132. .30007
/rpt_family="LIMD2"
complement(30295. .32620)
/rpt_family="LIPAS"
complement(30295. .32620)
                                                                                                                                                                                                                                                                                                                                         / Complement (32622. 33185)
/ The family="LiPA5"
33158. 34527
/ The family="LiMD2"
3458. 3453
/ The family="LiPA13"
/ The family="LiPA13"
/ The family="LiMD2"
36194. 3609
/ The family="LiMD2"
/ The family="LiMD2"
/ See family="LiMD2"
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/rpt_family="AT_rich"
36428. .37415
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AP001356 3 GI:9229949
HTG: HTGS_PHASE1; HTGS_DRAFT.
HOmo sapiens (human)
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AP001356/c
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AL928696 102448 bp DNA linear ROD 21-NOV-2002 Mouse DNA sequence from clone RP23-387G11 on chromosome 2, complete
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Mus musculus
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 102448)
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Xu, w. and Murphy, L.J.
Isolation and characterization of the mouse beta 2/neuroD gene
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Xu,W. and Murphy,L.J.
Direct Submission
Submitted (11-UN-1998) Physiology, University of Manitoba, 770
Bannatyne Ave., Winnipeg, MB R3E 0W3, Canada
Location/Qualifiers
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              Length 177456;
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Mus musculus beta2/neuroD gene, promoter and exon l.
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Pred. No. 3e+02;
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2091. .>2172
/product="beta2/neuroD"
/note="helix-loop-helix protein"
                         DB 2;
76;
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/mol_type="genomic DNA"
/grzain="C57BL/6N"
/db_xref="taxon:10090"
/chromosome="2"
                         90.0%; Score 18; DB ilarity 100.0%; Pred. No. 76; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                         NOTE: This is a 'working draft' sequence. It currently consists of sontigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
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Sequencing vector: PCR products; 100% of reads Chemistry: Dye-terminator Er-amersham; 100% of reads Chemistry: Dye-terminator Er-amersham; 100% of reads Assembly program: Phrap; version 0.990329 Consensus quality: 174936 bases at least Q40 Consensus quality: 17605 bases at least Q30 Consensus quality: 176462 bases at least Q20 Consensus quality: 176462 bases at least Q20 Quality coverage: 11.10x in Q20 bases; sum-of-contigs
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1 44797: contig of 44797 bp in length
198 44897: gap of 100 bp
898 77452: contig of 32555 bp in length
17552: gap of 100 bp
17552: gap of 100 bp
1849 132030: contig of 28196 bp in length
1749 105848: gap of 100 bp
131 132130: gap of 100 bp
131 154722: contig of 26182 bp in length
173 154822: gap of 100 bp
173 154822: contig of 22592 bp in length
173 155828: contig of 100 bp
17588: gap of 100 bp
17588: contig of 100 bp
17588: contig of 100 bp
17588: contig of 100 bp
17588: contig of 7040 bp in length
17589: 17268: gap of 100 bp
17468: gap of 100 bp
17468: gap of 100 bp
17468: gap of 100 bp
17745: contig of 4988 bp in length
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/organiam="Homo sapiens"
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/db_xref="taxon:9606"
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/note="assembly_fragment"
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/note="assembly_fragment"
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FEATURES

ORIGIN

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/mol_type="genomic_DNA"
/db_xref="taxon:9606"
/clone="RP11-28C3"
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Center clone name: 28_C_3
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/rpt_family="MIR"
1188. .1247
/rpt_family="MIR"
2104. .2105
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820. .885
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       AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL: Sw:, SWISSROT; Tr:, TREMBL; WP:, WORMPEP; Information the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-387G11 is from the RPCI-23 Mouse PAC Library constructed by the group of Pieter de Jong.

PROFIGURE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF PROFICE THENDER SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTION OF THE SECTI
                               Submitted (21-NoV-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, GBIO 15A, UK. E-mail enquiristes: Inhumpurey@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk Clone version replaced gi:25136705. Sequence from the Mouse Genome Sequencing Consortium Whole genome Shotgum may have been used to confirm this sequence. Sequence ashotgum apply have been used to confirm this sequence. Sequence data from the Whole genome shotgum alone has only been used where it has
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Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 140334)
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Homo sapiens, clone RP11-28C3, complete sequence.
ACO21802
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                                                                                                                                                                                                                                                                                                                                     Center: Wellcome Trust Sanger Institute
                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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                                                                                                                                                                                                                                                               a phred quality of at least 30.
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Best Local Similarity 94.74
Matches 18; Conservative
Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                            Center code: SC
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VERSION
KEYWORDS
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TITLE
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Anderson, S., Baldwin, J., Backerly, E., Beda, F.,
Boguslavkiy, L., Boukhgalter, B.,
Boguslavkiy, L., Boukhgalter, B.,
Brown, A., Burkett, G., Castle, A.,
Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P.,
DeArellano, K., Dewar, K., Domino, M., Doyle, M., Fenestor, J.,
Gardyna, S., Grant, G., Hagos, B., Heaford, M., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Handers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K.,
Macdonald, P., Marquis, M., McEwan, P., McGurk, A., McKernan, K.,
McPheeters, R., Meldrim, J., McEwan, P., McGurk, A., McKernan, K.,
Norman, C.H., O'Connor, T., O'Donnell, P., Ollvar, T. M., Peterson, K.,
Pierre, N., Pisani, C., Pollara, V., Raymond, C., Rilley, K., Rothman, D.,
Roy, A., Santos, R., Severy, P., Spencer, B., Stange-Thomann, N.,
Zimmer, A., vassiliev, H., Viel, R., Vo, A., Wyman, D., Ye, W.J.,
Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission

Submitted (20-JAN-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

CB 3 (bases 1 to 140334)

SBirren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Boguslavkiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chazaro, B., Cock, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Gorde, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Farro, S., Gorde, S., Gorde, S., Gorde, D., Galagan, J., Gardyna, S., Gorde, S., Gorde, S., Gordete, M., Graham, L., Grand-Pierre, N., Hagos, B., Heaford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., Norman, C.H., Michae, W., Murphy, T., Naylor, J., Nguyen, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phurkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Riee, C., Rogov, P., Spencer, B., Santos, R., Schauber, S., Schupback, R., Stanger, N., Schupback, R., Yell, R., Wall, R
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All repeats were identified using RepeatMasker:
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Center: Whitehead Institute/ MIT Center for Genome Research
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http://ftp.genome.washington.edu/RM/RepeatMasker.html
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------- Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="RPCI-11 Human Male BAC" complement(502. .677)
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repeat_region

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4207. .4503

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complement(10103. .10410)
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complement(10411. .10618)
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0619. 10737
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complement (6534..6819)

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6820. 6953

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6954. 7259

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complement (8519. .848)

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complement (8604..8905)

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complement (8604..8905)

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complement (8500..9603)

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complement (8500..9603)

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complement (8906..9064)
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10056. .10102
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10997. 11136

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11160. 11142
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AC133524

AC133524 GI:22830237

HTG5 PHASE1; HTG5_DRAFT; HTGS_FULLTOP.

Mus musculus (house mouse)

Eukaryota; Matazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.

Mus musculus

Eukaryota; Materston, R.H.

A (bases 1 to 189983)

I (bases 1 to 189983)

I (bases 1 to 189983)

S (breck Submission

AL (brease 1 to 189983)

S (breck Submission

AL (bases 1 to 189983)

AL (bases 1 to 189983)

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R (bases 1 to 18983)
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Mus musculus chromosome UNK clone RP23-43L4, WORKING DRAFT
SEQUENCE, 5 unordered pieces.
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                                                                                                                                                                               /rpt_family="Aludo"
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1720. .17525
/rpt_family="LiME3"
1752. .17683
/rpt_family="LiME3"
17684. .17994
/rpt_family="LiME3"
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complement (20485. .20550)
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14009. .14052
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14071. .14118
/rpt_family="(TG)n"
14804. .14864
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/rpt_family="AluJb"
21400. 21637
/rpt_family="MIR"
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17995. .18764
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18853. .18898
/rpt family="L1ME3"
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9216. 19541
rpt_family="AluSc"
                                                                                                                                       /rpt_family="MIR3"
16152. 16298
/rpt_family="MIR"
complement(16584...)
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                                                                                                    'rpt_family="MIR"
5850. .16050
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Best Local Similarity 94.7<sup>3</sup>
Matches 18; Conservative
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AC133524/c
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KEYWORDS
SOURCE
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ACO26086 191426 bp DNA linear HTG 01-SEP-2000
Homo sapiens chromosome 15 clone RP11-540N15, WORKING DRAFT
SEQUENCE, 26 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (19-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       * NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as "runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MO 63108, USA
On Sep 1, 2000 this sequence version replaced gi:8568910.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequencing vector: militial 100%
Sequencing vector: plasmid; 0%
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 180224 bases at least Q40
Consenus quality: 185399 bases at least Q30
Consenus quality: 185399 bases at least Q20
Insert size: 203000; agarose-fp
Insert size: 203000; agarose-fp
Quality coverage: 4.00 in Q20 bases; sum-of-contigs
Quality coverage: 4.34 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: Washington University Genome Sequencing Center
Center code: WUGSC
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1865: gap of unknown length
4193: contig of 2339 bp in length
4193: contig of 1850 bp in length
6143: contig of 1860 bp in length
6243: gap of unknown length
7809: contig of 1566 bp in length
7809: contig of 1849 bp in length
9758: contig of 1849 bp in length
1546: gap of unknown length
1546: gap of unknown length
18198: contig of 5502 bp in length
18208: gap of unknown length
18208: contig of 2738 bp in length
21825: contig of 3738 bp in length
21825: contig of 3565 bp in length
25547: contig of 3565 bp in length
25547: gap of unknown length
25547: gap of unknown length
25669: gap of unknown length
235543: contig of 2822 bp in length
235543: contig of 3565 bp in length
235543: contig of 3565 bp in length
235543: contig of 3565 bp in length
325543: contig of 3565 bp in length
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325543: contig of 3565 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----- Genome Center
                                                                                  AC026086
AC026086.4 GI:9958281
HTG; HTGS_PHASE1; HTGS_DRAFT
HOmo sapiens (human)
                                                                                                                                                                                                                                           1 (bases 1 to 191426)
Waterston, R.H.
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28569:
32543:
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39611:
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7810
9359
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9359
11839
11839
11829
225548
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32644
32643
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KEYWORDS
SOURCE
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                  LOCUS
DEFINITION
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                                     Submitted (14-SEP-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
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                                                                                                                                                                                                                                                                                Sequencing vector: M13; 0%
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-primer E7; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consenus quality: 18736 bases at least Q40
Consensus quality: 18736 bases at least Q20
Innert size: BAC96; agarose-fp
Insert size: BAC96; agarose-fp
Quality coverage: 12.95 in Q20 bases; sum-of-contigs
                                                                                                                                                                      Center: Washington University Genome Sequencing Center
Center code: WUGSC
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/note="assembly_name:Contig10"
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1. 189883
(organism="Mus musculus"
/mol type="genomic DNA"
/db xref="taxon:10090"
/chromosome="UNK"
                                                                                                     ----- Genome Center
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Best Local Similarity 94.79
Matches 18; Conservative
              Direct Submission
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AC026086/c
              TITLE
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                                                                               COMMENT
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48442: contig of 8531 bp in length 48442: contig of 8645 bp in length 54805: gap of unknown length 54805: gap of unknown length 662691: contig of 7486 bp in length 624905: gap of unknown length 624905: gap of unknown length 70784: contig of 7786 bp in length 70784: gap of unknown length 80513: contig of 9267 bp in length 80513: contig of 9267 bp in length 9341: gap of unknown length 9341: contig of 9429 bp in length 9341: contig of 9429 bp in length 9341: contig of 1848 bp in length 11399; contig of 1848 bp in length 11499; contig of 1848 bp in length 115099; gap of unknown length 115099; gap of unknown length 115099; gap of unknown length 116099; contig of 1848 bp in length 11609; gap of unknown length 11615; contig of 10100 bp in length 11615; contig of 10100 bp in length 11615; contig of 10100 bp in length 11615; contig of 10100 bp in length 11615; contig of 10100 bp in length 11615; contig of 2008 bp in length 1161642: gap of unknown length 1161642: gap of unknown length 1161642: gap of unknown length 1161642: gap of unknown length 1161642: gap of unknown length 1191426: contig of 2408 bp in length 1191426: contig of 2408 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1191426: contig of 2406 bp in length 1
length
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21983...25547
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note="assembly_name:Contig23"
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During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL: Sw:, SWISSPROT; TI:, TREMBL: WP:, WORMPEP; Information on the WORMPEP
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Mouse DNA sequence from clone RP23-412B2 on chromosome 4, complete
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Leongamornlert, D. B. Birect Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (13-AUG-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
nmquery@sanger.ac.uk sequence version replaced gi:20793071.
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146746 .167157 nome:Contig32"
167258 .186352 /note="assembly_name:Contig33"
186453 .188860 /note="assembly_name:Contig8"
188961 .191426 /note="assembly_name:Contig8"
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115100. 129243
/note="assembly_name:Contig30"
129344. 146645
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Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
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Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Yorng, G., Zainoun, J., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Direct Submission and Zody, M.

AL Submitted (21-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

A (bases I to 194546)

RESEarch, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barra, B., Wusbaum, C., Charago, E., Chang, J., Charago, B., Choepel, Y., Collymore, A., Cooke, P., DeArellano, K., Dewer, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzGerald, M., Gage, D., Galagan, J., Garham, L., Grand, Pletre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Machen, C., Macdonald, P., Major, J., Machews, C., Macdonald, P., Major, J., Meneus, L., Mihova, T., Mienga, V., Phunkhan, P., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhan, P., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhan, P., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhan, P., Schauer, S., Schupback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Viel, R., V., Zimmer, A. and Zody, M.
Direct Submission
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Smit, A.F.A. & Green, P. (1996-1997) http://ftp.genome.washington.edu/RM/RepeatMasker.html
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Center: Whitehead Institute/ MIT Center for Genome Research
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Contact: sequence_submissions@genome.wi.mit.edu
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/clone lib="RPC1-11 Human Male BAC"
441. 666
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/db_xref="taxon:9606"
/chromosome="15"
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6531. .6602
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/rpt_family="MER91A"
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/rpt_family="MBR112"
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complement(6342. .6
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Signature, M., Boduslavity, L., Boukhgatler, B., Brown, A., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Camarata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dekrellano, K., Dewar, K., Diaz, J.S., Collymore, A., Gookete, W., Grand-Pierre, N., Gade, S., Garde, S., Goyette, M., Grand-Pierre, N., Gade, B., Heaford, A., Horton, L., Hulme, W., Illev, I., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lahorine, R., Liu, G., Machean, C., Macdonald, P., Marquis, N., Matthews, C., McZarthy, M., McEwan, P., McKernan, K., Murphy, T., Naylor, J., Nowyen, C., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Flunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Strauss, N., Surauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Travers, M., Travis, N., Trigillo, J., Vassiliev, H., Viel, R., Wallson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M. Soung, S., Severy, Sound, S., Submission, M., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACOB7482 194546 bp DNA linear PRI 01-SEP-2002
Homo sapiens chromosome 15, clone RP11-540N15, complete sequence.
ACOB7482
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 194546)

Birren, B., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 15, clone RP11-540N15
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                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                         Length 193363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GGAAGGTTGAGTCAAGGAT 19
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         VECTOR: pBACe3.6.
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us-09-899-276c-8.rge

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1 (Dasses 1 to 208945)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC125890 208945 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-281JJ7, *** SEQUENCING IN PROGRESS
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
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HTG: HTGS PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
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                                                                                                                                                                                                                                                         2 GAAGGITGAGICAAGGAIT 20
                                                                                                                              Query Match
Best Local Similarity 94.7%;
Matches 18; Conservative
                                                repeat_region
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Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Monicular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23195060.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft" sequence. It currently

* Consists of 1 contigs. Gaps between the contigs.

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* The sequence will be replaced.
                                                                                                                                                                              Worley, K.C.
Direct Submission
Submitted (O2-JUL-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 208945)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yu.F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weise,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
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Contact: hgsc-help@bom.tmc.edu
Contact: hgroject Information
Center project name: GWLQ
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Center code: BCM

    .208945
    organism="Rattus norvegicus"

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clone_end:T7"
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note="clone_boundary
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10 (Dases I to 22485)

Muzny, D. Marte., Metaker, M. Lee., Abramzon, S., Adame, C., Alder, J., Alsbrooks, S., Amin, A., Anguiano, D., Allan, H., Alsbrooks, S., Amin, A., Anguiano, D., Anguiabechi, V., Royagi, A., Ayodgi, M., Baca, E., Baden, H., Blankenburg, K., Blari, E., Blankenburg, K., Blari, P., Brown, M., Blarian, B., Blari, P., Brown, M., Blayth, P., Brown, M., Blayth, P., Brown, M., Blayth, P., Brown, M., Cavazos, I., Ceasar, H., Center, A., Chavez, D., Chen, G., Chen, R., Reilly, S., Pall, H., Perez, A., Penz, L., L., Pennkoh, R., Reilly, R., Pelly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reilly, R., Reill
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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0; Mismatches 1; Indels
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HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOD.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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/note="wgs_contig"
140618. .141928
/note="wgs_contig"
207618. .208514
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                                                                                                                                                                                                                                                                                                                                      clone_end:Sp6
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Best Local Similarity 94.7'
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Worley, K.C.

Direct Submission

Submitted (17-SEP-2001) Human Genome Sequencing Center, Department Submitted (17-SEP-2001) Human Genetics, Baylor College of Medicine, One Medicular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

Stat Genome Sequencing Consortium.

Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department Of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On May 9, 2003 this sequence version replaced gi:22772229.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence contigs will be indicated in the feature table.
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* NoTE: This is a 'working draft' sequence. It currently

* NOTE: This is a 'working draft' sequence. It currently

* Consists of I contige. Gaps between the contige

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

I 224855. contig of 224855 bp in length.
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetry, J., Shvartsbeyn, A., Sisson, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Soag, J., Strong, R., Sutton, A., Tabor, P., Tabor, P., Taylor, T. aylor, T. Thomas, N., Thomas, A., Tingey, A., Trejos, Z., Usmani, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, G., Wallson, R., Wlexen, P., Weler, B., Wang, J., Wijht, R., Wilson, R., Wilson, R., Wadron, L., Yoon, V., Wright, D., Wright, R., Wilson, R., Wang, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., Von Weinstock, G. and Gibbs, R.A. Bitth, D.R., Holt, R.A., Smith, H.O., Winstell Shang, J., Tako, J.
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Contact: hgsc-help@bcm.tmc.edu
Conter project Information
Center project name: GCUZ
Center clone name: GCUZ
Center clone name: AL130-7M13
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88; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer; cervical carcinoma. Poustka A; Delius H, Human MCP-1 related oligonucleotide SEQ ID NO:8. Finzer P, (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM ВЪ. 06-JUL-2000; 2000EP-00114560. 06-JUL-2000; 2000EP-00114560. DNA; 20 11-MAR-2004 (first entry) ρ, Ą Roesl F, Soto U, Coy Zur Hausen H, Patzelt ADH13945 standard; EP1170372-A1. Homo sapiens 09-JAN-2002. ADH13945; ADH13945 

WPI; 2002-165895/22.

Disclosure; SEQ ID NO 8; 30pp; English.

Novel nucleic acid molecule encoding monocyte-chemoattractant-protein-1, useful in gene therapy, for treating atherosclerosis and cancer.

The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	Description	Adh13945 Human MCP	Adh13947 Human mon	Adh13938 Human mon	Ado03803 Human Cc1	Aas69735 DNA encod	Aac42300 Arabidops	Aac48378 Arabidops	Adq97989 Mouse can	Aac57918 Arachidon	Continuation (6 of	Aas20588 Human met	Aal20747 Human bre	Aall1857 Human bre	Acn82053 Breast ca	Aak56196 Human imm	Aah16869 Human cDN	Acn90528 Breast ca	Adg90903 Hepatic B	Adg90914 Hepatic s	Adg90913 Hepatic B
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The invention relates to a novel nucleic acid molecule (I) comprising a sequence encoding monocyte-chemoattractant-protein-1 (MCP-1) or a protein having the biological activity of MCP-1. A protein encoded by a nucleic acid of the invention has cytostatic, and antiarteriosclerotic activity. A nucleic acid of the invention may have a use in gene therapy. A compound of the invention is useful in the preparation of a medicament for the treatment of atherosclerosis or cancer e.g. cervical carcinoma. A pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. or carbonic atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
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                                                                                                                                                                                                                                      ds; human; monocyte-chemoattractant-protein-1; MCP-1; cytostatic; antiarteriosclerotic; gene therapy; atherosclerosis; cancer;
                                                                                                                                                                                               Human monocyte-chemoattractant-protein-1 related DNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       human; ds; animal model; age-related macular degeneration; AMD; gene knockout; Cc12-deficient; Ccr2-deficient; drusen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 600 BP; 213 A; 101 C; 150 G; 136 T; 0 U; 0 Other;
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Pred. No.
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Patzelt A;
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Zur Hausen H,
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pharmaceutical composition of the invention is useful for the treatment of diseases associated with dysregulation of MCP-1 expression, e.g. atherosclerosis or cancer. The present sequence is used in the exemplification of the invention.
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Pred. No. 53;
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Best Local Similarity 100.0%; Pred. No. 1.4;
Matches 20; Conservative 0; Mismatches 0; Indels
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                                                                                                           Sequence 20 BP; 6 A; 1 C; 8 G; 5 T; 0 U; 0 Other;
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H, Patzelt A;
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Homo sapiens EP1170372-A1

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DB 6; 80;

Query Match

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The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed consists and in gene therapy techniques to restore normal cativity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a cupplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and its binding partners are useful for treating disorders of supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (II) and its binding partners are useful for treating disorders of involving abbrrant protein expression or biological activity. The polypeptide and polymotelecide sequences have applications in capporation of mutations cand to produce other types of data and products dependent on DNA and amino acid sequences. Abs64197-AAS4564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                                                                                                                New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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90.0%; Pred. No. 1.1e+02;
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                                                                           Drmanac RT, Liu C,
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                          (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention relates to a novel methods and animal models for testing candidate drugs that can be used for the treatment or prevention of agerelated meaular degeneration (AMD). Specifically, it refers to administering a candidate drug to gene knockout mice, in particular CC12-deficient, CCr2-deficient and/ or a Cc12-deficient/Ccr2-deficient dual knockout mouse. The present invention describes analysing the knockout mouse eye for development or repression of drusen and/ or lipofuscin accumulation, as well as for the effect of a candidate drug on Bruch's membrane, retinal degeneration and/ or choroidal neovascularisation. Accordingly, such compositions exhibit ophthalmological activities and can be used for gene therapy purposes. This polymucleotide sequence is the human Cc12 gene and enchancer region DNA of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Testing candidate drug for treating age-related macular degeneration, by administering drug to Cc12-deficient, Ccr2-deficient knockout mouse, and analyzing development or regression of drusen and/or lipofuscin
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lipofuscin accumulation; Bruch's membrane; retinal degeneration; choroidal neovascularisation; ophthalmological; gene therapy.
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Mismatches 0; Indels 0;
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990S-0123548P-
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Best Local Similarity 90.0
Matches 18; Conservative
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007-0CT-1999)
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01-SEP-1999;
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New isolated cancer associated nucleic acids comprising at least 10 contiguous nucleotides, useful for diagnosing, preventing and/or treating cancers such as leukemia and lymphoma.
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                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cytostatic; Gene Therapy; cancer; leukemia; lymphoma; Mouse; ds
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0
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                                                                                                                                                                                                                                                                              .2e+02
                                                                                                                                                                                                                                                                             Pred. No. 1.26); Mismatches
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                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                            1 GGAAGGTTGAGTCAAGGATT 20
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99US-0159330P.
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ADQ97989 standard; DNA; 59002
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                                                                                                                                                                                                                                                                    84.0%;
                                                                                                                                                                                                                                                                              90.06;
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                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                               Local Similarity
es 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; biallelic marker; arachidonic acid metabolism; genotyping; detection; hybridisation; phenotype; haplotype; SNP; polymorphic base; single nucleotide polymorphism; hybridisation assay; sequencing assay; specific amplification assay; dentification; ERBM; 12-10-RBM; eicosanoid-related biallelic marker; 12-10-related biallelic marker; ds.
                                                              Sequence 59002 BP; 16030 A; 11777 C; 12009 G; 18102 T; 0 U; 1084 Other;
                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arachidonic acid metabolism related genomic biallelic marker #552
                                                                                                                             Length 59002;
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                                                                                                                                                                                        Indels
                                                                                                                         Score 16.8; DB 12;
                                                                                                                                                    Pred. No. 1.8e+02;
0; Mismatches 2;
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ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                                                                                  7393 GGAAGGATGAGTCAAGCATT 7374
                                                                                                                                                                                                                                                   1 GGAAGGTTGAGTCAAGGATT 20
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les 18; Conservative (
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07-MAY-1999;
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82.0%; Score 16.4; DB 3; Length 939;

Query Match

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ADQ97050 from base 500001 (Human cancer associated sequence HD: fragments LOCUS ADQ97050 Accession Adg97050
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; methionine aminopeptidase; protease; adrenal cortico adenoma; ds;
Cushing's syndrome; prostate embryonal carcinoma; colon tumour; brain;
hepatocellular carcinoma; foetal lung; testis; b cell; kidney; prostate;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid molecule encoding methionine aminopeptidase, useful for the development of human therapeutics and diagnostic compositions.
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Pred. No. 1.8e+02;
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Pred. No. 3.2e+02;
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                                                                                   548 GGAAGGTTGAGTCAAGCA 565
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                                                                                                                                                                                                                                                                                                                                                                                            66453 GAAGGTTGATTCAAGGAT
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                                                                                                                                                                                                                                           300001
400001
500001
600001
                                                                                                                                                                                                                                                                                                                   82.08;
                                                                                                                                                                                                                                                                                                                                  94.48;
                                                                                                                                                                                                                100001
                                                                                                                                                                                      Begin
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           Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                               17; Conservative
                                                                                                                                                       of
7
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                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
                                                                                                                                                                      into
                                                                                                                                         ADQ97050_5
Continuation (6 of 7)
                                                                                                                                                                      Sequence split in
Fragment Name
                                                                                                                                                                                                                      ADQ97050_2
ADQ97050_3
ADQ97050_4
ADQ97050_5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                  ADQ97050
                                                                                                                                                                                                                ADQ97050
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                                                                                                                                                                                                                                                                                                                   Query Match
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AAS20588/c
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                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                             RESULT 10
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Human breast cancer expressed polynucleotide 4314.
                                                                                                                                 Human; breast cancer; cell marker; cytostatic;
                              AAL11857 standard; cDNA; 433 BP
                                                                                                                                                                                                                                                         14-JAN-2000; 2000US-0176077P.
14-WAR-2000; 2000US-019167P.
29-WAR-2000; 2000US-019209P.
29-WAY-2000; 2000US-0193480P.
15-WAY-2000; 2000US-0205230P.
09-UDN-2000; 2000US-0211315P.
25-JUL-2000; 2000US-0211315P.
                                                                                                                                                                                                                                  10-JAN-2001; 2001WO-US000798
                                                                                   (first entry)
                                                                                                                                                                                  WO200151628-A2.
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                                                                                                                                                               Homo sapiens
                                                                                   07-DEC-2001
                                                                                                                                                                                                             19-JUL-2001
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                                                           AAL11857;
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Matches
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          RESULT 13
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                       AAL11857
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to human breast cancer expressed polymucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast calls. The polymucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and potentially preventing breast cancer. The polymucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
brain, hepatocellular carcinoma, foetal lung, testis and b cell, kidney
                                               Seguence 84495 BP; 23805 A; 16441 C; 17154 G; 25835 T; 0 U; 1260 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
          and prostate. This sequence represents genomic DNA encoding the human methionine aminopeptidase of the invention
                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New peptide useful as a marker for the diagnosis of breast cancer.
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                                                                       Query Match
80.0%; Score 16; DB 6; Length 84495;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                           Human breast cancer expressed polynucleotide 13204.
                                                                                                                                                                                                                                                                                                                   Human; breast cancer; cell marker; cytostatic; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 2342; 3695pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GAAGGITGAGICAAGGAIT 20
                                                                                                                                                 34427 GGAAGGTTGAGTCAAG 34412
                                                                                                                                                                                                                  AAL20747 standard; cDNA; 399 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; 2000US-0176077P.
; 2000US-0189167P.
; 2000US-0192099P.
; 2000US-0193480P.
; 2000US-0205230P.
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                                                                                                                             1 GGAAGGTTGAGTCAAG 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lillie J, Xu Y, Wang Y,
                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-451856/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       WO200151628-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-MAR-2000; 29-MAR-2000; 215-MAY-2000; 2
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14-MAR-2000;
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The invention relates to human breast cancer expressed polynucleotides (AAL07544-AAL26789) and methods of assessing whether a patient is afflicted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and polynetides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.
                                                                                                                         New peptide useful as a marker for the diagnosis of breast cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 433;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 433 BP; 122 A; 69 C; 143 G; 97 T; 0 U; 2 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 15.8; DB 4;
Pred. No. 3.3e+02;
0; Mismatches 2;
(MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Breast cancer related marker, seq id 3203.
                                              Lillie J, Xu Y, Wang Y, Steinmann K;
                                                                                                                                                                              Claim 1; Page 783; 3695pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    240 GAAGGTGGAGTCAAGAATT 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2 GAAGGITGAGICAAGGAIT 20
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                                                                                             WPI; 2001-451856/48.
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200 GAAGGIGGAGICAAGAATI 218

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2000US-0218290P.
2000US-0220964P.
2000US-0224518P.
2000US-0224513P.
2000US-022513P.
2000US-025213P.
2000US-025214P.
2000US-025214P.
2000US-025268P.
2000US-025268P.
2000US-022547P.
2000US-022548P.
2000US-022548P.
2000US-022548P.
2000US-022548P.
2000US-0226681P.
2000US-0225418P.
2000US-0225418P.
2000US-0225418P.
2000US-0225418P.
2000US-0225418P.
2000US-0225418P.
                                             2000US-0216647P.
2000US-0216880P.
2000US-0217487P.
2000US-0217496P.
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2000US-0231243P.
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19-MAY-2000;
07-JUN-2000;
36-JUN-2000;
36-JUN-2000;
07-JUL-2000;
11-JUL-2000;
11-JUL-2000;
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08-SEP-2000;
08-SEP-2000;
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08-SEP-2000;
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05-SEP-2000;
06-SEP-2000;
06-SEP-2000;
08-SEP-2000;
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14-AUG-2000;
14-AUG-2000;
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14-AUG-2000;
14-AUG-2000;
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 breast cancer which is encoded by a nucleic acid molecule comprising a nucleotide sequence (91). Further disclosed is an antibody that binds to the polypeptide of the invention. The activity of the polypeptide of the invention. The activity of the polypeptide of the invention may be described as evtostatic. The antibody is useful for detecting the presence of (1) in a sample. Nucleic acid molecules of the invention are useful in the detection of breast tumours. (1) is useful as a marker for breast cancer and in breast cancer therapy. Sequences given in records ACN78851-ACN92934 represent nucleic acid markers associated such breast cancer. Note: The sequence listing does not form part of the specification but may be obtained in electronic format from the USPTO web site at seqdata.uspto.gov/sequence.thml?DocID=20030099974
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                            Novel isolated polypeptide associated with breast cancer, useful for detecting presence of polypeptide in sample, as a marker for breast
                                                                                                                                                                                                                                                  invention relates to an isolated polypeptide (I) associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human immune/haematopoietic antigen encoding cDNA SEQ ID NO:1256.
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                                                                                                                                                                                                                                                                                                                                                                                                                              79.0%; Score 15.8; DB 11; Length 459; 89.5%; Pred. No. 3.3e+02; ive 0; Mismatches 2; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 459 BP; 130 A; 73 C; 148 G; 103 T; 0 U; 5 Other;
                                                                                                                                                                                                                           Disclosure; SEQ ID NO 3203; 36pp; English
                                                                                                                               Wang Y, Steinmann K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249 GAAGGTGGAGTCAAGAATT 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 GAAGGITGAGICAAGGAIT 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAK56196 standard; cDNA; 462 BP
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2000US-0180628P.
2000US-018464P.
2000US-0189374P.
2000US-019974P.
2000US-0190076P.
                                                        18-JUL-2002; 2002US-00198846
                                                                                18-JUL-2001; 2001US-0306220P
                                                                                                       (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-2001; 2001WO-US001354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 89.5
es 17, Conservative
                                                                                                                                                     WPI; 2003-787014/74.
                                                                                                                              Lillie J, Xu Y,
           US2003099974-A1
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04-FEB-2000;
24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
18-APR-2000;
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Matches
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treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the protein. (I) proteins and polymucleotides may be used to press the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of hemantopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54550 and AAM82169 represent sequences used in the exemplification of the present invention

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Rosen CA, Barash SC, Ruben SM
                                                                                                                                                                                                                                                                                                                                                         17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249264P.
17-NOV-2000; 2000US-0249297P.
17-NOV-2000; 2000US-024929P.
17-NOV-2000; 2000US-0249300P.
17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-025193P.
05-DEC-2000; 2000US-025198P.
05-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-025198P.
06-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251866P.
08-DEC-2000; 2000US-0251869P.
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2000US-0246611P.
2000US-0249207P.
2000US-0249207P.
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2000US-0246474P.
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2000US-0246476P.
2000US-0246476P.
2000US-0246476P.
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2000US-0246532P.
2000US-0246609P.
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2000US-0254097P.
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20-OCT-2000; 2
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
08-NOV-2000;
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08-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynucleotides may be used in the prevention, diagnosis and

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

WPI; 2001-483426/52. P-PSDB; AAM83415.

Claim 1; SEQ ID NO 1256; 3071pp + Sequence Listing; English.

Gaps ö Query Match 79.0%; Score 15.8; DB 4; Length 462; Best Local Similarity 89.5%; Pred: No. 3.38+02; Matches 17; Conservative 0; Mismatches 2; Indels C 4, 2005, 08:31:32 1 GGAAGGTTGAGTCAAGGAT 19 Search completed: August Job time : 16.2551 secs 183 g ਨੇ

Seguence 462 BP; 96 A; 134 C; 137 G; 91 T; 0 U; 4 Other;

BP259697 BP259697
AQ299288 H8 2 221 A
BU21070 60416428
AZ032695 RPCI-23-3
BQ403091 GA Ed005
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BW317210 BW327210
BW317210 BW327310
BW317210 BW327310
CD823901 BW25.050F
CL622087 PWIOINIGH
CL622087 PWIOINIGH

Run on

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AJ516664 Mytilus galloprovincialis haemolymph, gills, digestive AJ516664 Mytilus galloprovincialis haemolymph, gills, digestive gland, foot, adductor muscles and mantle Mytilus galloprovincialis cDNA clone GPPD00678, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                      Mytilus galloprovincialis (Mediterranean mussel)
Mytilus galloprovincialis
Mytilus galloprovincialis
Mytilus galloprovincialis
Mytiloidea; Mytilidae; Mytilus.

1 (bases 1 to 400)
Venier, P., Pallavicini, A., De Nardi, B. and Lanfranchi, G.
Towards a catalogue of genes transcribed in multiple tissues of
Mytilus galloprovincialis
Gene 314, 29-40 (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="haemolymph, gills, digestive gland, foot, adductor muscles and mantle" /clone lib="Mytilus galloprovincialis haemolymph, gills, digestive gland, foot, adductor muscles and mantle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               90.0%; Score 18; DB 1; Length 400;
100.0%; Pred. No. 3.3e+02;
ive 0; Mismatches 0; Indels
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/organism="Mytilus galloprovincialis"
/moltype="mRNA"
/db xref="taxon:29158"
/clone="GPPD00678"
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University of Padova
University of Padova
Via Ugo Bassi 58/b, Italy, 34100, Italy
Location/Qualifiers
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                                       AZ032695
BG442803
BG442803
BB442842
BB458766
AZ70649
AW037653
CN465627
BD587296
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AJ516664.1 GI:37650241
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CC6581634 CGT18161

AN922103 AN794272

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                                                                   August 4, 2005, 04:04:35; Search time 94.3968 Seconds (without alignments) 8064.741 Million cell updates/sec
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         GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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gb_htc::*;
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xref="taxon:10090"
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Dunn, D., Aoyagi, Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Roie, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Rodentia; Sciurognathi; Muridae; Murinae; Mus. (bases 1 to 361)

Adams, D.J., Biggs, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Flumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A. Dincet Submission
Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 15A, UK. http://www.sanger.ac.uk/MICER
  CR008527

Reverse strand read from insert in 5'HPRT insertion targeting and chromosome engineering clone MHPN202111, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AZ785398 16-FEB-200
2M0049B10R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGC2M0049B10 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0049 row: B column: 10
Seg primer: CACACAGGAAACAGCTATGACC
                                                      CRO08527
CR008527.1 GI:49741518
GSS; genome survey sequence; MICER.
Mus musculus (house mouse)

    .453
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/strain="C57BL/6J"

                                                                                                                                                                                                                                                                                                                                                       1. .361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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High quality sequence stop: 453.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
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Matches 18, Conservative
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Fax: 801 585 7177
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(http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynanically sheared by repeated passage through a was hydrodynanically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pwb12 (gil 4732114 gpl AR129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent B. coli XII0-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ALLU0780 SST210069 Normalized rat brain, Bento Soares Rattus sp. cDNA clone RRRBAL8 3' end, mRNA sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (REST) Catalog & Rat
                                                     /lab host="B. Coli strain XL10-Gold, T1-resistant, F-"/clone lib="Mouse 10kb plasmid UUGCIM library"/note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone lib="Normalized rat brain, Bento Soares"
/note="Organ: brain; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI"
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1 (bases 1 to 580)
Lee,N.H., Glodek,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (REST) Catalog &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rat Jundax
Gene Index
Unpublished (1998)
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@igr.org
Seq primer: M13-21.
Seq primer: M3-21.
Seq primer: M3-21.
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Pred. No. 6.8e+02;
0; Mismatches 1; Indels (
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/mol_type="mRNA"
/db_xref="ATCC (inhost):2023775"
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                                                                                                                                                                                      Laboratory Mouse DNA Resource
clone="UUGC2M0049B10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               406 GGAAGGTTGAGGCAAGGAT 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGAAGGTTGAGTCAAGGAT 19
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RESULT 5 AG180768/c DEFINITION

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ACCESSION

JOURNAL REFERENCE AUTHORS

TITLE

TITLE JOURNAL

COMMENT

FEATURES

ORIGIN

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ACCESSION VERSION KEYWORDS

REFERENCE AUTHORS

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SM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD

clade; Panicoideae; Andropogoneae; Zea.

E 1 (bases 1 to 284)

S Bhatti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,

Rouzard, K., Fuks, G., Yu, Y., Wing, R. and Messing, J.

Sequencing of the maize genome at PGIR (2003b)

L Unpublished (2003)

L Ontact: Bhatti, A.K.

Dr.Joachim Messing's lab

The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers

University
                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 832)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZWMBBC0482F11r ZMWBBc Zea mays genomic clone ZMMBBc0482F11 3', genomic survey sequence.
                                                                                                                                                                                                                                                                                                   Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
Noiversity of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3153 row: F column: 13
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="CIT_Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in
E-Coli DH10B"
                                                                                                                                                                                           Sequence-tagged connectors: A sequence approach to mapping and
                                                                                                                                                                                                   scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 832;
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Tel: 732 445 3801
Fax: 732 445 5735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .832
/organism="Homo sapiens"
/mol type="qenomic DNA"
/db_xref="taxon:9606"
/clone="plate=3153 Col=13 Row=F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 17.4; DB 8;
Pred. No. 7.3e+02;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 832.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 GAAGCTTGAGTCAAGGATT 420
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94.7%;
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Homo sapiens (human)
Homo sapiens
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Best Local Similarity
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CC836847
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Totoki, Y., Watanabe, H. and Sakaki, Y.

Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpes@qsc.riken.go.jp, WRL:http://hgp.gsc.riken.go.jp/,
T=1:81-45-503-9111, Fax:81-45-503-9170,
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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AQ898174 GI:6354364
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                                                                                                                                                                                                                                                                 GSS 09-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
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Pan troglodytes DNA, clone: RP43-053H03.TJ, genomic survey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="genomic_DNA"
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/clone="kt43-053H03.TJ"
/sea-male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fuiiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library RPCI-43
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87.0%; Score 17.4; DB 1; Length 580; 94.7%; Pred. No. 7e+02; 1:ve 0; Mismatches 1; Indels
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/organism="Pan troglodytes"
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Pan troglodytes
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R.Site 1 : EcoRI
R.Site 2 : EcoRI.
                                                                                                                      2 GAAGGITGAGICAAGGAIT 20
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AG180768.1 GI:16710448
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                      Best Local Similarity 94.7
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                sequence.
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  Query Match
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BG721914.1 GI:14001101
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Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA sequence.
BG721914
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Wersity of Utah
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AZ380590 537 bp DNA linear GSS 02-OCT-2000 1M0136P01R Mouse 10kb plasmid UUGCIM library Mus musculus genomic clone UUGCIM0136P01 R, genomic survey sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. I. bases I to 537)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R., Tingey, A., von Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
                                                                                                     /organism="Zea mays"
/mol type="genomic DNA"
/cultivar="B7"
/cultivar="B7"
/clone="ZMMBBC0482F11"
/lab host="E. coli DH108"
/clone lib="ZMMBBC"
/clone lib="ZMMBBC"
/note="Vector: pTARBAC1.3; Site_1: BamH1; Site_2: BamH1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          //lab_host="E. Coli strain Xil0-Gold, Tl-resistant, F-" /clone lib="Mouse 10kb plasmid UUGCIM library" /note="Vector: PWD42nv; Purified genomic DNA from M.musculus C57BL/6J (male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
                                                                                                                                                                                                                                                                                                               Query Match 85.0%; Score 17; DB 9; Length 284; Best Local Similarity 100.0%; Pred. No. 1e+03; Matches 17; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0136 row. P column: 01
Seg primer: CACACAGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Mus musculus"
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Location/Qualifiers
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/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:10090"
/clone="UUGC1M0136P01"
Seg primer: SP6
Class: BAC ends
High quality sequence start: 97.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (house mouse)
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AZ380590.1 GI:10494290
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GGAAGGTTGAGTCAAGG 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AZ380590/c
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was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMAPA2 (gil-A722114[gb]AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG721914 171 bp mRNA linear EST 08-MAY-2001
602695642F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4827611 5',
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                                                                                                                                                                                                                                                                                  Gaps
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0
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                                                                                                                                                                                                                                                Query Match 85.0%; Score 17; DB 8; Length 537; Best Local Similarity 100.0%; Pred. No. 1.1e+03; Matches 17; Conservative 0; Mismatches 0; Indels
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VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

DEFINITION

CC558114

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ACCESSION

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308 bp mRNA linear EST 11-AUG-2004
AJ792516 Antirrhinum majus whole plant Antirrhinum majus cDNA clone
AJ792516
                                                 CC675901 305 bp DNA linear GSS 19-JUN-2003 OGWEH38TH ZM_0.7_1.5_KB Zea mays genomic clone ZMMBMa0558H04,
                                                                                                                                                                                                                                                                                              Eukaryopia, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Liliopsida, Poales, Poaceae, PACCAD
clade, Panicoideae, Andropogoneae, Zea.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiids; Lamiales; Plantaginaceae; Antirrhineae;
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2achgo, S., Stueber K., Saedler, H., Sommer, H. and Schwarz-Sommer, Z.
Antirrinnum EST collection
Unpublished (2003)
Contact: Schwarz-Sommer Z
Molekulare Pflanzengenetik
MPI fuer Zechtungsforschung
Carl-von-Linne Weg 10, D-50829, Germany.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 305)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citck,R.W., Numberg,A., Robbins,D. and Lakey,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4577"
/clone="zwmBwa0558H04"
/clone=lib="zm_0.7 1.5_KB"
/note="woctor: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9712 Medical Center Drive, Rockville, MD 20850, USA
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90.0%; Pred. No. 1.38+03;
tive 0; Mismatches 2; Indels

    .308
    /organism="Antirrhinum majus"

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/strain="B73"
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Antirrhinum majus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fax: 301-838-0208
Email: whitelaw@tigr.org
                                                                                                  genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .305
/organism≃"Zea
                                                                                                                                                                           CC675901.1 GI:32080599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Cathy Whitelaw
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Other_GSSs: OGWEH38TV
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Class: sheared ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 301-838-5843
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Best Local Similarity
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The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V52 4E6
Fal: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240 htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering_information.htm). This work
was undertaken as part of the International BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Seg primer: 7.
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                                                                                                                                                                                                                                                                                                 281 bp DNA linear GSS 18-JUN-2003 CH240 466N17.T7 CHORI-240 Bos taurus genomic clone CH240_466N17, genomic survey sequence.
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
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/note="Vector: pTARBACI.3; Site 1: MboI; Site_2: MboI;
Hereford bull Li Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pleter de Jong"
                                                 Gaps
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84.0%; Score 16.8; DB 9; Length 281;
Best Local Similarity 90.0%; Pred. No. 1.3e+03;
Matches 18; Conservative 0; Mismatches 2; Indels
                                                 Indels
Pred. No. 1.2e+03;
. Migmatches 0;
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/strain="breed: Hereford"
/db_xref="taxon:9913"
/clone="CH240_466N17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Bos taurus"
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             100.0%;
                                                                                                            3 AAGGITGAGICAAGGAI
                                              17; Conservative
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Bos taurus
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Actinopterygii, Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.

1 (bases I to 335)

1 (bases I to 335)

1 (bases I to 335)

Direct Submission
Submitteed (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Submitteed (13-MAR-2003) The Sanger Institute, Wellcome Trust Genome Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. B-mail enquiries: Chunquery@sanger.ac.uk Unpublished
This sequence was generated from the T7 end of BAC 125C2 125C2 is part of the Daniokey BAC Library created by R. Plasterk and N.V. Keygene. Further details:

Keygene. Further details:

Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 345)
Okazaki,Y., Furuno,M., Kasukawa,T., Adachi,J., Bono,H., Kondo,S.,
Nikaido,I., Osato,N., Saito,R., Suzuki,H., Yamanaka,I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
                                                                                                                                                                                    Gaps
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BX160484
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                                                                                                                                         Length 308;
/mol_type="mRNA"
/db_xref="taxon:4151"
/db_cfone="018_211_n02"
/tisoue_type="whole plant"
/clone_lib="Antirrhinum majus whole plant"
                                                                                                                                                                                                                                                                                                                                                                       linear
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                                                                                                                                            Score 16.8; DB 1;
Pred. No. 1.3e+03;
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/tissue type="Testis"
/note="vector pIndigoBAC-536"
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                                                                                                                                                                                    0; Mismatches
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/mol_type="genomic DNA"
/db_xref="taxon:7955"
                                                                                                                                                                                                                                                                                                                                                                         335 bp
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                                                                                                                                              Query Match
Best Local Similarity 90.0%;
Matches 18; Conservative
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Best Local Similarity 90.0°
Matches 18; Conservative
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Ridyosawa, H., Yagi, K., Tomani, Y., Mangana, W., Migomi, A.,

Enclothed, C., Oursdon, M., Schrift, M., Brade, D., Bruic, W.,

Barilous, S., Beisel, K. W., Black, J.A., Brade, D., Bruic, W.,

Barilous, S., Beisel, K. W., Bake, J.A., Brade, D., Bruic, W.,

Enchia, C., Corbani, L. B., Cousing, J., Bruic, W.,

Fletcher, C. F., Perrent, A., Fracer, K. S., Dalla, E., Dragani, T.A.,

Fletcher, C. F., Perrent, A., Fracer, K. S., Dalla, E., Dragani, T.A.,

Fletcher, C. F., Perrent, A., Fracer, K. S., Dalla, E., Dragani, T.A.,

Garibold, M., Gissi, C., Godel, B., M., Manda, E., Brangani, T.A.,

Mallat, B., Harokaw, R., Jockeon, J.J., Jards, E., Majolet, D.R.,

Mallat, B., Harokaw, R., Jockeon, J.J., Jards, E., Majolet, D.R.,

Mallat, M., Marchani, L., Warenier, E., Mallat, R., Majolet, D.R.,

Mallat, M., Schindier, C., Seed, D., Testes, G., Secole, M., Shimada, K.,

Sandalin, A., Schneider, C., Seed, D., Testes, G., Secole, M., Shimada, K.,

Mallat, M., Schindier, M., Mallat, M., Maki, K., Seed, B., Warenier, M., Marchanier, M.,

Mallat, M., Stor, K., Shiraki, T., Waki, K., Sanda, J., Akawa, R.,

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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL):

DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html
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US-VJ-49-ULD-LIL14/C
; Sequence 12174, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
    APPLICANT: VENTER, J. Craig et al.
    APPLICANT: VENTER, J. Craig et al.
    TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
    TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REPRENCE: CLOOL307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/231,768
; PRIOR FILING DATE: 2000-10-20
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 2007012
; SOFTWARE: FREESEQ for Windows Version 4.0
; SEQ ID NO 12174
LENGTH: 153642
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 15635, Application US/09949016
Patent No. 6812339
GERERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF TILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
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12738, A
131552, A
5, Appli
11892, A
12572, A
15547, A
16847, A
16320, A
                                                        1, Appli
1, Appli
13589, A
                                                     Sequence 1, Appli
Sequence 1, Appli
Sequence 13318,
Sequence 13318,
Sequence 12738,
Sequence 17157,
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence 1, Sequence
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US-09-949-016-5415
US-08-15-751
US-08-915-751
US-09-296-275-1
US-09-949-016-13589
US-09-949-016-13318
US-09-949-016-12738
US-09-949-016-12738
US-09-949-016-1275
US-09-949-016-12655
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US-09-949-016-12655
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Pred. No. 1.1e+02;
0; Mismatches 2;
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; OTHER INFORMATION: n = A,T,C or
US-09-949-016-12174
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Best Local Similarity 90.v
  NAME/KEY: misc_feature
     776.00
776.00
776.00
776.00
776.00
776.00
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US-09-949-016-15635/c
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ORGANISM: Human
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NAME/KEY: allele
LOCATION: 439
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                                                                                                                                                                                                                                                        84.0%; Score 16.8; DB 4; Length 153643; 90.0%; Pred. No. 1.1e+02; tive 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 4; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1755, Application US/09621976

patent No. 6639063

geneRal INPORMATION:
APPLICANT: UNDORATION:
APPLICANT: Jobert, S.
FILE REFERENCE: GENSET. 054PR2

CURRENT APPLICANTON: BSTS and Encoded Human Proteins.
FILE REFERENCE: GENSET. 054PR2

CURRENT FILING DATE: 2000-07-21

NUMBER OF SEQ ID NOS: 19335

SOFTWARE: Patent.pm

SEQ ID NO 17595

LENGTH: 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 94.4%; Pred. No. 98;
Matches 17; Conservative 0; Mismatches
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 15635
LENGTH: 153643
                                                                                                                                                                                                                                                                                                                                         117870 GGAATGTTGAGTCAAGGTTT 117851
                                                                                                                                                                              ; NAME/KEY: misc_feature
; LCCATION: (1)...(153643)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15635
                                                                                                                                                                                                                                                                                                                        1 GGAAGGTTGAGTCAAGGATT 20
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                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 90.04
Matches 18; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-621-976-17595
                                                                                                                                        TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-621-976-17595
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US-09-641-638-552
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RESULT 5

USA-10-170-097-552

Sequence 552, Application US/10170097

Sequence 552, Application US/10170097

Sequence 100. 6794143

Sequence 100. 6794143

Sequence 100. 6794143

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Chemakov, Ilya

APPLICANT: Chemakov, Ilya

APPLICANT: Chemakov, Ilya

APPLICANT: Chemakov, Ilya

APPLICANT: Gonen, Annick

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

FILER REFERENCE: GEN-T114XC201

CURRENT APPLICATION NUMBER: US 09/641,638

PRIOR FILING DATE: 2000-08-16

PRIOR PILING DATE: 2000-08-16

PRIOR PILING DATE: 2000-08-16

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-02-12

PRIOR APPLICATION NUMBER: US 60/119,917

PRIOR APPLICATION NUMBER: US 60/119,917

PRIOR PILING DATE: 1999-02-12

PRIOR PILING DATE: 1999-02-12

PRIOR PILING DATE: 1999-02-12

PRIOR PILING DATE: 1999-02-12

PRIOR PILING DATE: 1999-03-33

PRIOR PILING DATE: 1999-03-33

PRIOR PILING DATE: 1999-03-33

PRIOR PILING DATE: 1999-03-13

PRIOR PILING DATE: 1999-03-13

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JOCATION: 439

JOCATION: 439

O'THER INPORMATION: 12-65-98: polymorphic base C or T

NAME/KEY: misc_binding

LOCATION: 419.-438

O'THER INFORMATION: 12-65-98.misl, potential

NAME/KEY: misc_binding

LOCATION: 440..459

O'THER INFORMATION: 12-65-98.mis2, potential complement

NAME/KEY: primer_bind

LOCATION: 342..360

O'THER INFORMATION: upstream amplification primer

NAME/KEY: misc_bind

LOCATION: 777..79

O'THER INFORMATION: downstream amplification primer

NAME/KEY: misc_binding

LOCATION: 427..451

O'THER INFORMATION: 12-65-98 potential probe

US-09-641-638-552
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82.0%; Score 16.4; DB 3; Length 939;
Best Local Similarity 94.4%; Pred. No. 1e+02;
Matches 17; Conservative 0; Mismatches 1; Indels C
    PRIOR APPLICATION NUMBER: US 09/275,267
PRIOR FILING DATE: 1999-03-23
PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
SEQ ID NO 552
LENGTH: 939
APPLICATION NUMBER: US 09/275,267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 GGAAGGTTGAGTCAAGCA 565
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                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo Sapiens
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APPLICANT: Zianghe YAN, Karen A. KETCHUM, Valentina DIFRANCESCO, Ellen M. BEASLEY TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS, TITLE OF INVENTION: USES THEREOF FILE SENCODING HUMAN PROTEASE PROTEINS, AND TITLE OF INVENTION: USES THEREOF FILE REFERENCE: CLOUISICAL CURRENT APPLICATION NUMBER: US/09/797,906 CURRENT APPLICATION NUMBER: US/09/797,906
                                   APPLICANT: VENTER, J. Craig et al.

ITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITLLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

ITLLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLOOL307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT APPLICATION NUMBER: US/09/941,755

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-30

PRIOR FILING DATE: 2000-10-30

PRIOR PLING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FREUSEQ for Windows Version 4.0

FENDING DATE: 2000-10-03

FENDER OF SEQ ID NOS: 207012

SOFTWARE: FREUSEQ for Windows Version 4.0
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Pred. No. 2e+02;
0; Mismatches 1; Indels 0;
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Pred. No. 2.6e+02;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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US-09-949-016-16549
Sequence 16549, Application US/09949016
Parent No. 6812339
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(670690)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: (1)...(84495)
CTHER INFORMATION: n = A,T,C or G
US-09-797-906-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/09797906 Patent No. 6329188
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Best Local Similarity 100.0%; Pi
Matches 16; Conservative 0;
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-797-906-3/c
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SEQ ID NO 3
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Pred. No. 2e+02;
0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                        NAME/KEY: primer bind
LOCATION: 777..797
OTHER INFORMATION: downstream amplification primer, complement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 82.0%; Score 16.4; DB 4; Length 939; Best Local Similarity 94.4%; Pred. No. 1e+02; Matches 17; Conservative 0; Mismatches 1; Indels
                                                                                                                               LOCATION: 440.7459
OTHER INFORMATION: 12-65-98.mis2, potential complement
FEATURE:
OTHER INFORMATION: 12-65-98 : polymorphic base C
                                                                                                                                                                                                       NAME/KEY: primer bind
LOCATION: 342..360
OTHER INFORMATION: upstream amplification primer
                                                                                                                                                                                                                                                                                                                                                                                                  COCATION: 427.751
COTHER INFORMATION: 12-65-98 potential probe US-10-170-097-552
                                                             LOCATION: 419.7438
OTHER INFORMATION: 12-65-98.mis1, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION: (1)....(670689)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12505
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Best Local Similarity 94.4%;
Matches 17; Conservative
                                                                                                  FEATURE:
NAME/KEY: misc_binding
                                         NAME/KEY: misc_binding
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US-09-949-016-14207
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LENGTH: 670689
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PRIOR APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SEQ ID NO 15821
LENGTH: 50563
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; LOCATION: (1)...(112132)
; OTHER INFORMATION: n = A,T,C or G
US-09-741-150-3
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Best Local Similarity 89.5*
Matches 17; Conservative
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ORGANISM: Human
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CRGANISM: Human
US-09-949-016-15821
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US-10-160-187-3/c
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US-09-741-150-3/c
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TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REPERENCE: CLOO1307

CURRENT PILING DATE: 2000-04-14

PRIOR PLILING DATE: 2000-10-20

PRIOR PLILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHAND THE PRIOR PLILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOUTHAND THE PRIOR PLILING DATE: 2000-09-08

LENGTH: 47555
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Sequence 1581, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
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Pred. No. 3.1e+02;
0; Mismatches 2;
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Best Local Similarity 89.57
                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity 89.5
Matches 17; Conservative
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CRGANISM: Human
US-09-949-016-12598
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US-09-949-016-15821
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Sequence 3, Application US/10160187

Sequence 3, Application US/10160187

Patent No. 620607

GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al.
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PROTEINS,
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CLOO0968D1V

FILE REPERENCE: CLOO0968D1V

CURRENT PILING DATE: 2002-06-04

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22

PRIOR FILING DATE: 2000-11-22
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ENCODING HUMAN PROTEASE PROTEINS, AND
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Score 15.8; DB 4; Length 50563;
Pred. No. 3.1e+02;
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                                                              Indels
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Pst Local Similarity 89.5%; Pred. No. 3.4e+02;
Matches 17; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09741150

Patent No. 643669

GENERAL INFORMATION:
APPLICANT: GUEGLER, Karl et al
TITLE OF INVENTION: ISOLATED HUMAN PROTEASE PRO
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENC
TITLE OF INVENTION: UNCLEIC ACID MOLECULES ENC
TITLE OF INVENTION UNMBER: US/09/741,150
CURRENT FILING DATE: 2000-12-21

NUMBER OF SEQ ID NOS: 4
SEQ ID NO 3
LENGTHAN 112132
                                                           0; Mismatches
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FACELL NO. 9012239;
FACELL NO. 9012230;
FACELL NO. 9012230;
FACELL NO. 9012230;
FACELL OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
FRIOR APPLICATION NUMBER: 60/241,755
FRIOR FILING DATE: 2000-10-20
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-10-03
FRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOUTHARD FACES OF Windows Version 4.0
SEQ ID NO 15:094
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Bacent No. 6812339
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
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                                                                                                                                                                                                                                                                                          Query Match 79.0%; Score 15.8; DB 4; Length 112132; Best Local Similarity 89.5%; Pred. No. 3.46+02; Matches 17; Conservative 0; Mismatches 2; Indels 0;
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79.0%; Score 15.8; DB 4; Length 209210;
Best Local Similarity 89.5%; Pred. No. 3.5e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0;
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 3
LENGTH: 112132
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                                                                                                                                                                   NAME/KEY: misc_feature; LCCATION: (1)...(112132); CTHER INFORMATION: n = A,T,C or GUS-10-160-187-3
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LOCATION: (1)...(209210)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                              2 GAAGGTTGAGTCAAGGATT 20
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                                                                                                                     ORGANISM: Homo sapien
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US-09-949-016-15094
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ORGANISM: Human
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US-09-949-016-12465
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                                                                                                TYPE: DNA
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USO8_NEW_PUB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

11: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

12: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

13: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

14: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

15: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

16: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

17: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

18: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

19: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

21: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

23: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

24: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

25: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

26: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

27: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

28: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

29: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

22: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

23: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

24: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

25: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

26: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

27: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

28: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

29: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

20: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

20: /cgn2_6/ptod
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                        OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-899-276C-8
20
1 ggaaggttgagtcaaggatt 20
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                          Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 10, Appli Sequence 10, Appli Sequence 1, Appli Sequence 4, Appli Sequence 816, App Sequence 1623, App
SUMMARIES	20 9 US-09-899-276-8 21 9 US-09-899-276-10 000 9 US-09-899-276-1 93 19 US-10-685-705-4 72 21 US-10-950-009-816 117 19 US-10-437-963-16253 39 17 US-10-170-097-552
DB	9 9 19 17
, i	1176
* Query Match	20 100.0 17 85.0 17 85.0 17 85.0 .8 84.0 .8 84.0
Score	20 20 17 17 16.8 16.8
Result No.	14064866

2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 2552, Ag 255	Sequence 56906, A Sequence 7, Appli Sequence 287, App Sequence 287, App Sequence 3, Appli Sequence 17642, A Sequence 17642, A Sequence 17590, A Sequence 17590, A Sequence 17590, A Sequence 17590, A Sequence 12, Appli Sequence 5, Appli
10 - 926 - 684 - 55 10 - 741 - 601 - 95 10 - 741 - 601 - 95 10 - 741 - 600 - 21 10 - 424 - 599 - 13 10 - 622 - 135 - 68 10 - 632 - 36 10 - 632 - 68 10 - 632 - 68 10 - 632 - 68 10 - 632 - 68 10 - 632 - 68 10 - 632 - 68 10 - 632 - 68 10 - 632 - 68 10 - 632 - 68 10 - 632 - 68 10 - 632 - 12 10 - 135 - 135 - 13 10 - 135 - 135 - 13 10 - 135 - 135 - 13 10 - 135 - 135 - 13 10 - 135 - 135 - 13 10 - 135 - 135 - 13 10 - 135 - 135 - 13 10 - 135 - 135 - 13 10 - 135 - 135 - 13 10 - 135 - 135 - 13 10 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 135 - 1	US-10-437-963-56906 US-10-481-582-7 US-09-997-722-250 US-10-322-281-287 US-09-741-150-3 US-10-741-601-3 US-10-741-601-5641 US-10-741-600-17642 US-10-741-600-17590 US-10-317-883A-12 US-09-844-653-5
10001111111111111111111111111111111111	121 121 121 131 101 101
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8 0 11 11 11 11 11 11 11 10 0 8 8 11 10 11 11 11 11 11 11 11 11 11 11 11	4 5 5 6 6 7 4 4 4 4 4 4 4 5 6 6 6 7 8 8 6 9 7 8 8 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9
0 0000 00000 0	0 0000

## ALIGNMENTS

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US-09-899-276-8

Sequence 8, Application US/09899276

Sequence 8, Application US/09899276

Sequence 8, Application US/09899276

Sequence 8, Application US/09899276

Sequence 8, Application US/09899276

GENERAL INFORMATION:

APPLICANT: Rosi, Frank

APPLICANT: Coy, Johannes

APPLICANT: Coy, Johannes

APPLICANT: Poultus, Haid

APPLICANT: Parzelt, Andemarie

APPLICANT: Parzelt, Andrea

FILE REFERENCE: 01267-023

CURRENT APPLICATION NUMBER: US/09/899,276

CURRENT APPLICATION NUMBER: US/09/899,276

CURRENT FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-07-06

PRIOR FILING DATE: 2000-07-06

MUMBER OF SEQ ID NOS: 12

SEQ ID NO 8

LENGTH: 20

TYPE: DAM

ORGANISM: Artificial Sequence

FEATURE:

FEATURE:

CHER INFORMATION: Part of 3'-DHSR
```

100.0%; Score 20; DB 9; Length 20;

Query Match

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APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Kentucky Research Foundation
APPLICANT: University of Methods And Animal Model For Analyzing Age-Related Macular
TITLE OF INVENTION: Degeneration
FITLE OF INVENTION: Degeneration
FILE REPERBINCE: 050229-0415
CURRENT APPLICATION NUMBER: US/10/685,705
CURRENT APPLICATION NUMBER: 60/422,096
PRIOR PILING DATE: 2002-10-30
SOFTWARE: Patentin version 3.2
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-950-009-816/C

Sequence 816, Application US/10950009

publication No. US20050069934A1

GENERAL INFORMATION:
APPLICANT: BERKA, Randy
APPLICANT: BERKA, Randy
TITLE OF INVENTION: Methods For Monitoring Gene Expression
FILE REFERENCE: 10541-200-US
CURRENT PILING DATE: 2004-09-24
PRIOR APPLICATION NUMBER: 60/506,140
PRIOR PILING DATE: 2004-09-24

PRIOR PILING DATE: 2004-09-24

PRIOR PILING DATE: 2004-09-25

NUMBER OF SEQ ID NOS: 1190

SOFTWARE: PASKSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 11793;
Query Match 85.0%; Score 17; DB 9; Length 600; Best Local Similarity 100.0%; Pred. No. 1.3e+02; Matches 17; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 1.6
Matches 17; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                  Sequence 4, Application US/10685705
Publication No. US20040177387A1
GENERAL INFORMATION:
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                                                                                                     1 GGAAGGTTGAGTCAAGG 17
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ORGANISM: Trichoderma reesei
US-10-950-009-816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 90.0°
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 6
US-10-437-963-16253
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GENERAL INCORDING.

APPLICANT: Socto, Ubaldo

APPLICANT: Soto, Ubaldo

APPLICANT: Coy, Johannes

APPLICANT: Coy, Johannes

APPLICANT: Coy, Johannes

APPLICANT: Delius, Haiomarie

APPLICANT: Delius, Haiomarie

APPLICANT: Delius, Harald

APPLICANT: Patzelt, Andrea

TITLE OF INVENTION: No. US20020106355Alel Regulatory Sequences of the MCP-1 Gene

PILE REFERENCE: 012627-023

CURRENT APPLICATION NUMBER: US/09/899,276

CURRENT APPLICATION NUMBER: US/09/899,276

CURRENT APPLICATION NUMBER: BP 00 114 560.6

PRIOR FILING DATE: 2000-07-06

NUMBER OF SEQ ID NOS: 12

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO.
                                                                                                                                                                                                                                                                                                                      APPLICANT: Rosl, Frank
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Ubaldo
APPLICANT: Soto, Delius, Hajo
APPLICANT: Finzer, Annemarie
APPLICANT: Pustek, Annemarie
APPLICANT: Pustek, Annemarie
APPLICANT: Patzelt, Andrea
TITLE OF INVENTION: No. US20020106355Alel Regulatory Sequences of the MCP-1 Gene
TITLE REFERENCE: 012627-023
CURRENT APPLICATION NUMBER: US/09/899,276
CURRENT APPLICATION NUMBER: US 00 114 560.6
PRIOR APPLICATION NUMBER: EP 00 114 560.6
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 12
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 120
LENGTH: 21
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                                          0; Indels
                      Pred. No. 2.7;
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            100.0%; Prec. ...
                                                                                                                                                                                                                                                     Sequence 10, Application US/09899276
Patent No. US20020106355A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Application US/09899276 Patent No. US20020106355A1
                                                                                         1 GGAAGGTTGAGTCAAGGATT 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Artificial Sequence
                      Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
US-09-899-276-1
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                                                                                                                                                                                                              RESULT 2
US-09-899-276-10
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US-10-926-684-552

Sequence 52, Application US/10926684

Publication No. US20050014190A1

SEGNERAL INFORMATION:
APPLICANT: Blumenfeld, Marta
APPLICANT: Bougueleret, Lydie
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Chumakov, Ilya
APPLICANT: Cohen, Annick
ITILE OF INVENTION: CARRYING
FILE REFERENCE: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM
FILE REFERENCE: GENES INVOLVED IN ARACHIDONIC ACID
FRIOR FILING DATE: 2002-06-10
FRIOR FILING DATE: 2000-08-16
FRIOR FILING DATE: 2000-08-16
FRIOR APPLICATION NUMBER: US 60/133,200
FRIOR APPLICATION NUMBER: US 60/133,200
FRIOR FILING DATE: 1999-03-13
FRIOR FILING DATE: 1999-03-13
FRIOR FILING DATE: 1999-03-12
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
FRIOR FILING DATE: 1999-02-12
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FRIOR FILING DATE: 1999-03-13
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                                                                                                                                                                                                                                          NAME/KEY: primer bind
LOCATION: 777..757
OTHER INFORMATION: downstream amplification primer, complement
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                                                           INFORMATION: 12-65-98.mis2, potential complement
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LOCATION: 440.7459
OTHER INFORMATION: 12-65-98.mis2, potential complement
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OTHER INFORMATION: 12-65-98 : polymorphic base C or T
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16.4; DB 17;
Pred. No. 2.7e+02;
                                                                                                                   NAME/KEY: primer_bind
LOCATION: 342..360
OTHER INFORMATION: upstream amplification primer
FEATURE:
                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY: misc_binding
; LOCATION: 427..451
; OTHER INFORMATION: 12-65-98 potential probe
US-10-170-097-552
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
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LOCATION: 419..438
OTHER INFORMATION: 12-65-98.misl, potential
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    548 GGAAGGTTGAGTCAAGCA 565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 94.4%;
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
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                                                                        APPLICANT: LA ROVALION:
APPLICANT: LA ROVALIC, David K.
APPLICANT: Show, Yihua
APPLICANT: Show, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Brown Sarbazuk, Brad
APPLICANT: Brown Sarbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REPERENCE: 38-21(5321)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT APPLICATION NUMBER: US/10/437,963
KUNMER OF SEQ ID NOS: 204966
SEQ ID NO 16253
LENGTH: 1817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 552, Application US/10170097

Publication No. US20030228582A1

GENERAL INFORMATION:

APPLICANT: Blumenfeld, Marta

APPLICANT: Blumenfeld, Marta

APPLICANT: Cohen, Annick

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

FILE REFERENCE: GEN-T114XC2D1

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

FILE REFERENCE: GEN-T114XC2D1

CURRENT APPLICATION NUMBER: US 09/641,638

PRIOR APPLICATION NUMBER: US 09/502,330

PRIOR APPLICATION NUMBER: US 09/502,330

PRIOR PILING DATE: 1090-02-11

PRIOR PILING DATE: 1999-05-07

PRIOR PILING DATE: 1999-05-07

PRIOR FILING DATE: 1999-02-12

PRIOR FILING DATE: 1999-02-12

NUMBER OF SEQ ID NOS: 1304

SEQ ID NO 552

LENGTH: 939

LENGTH: 939

LENGTH: 939
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 84.0%; Score 16.8; DB 19; Best Local Similarity 90.0%; Pred. No. 1.8e+02; Matches 18; Conservative 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Clone ID: PAT_MRT4530_22019C.1
US-10-437-963-16253
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LOCATION: 419..438
OTHER INFORMATION: 12-65-98.misl, potential
FEATURE:
Sequence 16253, Application US/10437963
Publication No. US20040123343A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 GGACGTGGAGTCAAGGATT 148
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ORGANISM: Oryza gativa
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LOCATION: 439
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| US-10-741-601-13271/c
| Sequence 13271, Application US/10741601
| Publication No. US20040166519A1
| Publication No. US20040166519A1
| Publication No. US20040166519A1
| TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
| TITLE OF INVENTION: GENETIC POLYMORPHISMS OF DETECTION AND USES THEREOF
| TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
| FILE REFERENCE: CL001500
| CURRENT PAPLICATION NUMBER: US/10/741,601
| CURRENT FILING DATE: 2003-12-22
| NUMBER OF SEQ ID NOS: 26415
| SEQ ID NO 13271
| LENGTH: 201
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Publication No. US20040166519A1

GENERAL INFORMATION:

TUTLE OF INVENTION: GENERAL

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: UNDERS. US/10/741,601

CURRENT APPLICATION NUMBER: US/10/741,601

CURRENT FILING DATE: 2003-12-22

NUMBER OF SEQ ID NOS: 26415

SOFTWARE: PESELSEQ for Windows Version 4.0

LENGTH: 201
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                                           FEATURE:
NAME/KEY: primer bind
LOCATION: 777..797
CHER INFORMATION: downstream amplification primer, complement
FEATURE:
NAME/KEY: misc_binding
LOCATION: 427..451
COTHER INFORMATION: 12-65-98 potential probe
US-10-926-684-552
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82.0%; Score 16.4; DB 21; Length 939;

Best Local Similarity 94.4%; Pred. No. 2.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 79.0%; Score 15.8; DB 19; Best Local Similarity 89.5%; Pred. No. 4.7e+02; Matches 17; Conservative 0; Mismatches 2;
LOCATION: 342..360
OTHER INFORMATION: upstream amplification primer
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                                                                                                                                                                                                                                                                                                                                                                                                                     1 GGAAGGTTGAGTCAAGGA 18
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; ORGANISM: Homo sapiens
US-10-741-601-13271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
CORGANISM: Homo sapiens
US-10-741-601-9597
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US-10-741-601-9597
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2 GAAGGTTGAGTCAAGGATT 20

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Sequence 130815, Application US/10424599

Publication No. US20040031072A1

GENERAL INFORMATION

APPLICANT: La Rosa Thomas J

APPLICANT: Zhou Yihua

APPLICANT: Cao Yongwei

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53223)B

CURRENT APPLICATION NUMBER: US/10/424,599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Segurne 31551, Application US/10741600
Sequence 31551, Application US/10741600
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: WYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE REPERENCE: GL001499
FULL REPERENCE: G.001499
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 31551
LENGTH: 201
                                                                                                                   APPLICATION OF US205026169A1
Sequence 23956, Application US/10741600
Sequence 23956, Application No. US20050026169A1
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele et al.
TITLE OF INVENTION:
TITLE OF INVENTION: MYCOARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
TITLE APPLICATION NUMBER: US/10/741,600
CURRENT APPLICATION NUMBER: US/10/741,600
CURRENT FILING DATE: 2003-12-22
NUMBER OF SEQ ID NOS: 73997
SEQ ID NO 23956
LENGTH: 201
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89.5%; Pred. No. 4.7e+02;
tive 0; Mismatches 2; Indels 0;
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Pred. No. 4.7e+02;
0; Mismatches 2;
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Best Local Similarity 89.5%;
Matches 17; Conservative (
64 GAAGGATGAGTCATGGATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17; Conservative
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US-10-741-600-31551
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US-10-741-600-23956
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Best Local Similarity
Matches 17; Conserv
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US-10-741-600-31551/c
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Search completed: August
Job time: 37.6761 secs
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Sequence 23154, Application US/10425115
Sequence 23154, Application US/20040214272A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Labou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Yihua
APPLICANT: Chou, Youla
APPLICANT: Chou, Yihua
APPLICANT: Chou, Youla
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APPLICANT: Chou, Youla
APPLICANT: Shou, Youla
APPLICANT: Shou, Youla
APPLICANT: Shou, Youla
APPLICANT: 38-21 (5)2223 B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 23154
LENGTH: 367
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Sequence 84482

Publication No. US20040214272A1

Publication No. US20040214272A1

Publication No. US20040214272A1

SEGNERAL INFORMATION:

APPLICANT: La Rocal Thomas J.

APPLICANT: La Novalic, David K.

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(51222)8

FULL REFERENCE: 38-21(51222)8

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 84482

LENGTH: 394
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                                                                                                                                                                                                                                                Length 366;
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89.5%; Pred. No. 5e+02;
tive 0; Mismatches 2;
                                                                                                                                                                      ; OTHER INFORMATION: Clone ID: PAT_MRT3847_89133C.1
US-10-424-599-130815
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                                                                                                                                                                                                                                                                                                                                                                                      108 GGAAGGTAGAGTTAAGGAT 90
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CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 285684
SEQ ID NO 130815
LENGTH: 366
TYPE: DNA
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Matches 17; Conservative
                                                                                                                    ORGANISM: Glycine max FEATURE:
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ORGANISM: Zea mays
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 14
US-10-425-115-23154/c
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CQ724136 Sequence
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BC009716 Homo sapi
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/note="MAP TO AC005549.1~EXPRESSED IN HELA, SIGNAL = 2.1"
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human hela cells or other human cervical epithelialcells
Patent: WO 0157278-A 5501 09-AUG-2001;
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68.2%; Pred. No. 1.7e-24;
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(c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/mol_type="unassigned DNA"

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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human bone marrow
Patent: WO 0157276-A 5703 09-AUG-2001;
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/db_xref="taxon:9606"
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- 2.4"
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human placenta
Patent: WO 0157272-A 5739 09-AUG-2001;
Acomica, Inc. (US)
Location/Qualifiers
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96.9%; Score 157; DB 6; Length 360;
Best Local Similarity 68.2%; Pred. No. 1.7e-24;
Matches 107; Conservative 50; Mismatches 0; Indels
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96.9%; Score 157; DB 6; Length 360;
Best Local Similarity 68.2%; Pred. No. 1.7e-24;
Matches 107; Conservative 50; Mismatches 0; Indels
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5739 from Patent WO0157272.
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/organism="Homo sapiens"
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Location/Qualifiers
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CQ096880/c
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/organism="Homo sapiens"
/mol type="unassigned DNA"
/db xref="taxon:9606"
/note="MAP TO AC005549.1-EXPRESSED IN HEART, SIGNAL = 2.6"
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HUMAN GENOME-DERIVED SINGLE EXON NUCLBIC ACID PROBES USEFUL FOR MANALYSIS OF GENE EXPRESSION IN HUMAN ADULT LIVER<130> PB 0004 WO 3<150> US 60/180,312<151> Of February 2000 (04.02.00)<150> US 60/180,312<151> Of February 2000 (26.05.00)<150> US 60/207,456<151> 26 May 2000 (26.05.00)<150> US 09/632,366<151> 03
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Human genome-derived single exon nucleic acid probes useful for
analysis of gene expression in human lung
Patent: WO 01860003-A 5889 15-NOV-2001;
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Human genome-derived single exon nucleic acid probes useful
analysis of gene expression in human brain
Patent: WO 0157275-A 5534 09-AUG-2001;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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68.2%; Pred. No. 1.7e-24;
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68.2%; Pred. No. 1.7e-24;
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Sequence 5534 from Patent WO0157275.
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/organism="Homo sapiens"
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CQ294784.1 GI:41255361
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Best Local Similarity 68.2%
Matches 107; Conservative
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Matches 107; Conservative
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/note="MAP TO AC005549.1~EXPRESSED IN ADULT LIVER, SIGNAL
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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= 3.7"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
August 2000 (03.08.00)<150> GB 24263.6<151> 03 October 2000 (03.00 to 150> US 60/236, 359<151> 27 September 2000 (27.09.00)<150> US 60/236, 369<151> 21 September 2000 (27.09.00)<150> US 60/234, 687<151> 21 September 2000 (21.09.00)<150> US 09/608, 408<151> 30 June 2000 (30.06.00)<170> Molecular Dynamics Sequence Listing Engine Patent: WO 0157273-A 5816 09-AUG-2001; Aeomica, Inc. (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Penn, S.G., Hanzel, D.K., Chen, W. and Rank, D.R.
Human genome-derived single exon nucleic acid probes useful for analysis of gene expression in human fetal liver
Patent: WO 015/2277-A 5805 09-AUG-2001;
Aeomica, Inc. (US)
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ilarity 68.2%; Pred. No. 1.7e-24;
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Human JE gene encoding a monocyte secretory protein, exon 3.
M28225 M26035
M28225.1 GI:339005
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 478)
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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               CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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Mol. Cell. Biol. 9 (11), 4687-4695 (1989)
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Sequence 21 from Patent WO02097127.
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join (M28223.1:669. .675, M28224.1:1. .118,1. .103)
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Rollins, B.J., Stier, P., Ernst, T. and Wong, G.G.
Unpublished (1989)

Original source text: Human lung fibroblast W138 cell line, DNA,
clones hJE-34 and lambda-hJE-7.

[2] sites for [1]

Draft entry and computer readable sequence for [1] kindly provided
by B.J.Rollins 17-ULL-1989.

Location/Qualifiers
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                   /organism="Homo mapiens"
/organism="genomic DNA"
/mol_type="genomic DNA"
/db zef="taxon:9606"
/cell_line="W138"
/cell_type="fibroblast"
/issue_type="lung" ...675,M28224.1:1. ..118,1. .478)
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                                                                                                                                                                                                                                                                                                                                                                              gene="JE"
|oin(M28223.1:600. .675,M28224.1:1. .118,1.
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Methods for assessing and treating leukemia
Patent: WO 03038129-A 97 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
Location/Qualifiers
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    .482
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/mol_type="unassigned DNA"

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Sequence 97 from Patent WO03038129.
AX774781
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/gene="JE"
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PAT 08-OCT-2004
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Lyamichev, V., Skrzpczynski, Z., Allawi, H.T., Wayland, S.R., Takova, T. and Neri, B.P.
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Charge tags and separation of nucleic acid molecules
Patent: W0 02063030-A 72 IS-AUG-2002;
THIRD WAYE TECHNOLOGIES, INC. (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 254
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96.9%; Score 157; DB 6; Length 64
Best Local Similarity 68.2%; Pred. No. 1.9e-24;
Matches 107; Conservative 50; Mismatches 0; Indels
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                       ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 351
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                                         126 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT
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Sequence 72 from patent US 6780982.
AR567996
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                                                                                                                                                                                            AR567996.1 GI:53986227
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synthetic construct
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Matches 107; Conservative
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AR567996
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AX698741
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VQRLASYRRITSSKCPKEAVIFKTIVAKEICADPKQKWVQDSMDHLDKQTQTPKT"
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Rollins, B.J., Stier, P., Ernst, T. and Wong, G.G.

The human homolog of the JE gene encodes a monocyte secretory protein.
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join[M30816.1:600. .675, M31625.1:6. .123,6. .111)
/note="monocyte secretory protein"
/codon_start=1
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                                                  Length 482;
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M31626
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Best Local Similarity 68.2%; Pred. No. 1.8e-24;
Matches 107; Conservative 50; Mismatches 0; Indels
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                                                                                                                                                                                                                                                           /note="monocyte secretory protein"
                                                  Query Match 96.9%; Score 157; DB 6; L
Best Local Similarity 68.2%; Pred. No. 1.8e-24;
Matches 107; Conservative 50; Mismatches 0;
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90097880
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/note="MSP mRNA and introns"
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Unknown number of bp after segment 2.
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/db xref="taxon:9606"
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/note="MSP, intron B"
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Location/Qualifiers
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3 of 3
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Homo sapiens
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1 (bases 1 to 661)
Horwitz, K.B. and Richer, J.
Progesterone receptor-regulated gene expression and methods related thereto
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                                                                                                                                                                                    linear PAT 08-OCT-2004
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                           1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 60
195 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 254
                                             255 TTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACTTGAACACTCCACA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
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96.9%; Score 157; DB 6; Length 661;
Best Local Similarity 68.2%; Pred. No. 1.9e-24;
Matches 107; Conservative 50; Mismatches 0; Indels
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                                                                                                                                                                                         DNA
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Location/Qualifiers
1. .61
/organism="unknown"
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Sequence 104 from patent US 6750015.
ARS59337
ARS59337.1 GI:53968753
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AR55937
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162
1 cttcaagaccattgtggcca.....nnnnnnnnnnnntgatca 162
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                             OM nucleic - nucleic search, using sw model
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33. geneseqn2000s:*
43. geneseqn2001as:*
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65. geneseqn2001bs:*
66. geneseqn2001as:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aai15568 Probe #55	Aba57500 Human foe	Aai37053 Probe #57	Aba26988 Probe #54	Aak31146 Human bon	Aak05543 Human bra	Abs30826 Human liv	Abs05898 Human gen	Abv96715 Human pan	Abv97697 Human pan	Acc46770 Human COP	Adn95619 Human BEC	Adp13526 Renal cel	Ade84878 Farnesyl	Abs68800 Human mon	Aaa74882 Human che	Aag85370 Chemoattr	Aax80631 Monocyte	Aad58817 Human mon	Add18494 Human pro
SUMMARIES	ΩI	AA115568	ABA57500	AAI37053	ABA26988	AAK31146	AAK05543	ABS30826	ABS05898	ABV96715	ABV97697	) ACC46770.	L ADN95619	2 ADP13526	) ADE84878	ABS68800	AAA74882	AAQ85370	AAX80631	) AAD58817	) ADD18494
	Ouery Match Length DB	360 4	360 4	360 4	360 4	360 4	360 4	360 4	360 6	473 6	475 6	478 1(	478 13	478 12	482 1(	647 6	661 3	725 2	725 2	725 10	725 1(
dip.	Ouery Match I	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	96.9	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96	6.96
	Score	157	157	157	157	157	157	157	157	157	157	157	157	157	157	157	157	157	157	157	157
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at ftp.wipo.int/pub/published_pct_sequences

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The invention relates to a single exon nucleic acid probe for measuring human gene expression in a sample derived from human foetal liver. The single exon nucleic acid probes may be used for predicting measuring and displaying gene expression in samples derived from human fetal liver. The present sequence is a single exon nucleic acid probe of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n genome-derived single exon nucleic acid probes useful for analyzing expression in human fetal liver.
                                                                                                                                                                                                                                                                        foetal liver; gene expression; single exon nucleic acid probe; ss.
                                                                                                                                                                                                                  9
microarray, which can be used for measuring human gene expression in a sample derived from human cervical epithelial cells. By measuring gene expression, the probes are therefore useful in grading and/or staging of diseases of the cervix, notably cervical cancer. Note: The sequence for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                       CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCCAAGCAGAAGTGGGTTCAGGA
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                                                                                                                                                      DB 4; Length 360;
                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      foetal liver single exon nucleic acid probe #5805
                                                                                                                      Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                       NNINNINNINNINNINNINNINNINNINNINNINNIN 157
                                                                                                                                                                                                                                                                                                                                                          ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 202
                                                                                                                                                                                   0;
                                                                                                                                                      96.9%; Score 157; DB 4 68.2%; Pred. No. 0.73; iive 50; Mismatches
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; 2000US-0207456P.
; 2000US-00608408.
; 2000US-0234687P.
; 2000US-0234687P.
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                                                                                                                                                          Query Match
Best Local Similarity 68.2
Matches 107; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-483447/52
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30-JUN-2000; 2
03-AUG-2000; 2
21-SEP-2000; 2
27-SEP-2000; 2
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                                                                                                                   299
                                                                                                                                           298 TICCAIGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACTTGAACACTCCACT 239
                                                                                                              1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                            Length 360;
                                                                                                                                                                                                                                                                                                                                                                                       Probe; microarray; human; placenta; antenatal diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                 Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                               ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 202
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                                         96.9%; Score 157; DB 4;
68.2%; Pred. No. 0.73;
iive 50; Mismatches 0.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression in human placenta.
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30-JUN-2000; 2000US-00608408.
03-AUG-2000; 2000US-00632366.
27-SEP-2000; 2000US-0234587P.
27-SEP-2000; 2000US-0234559P.
04-OCT-2000; 2000GB-00024263.
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ID AAI37053 standard; DNA; 360
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                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hanzel DK,
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Matches 107; Conserv
                                               Query Match
Best Local Similarity
Matches 107; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart. The present sequence is one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                 299
                                                                                 Single exon nucleic acid probes for analyzing gene expression in human
                    CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                                           Probe #5454 for gene expression analysis in human heart cell sample.
                                                                                                                                                                                                                                                                                                                                                                           gene expression, heart; microarray, vascular system; probe; vascular disease; hypertension; cardiac arrhythmia;
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                                                                                                                             ACCCAAGAATCTGCAGCTAACTTATTTCCCCTAGCT 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 5454; 530pp; English.
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                                                                                                                                                                                                                                             BP.
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30-JUN-2000; 2000US-0669408.
03-MUG-2000; 2000US-0632466.
21-SEP-2000; 2000US-0234687P.
27-SEP-2000; 2000US-023599P.
04-OCT-2000; 2000GB-00024263.
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                                                                                                                                                                                                                                                                                                                                                                                                           congenital heart disease; ss
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                                                                                                                                                                                                                                            ABA26988 standard; DNA; 360
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                                                                                                                                                                                                                                                                                                                                                                                          cardiovascular
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The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human bone marrow. They can be used to measure gene expression in bone marrow samples, which may enable the improved diagnosis and treatment of cancers such as lymphoma, leukaemia and myeloma. The present sequence is one of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genome-derived single exon nucleic acid probes useful for analyzing
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358 CTTCAAGACCATTGTGGCCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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microarray; cancer; leukaemia; lymphoma; myeloma; 88.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human bone marrow expressed single exon probe SEQ ID NO: 5703.
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                                                                                                                                                                                                     202
                                                                                                                                                       238 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W, Rank DR;
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; 2000US-00608408.
; 2000US-00632366.
; 2000US-0234687P.
; 2000US-0236359P.
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Matches 107; Conservative
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21-SEP-2000;
27-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention provides a number of single exon nucleic acid probes which are derived from genomic sequences expressed in the human brain. They can be used to measure gene expression in brain cell samples, which may enable the diagnosis and improved treatment of nervous system diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia, epilepsy and cancers. The present sequence is one of the probes of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                          Human; brain expressed exon; gene expression analysis; probe; microarray; Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   exon nucleic acid probes for analyzing gene expression in human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 4; SEQ ID NO 5534; 650pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 157; DB 4; Length 360;
Pred. No. 0.73;
0; Mismatches 0; Indels
                                                                                                                                                     Human brain expressed single exon probe SEQ ID NO: 5534.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 360 BP; 121 A; 65 C; 77 G; 97 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 202
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Rank DR;
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                                                                                                                                                                                                                                                                                                                                                                                                                 (MOLE-) MOLECULAR DYNAMICS INC.
                                                                                  BP.
                                                                                                                                                                                                                                                                                                                              2000US-0207456P.

2000US-00608408.

2000US-00632366.

2000US-0234687P.

2000US-0236359P.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Chen W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96.9%;
68.2%;
                                                                                                                                                                                                                                                                                               30-JAN-2001; 2001WO-US000667
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                                                                                  AAK05543 standard; DNA; 360
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Best Local Similarity 68.2'
Matches 107; Conservative
                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                         Hanzel DK,
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                                                                                                                                                                                                                                                  WO200157275-A2.
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03-AUG-2000;
21-SEP-2000;
                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                       04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                 27-SEP-2000;
                                                                                                                                                                                                                                                                                                                                  26-MAY-2000;
                                                                                                                                05-NOV-2001
                                                                                                                                                                                                                                                                          09-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention
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                                                                                                         AAK05543;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Penn SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Single
                                                                      AAK05543,
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The invention relates to a single exon nucleic acid probe (SENP) (1) for measuring human gene expression in a sample derived from human adult liver, comprising one of 13109 defined nucleotide sequences given in the specification (or complements) fragments). The probe hybridises at high stringency to a nucleic acid molecule expressed in the human adult liver. CC (1) may be used for predicting, measuring and displaying gene expression in samples derived from human adult liver. The genes identified may be involved in genetic liver diseases such as cirrhosis, chyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is associated with coronary heart disease. ABS25011-ABS3105 represent human CC associated with coronary heart disease. ABS25011-ABS3105 represent human CC sequence information for this patent does not appear in the printed sequence information for this patent does not appear in the printed specification but was obtained in electronic format directly from WIPO at fip. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genome-derived single exon nucleic acid probes useful for analyzing gene expression in human adult liver.
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0
                                                                                                                                                                                                                            Human; single exon nucleic acid probe; liver; cirrhosis;
hyperlipoproteinaemia; hyperlipidaemia; hypercholesterolaemia;
coronary heart disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.9%; Score 157; DB 4; Length 360; 68.2%; Pred. No. 0.73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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                                                                                                                                                                            Human liver single exon probe, SEQ ID No 5816
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                    BP.
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2000US-00608408.
2000US-00632366.
2000US-0234687P.
2000US-0236379.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30-JAN-2001; 2001WO-US000664
ABS30826/c
ID ABS30826 standard; DNA; 360
                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-488898/53.
                                                                                                                                                                                                                                                                                                                                                                                                        WO200157273-A2.
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27-SEP-2000;
04-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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03-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      04-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAY-2000;
                                                                                                                                 25-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-AUG-2001
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                                                                          ABS30826;
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The inventorial probes for measuring gene expression in a sample excludible of the inventorial probes for measuring gene expression in a sample derived from human lung comprising single exon mucleic acid probes having one of from human lung comprising single exon mucleic acid probes having one of the inventorial complements or the 12387 open reading frames derived from the 12614 probes. Also included are a microarray comprising the novel set of probes which hybridise at high stringency to a nucleic cacid expressed in the human lung, comprising ene expression in a sample of the numan lung, comprising (a) contacting the array with a collection of detectably labeled nucleic acids derived from human lung mRNA, and (b) measuring the label detectably bound to each probe of the array; identifying exons in a eukaryotic genome, comprising (a) algorithmically predicting at least one exon from genomic sequences of the eukaryote; and (b) detecting specific hybridisation of detectably cannot be a fragment identical to the predicted exon, the probe is included in the above mentioned microarray; assigning exons to a single gene, comprising (a) identifying exons from genomic sequence by the method cabove and (b) measuring the expression of each of the exons in several tissues and/or cell types using hybridisation to a single exon microarrays having a probe with the exon, where a common pattern of expression of the exons in the specification, or encoded by the conservation of the exons should be assigned to a single gene; a peptide comprising on the exons should be assigned to a single gene; and expression or the probe with the exons appetue and performent and performent and performent and performent and performed to a single gene; and expense that the expression of the exons in the specification, or encoded by the
                                                                                                                                                                                                                                                                                                       Hermansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis; pulmonary histiocytosis; lymphangioleiomyomtosis; Karagener syndrome; pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia; pulmonary dyskinesis; pulmonary hypertension; hyaline membrane disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spatially-addressable set of single exon nucleic acid probes, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a spatially-addressable set of single exon
                                                                                                                                                                                                                 Human; ds; single exon probe; asthma; lung cancer; COPD; ILD;
chronic Obstructive pulmonary disease; interstitial lung disease;
familial idiopathic pulmonary fibrosis; neurofibromatosis;
tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
                                                                                                                                                                      Human genome-derived single exon probe from lung SEQ ID No 5889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   measure gene expression in human lung samples.
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                           ABS05898 standard; DNA; 360 BP.
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30-JUN-2000; 2000US-00608408
03-AUG-2000; 2000US-00632366.
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                                                                                                                      (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                      19-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-NOV-2001
                                                                      ABS05898
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ABS05898/c
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ABV96715 standard; cDNA; 473 BP.

ABV96715

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               analysis, and for identifying exons in a gene, particularly using human lung derived mRNA and for the study of lung diseases such as aethma, lung cancer, chronic obstructive pulmonary disease (COPD), interstitial lung disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis, tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-budlak syndrome, sarcoidosis, pulmonary hemosiderosis, pulmonary histocytosis, lymphangioleiomyomtosis, pulmonary alveolar proteinosis, Karagener syndrome, fibrocystic pulmonary dysplasia, primary ciliary present sequence is a single exon probe of the invention. Note: The sequence data for this parent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTCCATGGACCACCTGGACAAGCCAAACCCGAAGACTTGAACACTCACACA 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The probes are used for gene expression
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                                                                                                                                                                                                                                                                                                                                                       6; Length 360;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.9%; Score 157; DB 6
68.2%; Pred. No. 0.73;
tive 50; Mismatches
                                                                                                                                                                                                                                                                    at ftp.wipo.int/pub/published_pct_sequences
probes/open reading frames (ORF).
                                                                                                                                                                                                                                                                                                                                                                                              Matches 107; Conservative
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Best Local Similarity
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Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;
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2001US-0278651P.
2001US-0287112P.
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2001US-0305484P
                                                                                                                                                                                                                                                                                                                                                                          cytostatic; tumour; gene; ss
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2001US-0333626P
                                                                                                                                                             14-JAN-2003 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
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21-MAR-2001;
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                                                                            ABV96715;
THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE STATE OF THE S
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New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic

Hepler WT,

Persing DH,

Lodes MJ,

Kalos MD,

Benson DR,

(CORI-) CORIXA CORP.

WPI; 2002-627435/67.

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Query Match
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                                                                                                              The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences consisting of at least 20 contiguous residues of (a); (d) sequences that hybridize to (a), under moderately corridations; (e) sequences having at least 75 or 90% identity to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-CC ABP66837) encoded by (I) and oligonucleotide can be used to detect cancer in a patient and compositions comprising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and proparation of ribozyme molecules for inhibiting expression of the tumour CC polypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence data for this patent did not form part of the primed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published_pct_sequences
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.2%; Pred. No. 0.8;
Matches 107; Conservative 50; Mismatches 0: Indele
                                                                  Claim 1; SEQ ID NO 2123; 300pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 473 BP; 129 A; 121 C; 89 G; 134 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP.
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2001US-0287112P.
2001US-0391631P.
2001US-0305484P.
2001US-0313999P.
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2001US-0265682P.
2001US-0267568P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABV97697 standard; cDNA; 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2002; 2002WO-US002781
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09-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-2003
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ABV97697/c
             cancer
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             \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}^{\mathbf{X}} \mathbb{F}_{\mathbf{X}}
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The invention relates to an isolated polynucleotide (I) comprising: (a) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b) complements of (a); (c) sequences that hybridize to (a), under moderately cresidues of (a); (d) sequences that hybridize to (a), under moderately creditions: (e) sequences having at least 75 or 90% identity cit (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer or a patient and compositions complising polypeptides, polynucleotides, antibodies, fusion proteins, T cell populations and antigen presenting cells expressing the polypeptide are useful in treating pancreatic cancer and stimulating an immune response. The polynucleotides can be used as probes or primers for nucleic acid hybridisation, in the design and proteins in the tumour colls, in vaccines and for gene colypeptides and proteins in the tumour cells, in vaccines and for gene therapy. Note: The sequence date for this patent did not form part of the from WIPO at ftp.wipo.int/pub/published_pot_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; chronic obstructive pulmonary disease; COPD; chronic lung disease;
                                                                                                      New isolated polynucleotide and pancreatic tumor polypeptides, useful for diagnosing, preventing and/or treating cancer, particularly pancreatic cancer.
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Jiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            96.9%; Score 157; DB 6; Length 475; 68.2%; Pred. No. 0.8; ive 50; Mismatches 0; Indels
                                                                                                                                                                                                                         Claim 1; SEQ ID NO 3105; 300pp + Sequence Listing; English.
      Hepler WT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 475 BP; 134 A; 90 C; 122 G; 129 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human COPD related protein encoding cDNA SEQ ID NO:21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Persing DH,
         Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAY-2002; 2002WO-EP005835.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACC46770 standard; cDNA; 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 107; Conservative
         Kalos MD,
                                                               WPI; 2002-627435/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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            Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACC46770;
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Example 1; SEQ ID NO 542; 176pp; English.

WPI; 2003-876899/81.

P-PSDB; ADN95618

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                                                                                                                                                                     The present invention describes a method for predicting, diagnosing or prognosing chronic lung disease by detecting a chronic obstructive pulmonary disease (COPD) gene related polymucleotide (see ACC46750 to ACC46777, which encode the COPD related proteins in ABP96779 to ABP96806). The method is useful for predicting, diagnosing or prognosing encoded by them from the present invention (I) can be used for treating or preventing chronic lung disease in a mammal. (I) can be used for treating or preventing chronic lung disease in a mammal. (I) can be used in an animal model for determining the efficacy, toxicity, or side effects of treatment with (I), and determining the mechanism of action of (I).

ACC46778 to ACC46903 represent COPD related PCR primers and probes used in an example from the present invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Predicting, diagnosing or prognosing chronic lung disease, by detecting a chronic obstructive pulmonary disease (COPD) gene in a biological sample.
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   ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
Hall R, Schulze T, Kroegel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alitalo K, Makinen T, Petrova T, Saharinen P, Saharinen J;
                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 10; Length 478;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 478 BP; 142 A; 91 C; 78 G; 167 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 ACCCAAGAATCTGCAGCTAACTTATTTCCCCTAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                           96.9%; Score 157; DB 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human BEC/LEC-related gene sequence SeqID542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 68.2%; Pred. No. 0.81
Matches 107; Conservative 50; Mismatches
Kallabis H,
                                                                                                                                        Claim 8; Page 110; 214pp; English
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Gehrmann M,
                                 WPI; 2003-140492/13.
P-PSDB; ABP96799.
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Oellers N,
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This invention relates to a method of differentially modulating the growth or differentiation of blood endothelial cells (BEC) or lymphatic conductial cells (AEC) comprises contacting endothelial cells with a composition comprising an agent that differentially modulates blood or composition comprising an agent that differentially modulates blood or lymphatic endothelial cells. Treating hereditary lymphoedema comprises and entire a mutation in at control and human subject with lymphoedema and with a mutation in at least one allele of a gene encoding a LEC protein, where the mutation of correlates with lymphoedema in human subjects, and with the proviso that composition comprising a lymphatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymbatic growth agent selected from VEGF-C or VEGF-D polypeptides and polymucleotides. The invention may be useful for the development of compounds with an antiangiogenic, cytosteatic, consolved and sevel lymphatic endothelial cells, in treating herethed is useful in modulating the growth or differentiation of blood is useful in modulating the growth or differentiation of blood endothelial cells or lymphatic endothelial cells, in treating a medicament for predisposition to the disorder or in monitoring the efficacy or toxicity of a drug on endothelial cells. The agent is useful in manufacturing a medicament for the treatment for the disferential modulation of blood vessel endothelial cell or lymphatic growth agent may also be used in manufacturing a medicament for the treatment of hereditary lymphoedema resulting from a mutation. The lymphatic growth agent may also be used in manufacturing a constraint of hereditary lymphoedema resulting for a midicament for the treatment of hereditary lymphoedema resulting to sequence of other diseases and cancer metastasis via the lymphatic system. The present sequence is that of a human LEC/BEC differentially sequence does not other diseases and control of the method of the invention Note: This sequence does not appear in the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTCCATGGACCACCTGGACAAGCAAACCCCAAACTCCGAAGACTTGAACACCCACTCCACA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cricaagaccarreregeccaaggagarcrerecreaccccaaggagargreegr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 478 BP; 142 A; 91 C; 78 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Renal cell carcinoma differentially expressed gene #262.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 157
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Twine NC, Sloni DK;

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(TWIN/) (BURC/) (TREP/)

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The invention relates to a method of determining whether a patient will respond to treatment with a farnesyl transferase inhibitor (FTI), by analyzing the expression of gene that is differentially modulated in the presence of an FTI. The method is useful for determining whether a patient will respond to treatment with a FTI such as (B)-6-[amino(4-chlorophenyl)(1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl).1-methyl-1H-imidazol-5-yl)methyl]-4-(3-chlorophenyl).1-patient with leukemia with FTI if the analysis indicates that the patient will respond. This sequence corresponds to a gene whose expression may be modulated in the presence of FTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 TTCCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACTTGAACACTCCCACA 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Determining whether a patient will respond to treatment with a farnesyl transferase inhibitor, by analyzing the expression of gene that is differentially modulated in the presence of the inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CTTCAAGACCATTGTGGCCAAGGAGATCTGTGTGTGACCCCAAGCAGAAGTGGGTTCAGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Phosphoramidite; INVADER assay cleavage reaction; FEN1; cleavase; nucleic acid separation; DNA polymerase; human; MCP-1; ubiquitin; monocyte chemoattractant protein-1; gene; ss.
farnesyl transferase inhibitor; gene expression;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.9%; Score 157; DB 10; Length 482; 68.2%; Pred. No. 0.81; ive 50; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 482 BP; 143 A; 92 C; 79 G; 168 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human monocyte chemoattractant protein-1 (hMCP-1) RNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 97; 346pp; English.
                                                                                                                                                                                                                                                                                                                                                                          (ORTH ) ORTHO CLINICAL DIAGNOSTICS INC.
       ss; cytostatic; farnesyl trans
quinolinone; leukemia; cancer.
                                                                                                                                                                                                               30-OCT-2002; 2002WO-US034784.
                                                                                                                                                                                                                                                        30-OCT-2001; 2001US-0338997P.
30-OCT-2001; 2001US-0340081P.
30-OCT-2001; 2001US-0340938P.
30-OCT-2001; 2001US-0341012P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABS68800 standard; RNA; 647
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                                                                               Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relate to a method of diagnosing (MI) non-blood disease
such as solid tumor by providing peripheral blood sample of human having
cuch as solid tumor by providing peripheral blood sample of human having
concluded disease, and comparing an expression profile of specific genes
concluded an anomuclar cells (PBMCs) of paintents having the disease as
compared to PBMCs of normal humans. The method is useful for diagnosing
compared to PBMCs of normal humans. The method is useful for diagnosing
compared to PBMCs of normal humans. The solid tumor is chosen from
non-blood disease such as solid tumor. The solid tumor is chosen from
con-blood disease such as solid tumor. The solid tumor is chosen from
semple is a whole blood sample (claimed). (MI) is useful for identifying
sample is a whole blood sample (claimed). (MI) is useful for identifying
sample at that are differentially expressed in peripheral blood samples
cisplated at different stages of progression, development or treatment of
scand/or other solid tumors. This sequence corresponds to a gene that
cisplated at differentially expressed and detected by the method of the invention.
(Note: this sequence is not given as part of the printed specification
but was obtained from WIPO in electronic format at
citp.wipo./pub/published_pot_sequences).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Diagnosing non-blood disease such as solid tumor, involves comparing differential expression profile of specific genes in peripheral blood sample of subject with reference expression profile of specific genes.
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                                                                                                                                                                                                                                                                                                                                          Stover JA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 478 BP; 142 A; 91 C; 78 G; 167 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                             Dorner A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 157
                                                                                                                                                                                                                                                                                                                                          Trepicchio WL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 262; 350pp; English.
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                                           21-NOV-2003; 2003WO-US037481.
                                                                                      21-NOV-2002; 2002US-0427982P-03-APR-2003; 2003US-0459782P-
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                                                                                                                                                                                                                                                                                                                                             Burczynski ME,
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Matches 107; Conservative
                                                                                                                                                                             TWINE N C.
BURCZYNSKI M E.
TREPICCHIO W L.
DORNER A.
STOVER J A.
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Query Match

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RESULT 14 ADE84878 ADE84878;

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Gaps

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Search completed: August 4, 2005, 16:54:09 Job time : 226 secs

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Query Match 96.9%; Score 157; DB 6; Length 647; Best Local Similarity 55.4%; Pred. No. 0.89; Matches 87; Conservative 70; Mismatches 0; Indels

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xv24b04.x

ill7e04.x AV717017

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AV734336 UI-CF-EC1 UI-CF-EC1 UI-CF-DU1 UI-H-DH0-UI-H-EZ0-

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AV661469 GLC Homo sapiens cDNA clone GLCGSG05 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                            Bukaryottai Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

Ku, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X., Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W., Hu, G., Chen, Z. and Han, Z. and Han, Z. and Han, Z. and Han, Z. and Han, Z. Insight into hepatocellular carcinogenesis at transcriptome level
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  by comparing gane expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="GLC"
/note="Vector: pBluescript sk(-); Site_l: EcoRI; Site_2:
Khol"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
Chinese National Human Genome Center at Shanghai
Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hang@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="fQLGGSGOS"
/tissue=type="corresponding non cancerous liver tissue"
/lab_host="SOLR"
                                                                                                                                                                                                                                                ALIGNMENTS
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                                        BUS80675
AL697816
AV716988
AW773091
BU730951
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BM973445
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DEFINITION
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AUTHORS
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AW967017 EST379091
BX490080 DKRZP686B
BM704915 UI-E-CII-
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MR0-AN008
wc84b06.x
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AV714555 AV714555
                                                                                  (without alignments)
3732.695 Million cell updates/sec
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                                                                                                                                       cttcaagaccattgtggcca.....nnnnnnnnnnnntgatca 162
                                                                        August 4, 2005, 16:43:00; Search time 1652 Seconds
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BF081639 N
AI692798 N
AV735130 A
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                                                                                                                                                                                                                 68479088
          GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                          34239544 seqs, 19032134700 residues
                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                  - nucleic search, using sw model
                                                                                                                SEQ13-8698-9073-50N-TGATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AW967017
BX490080
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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9b_htc:

9b_est3:

9b_est4:

9b_est6:

9b_gss1:

9b_gss2:
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Score

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Result

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Gaps

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96.9%; Score 157; DB 1; Length 432; 68.2%; Pred. No. 1.1e-21; ive 50; Mismatches 0; Indels

Query Match 96.9 Best Local Similarity 68.2 Matches 107; Conservative

ORIGIN

AA877558 nrO5f01.8 BE326715 hr63g10.x BM99756 UT-H-DHO-BM708613 UI-E-CII-AW584110 hg55g02.x BM88255 TMM174 Hu BQ631442 ill7004.y

AW594110 BM888255 BQ631442

nr05f01.8 hr63g10.x

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19
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AI478647/c
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                                                           241 CTTCAAGACCATTGTGGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGAGGGGTTCAGGA 300
                                             Unpublished (1995)
Conteat: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
High quality sequence stops: 305
Source: IMAGE Consortium, LIALL
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                            361 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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High quality sequence stop: 305.
Location/Qualifiers
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Homo sapiens
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96.9%; Score 157; DB 7; Length 446; 68.2%; Pred. No. 1.1e-21; ive 50; Mismatches 0; Indels

Query Match Best Local Similarity 68.2 Matches 107; Conservative

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Unpublished (1997)
Unpublished (1997)
Unpublished (1997)
Email: cgapbs-r@mail.nih.gov
Tissue procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
EDMA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.4.G.B. Consortium/LINL at:
www-bio.llnl.gov/bbrp/lange/image.html
Insert Length, 1975 Std Error: 0.00
                                                                                                                                                                                                                                                                                         AI478647
tm54f08.xl NCI_CGAP_Kidll Homo sapiens cDNA clone IMAGE:2161959 3'
similar to gab:W34545 MONOCYTE CHEMOTACTIC PROTEIN 1 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    423
                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi; Mammalia, Eutheria, Primates; Catarrhini, Hominidae, Homo. I (bases 1 to 486).
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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                                                                                                                                                        121 NAMININAMININAMININAMININAMININAMININAMININAMININA 157
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High quality sequence stop: 444.
Location/Qualifiers
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Homo sapiens
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Best Local Similarity 68.2
Matches 107; Conservative
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AV714555 DCB Homo sapiens cDNA clone DCBADG05 5', mRNA sequence.
AV714555 LGI:10796072
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                                  Mammalia; Eutheria; Primates; Catarrhin; Hominidae; Homo.
1 (bases 1 to 513)
Xu.x. Gul, J., Liu, F., Qu, J., Zhao, M., Li, Y., Huang, Q., Zhou, J., Chang, Z., Xu, S., Gu, W., Tu, Y., Gao, G., Xiao, H., Li, N., Qian, B., Gao, X., Cheng, Z., Xu, S., Gu, W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Homo sapiens CDNA DCB clones
Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pTriplEx2; Site_1: sfilA; Site_2: sfilB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                              250 ACCCAAGAATCTGCAGCTAACTTATTTCCCCTAGCT 286
                                                                                                                  157
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                                                                                                                                                                                                                                                                            Los/1147 Solution 1206 bp mRNA linear EST 24-JUN-2003 [421d04.yl Human Iris cDNA (Normalized): fg Homo sapiens cDNA clone captants sequence.
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Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of adult human iris for the NEIBank
Project: steroid-response factors and similarities with retinal
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llarity 68.2%; Pred. No. 1.2e-21;
Conservative 50; Mismatches 0; Indels
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Section on Molecular Structure and Function
National Eye Institute
6/331, NIH, Bethesda, MD 20892-2740, USA
                                                                                                                                           362 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 326
                                                                                                         Email: graeme@helix.nih.gov
Plate: 21 row: d column: 04
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Mol. Vis. 8 (4), 185-195 (2002)
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Homo sapiens
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Fax: 301 496 0078
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Matches 107;
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                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
   Tissue Procurement: M. Bento Soares, Ph.D.
   Tissue Procurement: M. Bento Soares, Ph.D.
   CDNA Library Preparation: M. Bento Soares, Ph.D. and M.Fatima
   Bonaldo, Ph.D.
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Washington University Genome Sequencing Center
   Clone distribution: NCI-CGAP clone distribution information can be
   found through the I.M.A.G.E. Consortium/LLNL at:
   info@mages-llnl.gov
   Seq primer: -40UP from Gibco
   High quality sequence stop: 425.
   info@mac.lonl/Qualifiers
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 541)
                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. La (bases 1 to 520)
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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//organism="Homo sapiens"
/mol_type="mRNA"
/db_xef="taxon:19606"
/clone="IMM6E:142186"
/tissue_type="lymphocyte"
/lab_host="DH10B (phage-resistant)"
/clone_lib="Soares NPBMC"
/note="Organ: blood; Vector: pT713D-Pac; Site_1: Not1;
Site_2: ECORI; 1st_strand cDNA was primed with a Not I
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REFERENCE

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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NGI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
infoamage.llh.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 471.
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/note="Organ: kIdney; Vector: pT773D-Pac (Pharmacia) with
/note="Organ: kIdney; Vector: pT773D-Pac (Pharmacia) with
a modified polylinker; Site 1: NOt 1; Site 2: ECO RI;
Plasmid DNA from the normalized library NCI CGAP Kid3 was
prepared, and ss circles were made in vitro. Pollowing HAP
purification, this DNA was used as tracer in a subtractive
hypridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneIDS 132236-1323911, 1456007-1456775, and
150652-150285). Subtraction by Bento Soares and M.
Patima Bonaldo. "
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1 (bases 1 to 542)

Melton, D., Meadows, A., Clifton, S., Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R., Williams, T., Jackson, Y. and
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP)
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68.2%; Pred. No. 1.3e-21;
iive 50; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/lab host="DH108"
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Homo sapiens
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                                                                  Tumor Gene Index
Unpublished (1997)
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AW967017.1 GI:8156853
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AW967017
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                                                                                                                                                                                                                                 Good hit to opposite strand read. ..wrong orientation BUT PASSED FOR MOUSE-PANCREAS VERIFICATION
MOUSE-PANCREAS VERIFICATION
Possible reversed clone: similarity on wrong strand
Seq primer: -40RP from Gibco
High quality sequence stop: 542.
Location/Qualifiers
1. 542
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7440h06.x1 NCI CGAP CO16 Homo sapiens cDNA clone IMAGE:3318491 3' similar to SW:SY02 HUMAN P13500 SMALL INDUCIBLE CYTOKINE A2 BFS90622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Organ: Pancreas, Vector: pBluescript SK(-); Site_1:
Not1; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agraces egl. Average insert size ~lkb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Mctabolism Div. (Alan Permutt Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinous@imgate.wustl.edu, Tel:
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                Other ESTS: ill7e04.yl
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     203 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 262
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
I (basea I to 544.ncbi.nlm.nih.gov/ncicgap.
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                   Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp harvard.edu
This read is a 3' RESEQUENCE of a previously sequenced pancreas
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                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="IMAGE:6030414"
/tissue_type="Purified pancreatic islet"
/lab_hogt="DH10B"
/clone_lib="HR85 islet"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         323 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 359
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                                                                                                                                                                                                                                                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:9606"
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Unpublished (1997)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP Clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stopp: 443.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="NOI_CGAP_Col6"
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_l: Not I; Site_2: Bco RIP Plasmid DNA from the normalized library NCI CGAP Col0 was prepared, and so circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351)
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EST379091 MAGE reseguences, MAGJ Homo sapiens CDNA, mRNA seguence.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Hedde, P., Qi, R., Abernathy, K., Dharap, S., Gaspard, R., Gay, C., Holt, I.E., Saeed, A.I., Sharov, V., Lee, N.H., Yeatman, T.J. and Quackenbush, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Subtraction by Bento Soares and M. Fatima Bonaldo.
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Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 3528
Fax: 301 838 0208
Email: john@deligr.org
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3318491"
/tissue_type="colon tumor, RER+"
/lab_hogt="DH10B"
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DKFZp686B1371_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DKFZp686B1371_r', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKF2); Email s.wiemann@dkfz-heidelberg.de;
sequenced by MediGenomix (Martinsried/Germany) within the cDNA
sequencing consortium of the German Genome Project. No sl sequence
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                                                                                                                                                                                                                                                                                                                     298 TICCATGGACCACCTGGACAAGCAAACCCAAACTCCGAAGACTTGAACACTCCACA 357
                                                                                                                                                                                                                                                                                      238 cricaagaccarigiggccaaggagarcrgrgcrgaccccaagcagaagrgggrrcagga 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W., Well, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S. EST (Ottenwaelder, B., Obermaier, B., Deutschenbaur, S., Mewes, H.W.,
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Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hlcc3)"
Site_1: SfiIA; Site_2: SfiIB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.
Location/Qualifiers
                                                                                                                                                                                                                                               1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone (DKFZp686B1371) is available at the RZPD in Berlin.
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                                                                                                                                                                          Length 548;
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                                                                                                    /clone_lib="MAGE resequences, MAGJ"
/note="Vector: pBluescriptSKm"
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                                                                                                                                                                          Query Match 96.9%; Score 157; DB 2; Best Local Similarity 68.2%; Pred. No. 1.3e-21; Matches 107; Conservative 50; Mismatches 0.
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/note="Vector: pTriplEx2;
cDNA-collection"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /mol_type="mRNA"
/db_xref="taxon:9606"
/db_clone="DKPEQ68B1371"
/dev_stage="adult"
/lab_host="DH10B"
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                                                organism="Homo sapiens"
                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 549)
     Location/Qualifiers
1. .548
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Best Local Similarity 68.2<sup>§</sup>
Matches 107; Conservative
Seq primer: Reverse
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Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: MIPS
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Homo sapiens
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COMMENT
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Gaps

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// db xref="taxon:966"
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// clone lib="U1-B-CII"
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// clone lib="U1-B-CII"
// clone lib="U1-B-CII"
// clone lib="U1-B-CII"
// clone lib="U1-B-CII"
// clone lib="U1-B-CII"
// clone lib="U1-B-CII"
// clone lib="U1-B-CII"
// u1-B-CII is a normalized cDNA library containing the following tissue(s): RPB and Choroid. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6: 791-806, 1996. First strand cDNA synthesis was primed with an oligo-dI primer containing a synthesis was primed with Not I, and cloned directionally into pT/T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT) ls tail. The sequence tag for this library is According the visual System, supported by National Bye Institute (NBI)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coordinated Laboratory for Computational Genomics
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRF, Iowa City, IA 5242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Bmail: bento-soares@uiowa.edu
Tissue Procurement: Dr. Gregg Hageman
cDNA Library preparation: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, Univeristy of Iowa
Clone Distribution: Researchers may obtain clones from Research
Genetics (www.resgen.com)
Seg primer: M13 Reverse.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   563 bp mRNA linear EST 28-FEB-2002
UI-E-CII-agf-h-04-0-UI.rl UI-E-CII Homo sapiens cDNA clone
UI-E-CII-agf-h-04-0-UI 5', mRNA secuence
                                                                                                                                                                                  263 CTTCAAGACCATTGTGGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAGAGTGGGTTCAGGA 322
                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 563)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
   9
CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                                                                                                                                                                                                           383 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 419
                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Res. 6 (9), 791-806 (1996)
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ORIGIN

ઠે 셤 8 셤 ò RESULT 13 AA614521/c DEFINITION

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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE REFERENCE

JOURNAL

COMMENT

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1 (bases 1 to 565)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V.,
O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asingson@ludwig.org.br
Email: asingson@ludwig.org.br
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=MR0-AN0084-190
900-002-f07kf1=2000-00-19&t4=1)
Seq primer: puc 18 forward
High quality sequence stop: 374.
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//mol type="making"
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MRO-AN0084-190900-002-£07 AN0084 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for ancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                       477 cricaadaccarigigaccaaggagarcrerecteaccccaagcagaagregerrcagga
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20202663
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   0; Indels
                                                                                                                                                                                                                                                                                                                                          357 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 321
   Mismatches
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BF081639.1 GI:10875469
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Conservative
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107;
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       Matches
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PUBMED
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BF081639
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www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 811 Std Error: 0.00
Seq primer: -40ml3 #wd ET from Amersham
High quality sequence stop: 463.
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                                                                                                                                                                                                                                                                   233 CTTCAAGACCATGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 292
                                                                                                                                                                                                                                                                                                                                          np49b05.s1 NCI CGAP Br1.1 Homo sapiens cDNA clone IMAGE:1129617 3' similar to gb:M24545 MONOCYTE CHEMOTACTIC PROTEIN 1 PRECURSOR
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 565)
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="female, pooled"
/tiseue type="breagt"
/lab host="bH10B"
/clone lib="NCI_CGAP_Br1.1"
/note="Vector: pT773D-Pac (Pharmacia) with a modified
                                                                                                                                                                                                   1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
                                                                                                                                          Gaps
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                                                                Length 563;
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Pred. No. 1.3e-21;
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                                                            Score 157; DB 4;
Pred. No. 1.3e-21;
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/db_xref="taxon:9606"
/clone="IMAGE:1129617"
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AA614521.1 GI:2466717
                                                        96.9%;
68.2%;
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Unpublished (1997)
                                                                                                                                Matches 107; Conservative
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Best Local Similarity
                                                                Query Match
Best Local Similarity
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source

ORIGIN

FEATURES

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time : 1657 secs

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Job
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Email: cgapbs-r@mail.nih.gov
Life Technologies catalog #: 11548-013

Life Technologies catalog #: 11548-013

Lone distribution: WCI-CGAP Clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

Www-bio.llnl.gov/bbrp//ange/fange.html
Insert Length: 707 Std Error: 0.00

Seq primer: 40UP from Gibco
Req primer: 40UP from Gibco
Req primer: Longth: Sequence stop: 417.
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/lab host="DH10B"
/clone_lib="NCI CGAP Pan1"
/note="Oxgan: pancreas; Vector: pCMV-SPORT6; Site_1: Sal1;
/note="Oxgan: pancreas; Vectorinomally. Primer: Oligo dT.
Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.72 kb. Life Technologies catalog #:
11548-013"
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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/organism="Homo sapiens"
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Search completed: August 4, 2005, 17:38:36

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Copyright (c) 1993 - 2005 Compugen Ltd.
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4 US-09-545-894-3 3 US-08-744-419-1 3 US-09-316-887A-15 4 US-09-463-451-29 4 US-09-463-451-29 4 US-09-463-628-37 4 US-09-646-028-39 4 US-09-646-028-49 5 US-09-646-028-49 1 US-08-56-028-49 2 US-09-646-028-49 1 US-08-250-958-3 2 US-08-95-1268-1 2 US-08-95-1268-1 3 US-08-95-1268-1 3 US-08-95-1268-1 3 US-08-95-1268-1	ALIGNMENTS  or Zbigniew T. R. a Tags and the Separatio : US/09/777,430C 3.1 ence	tch  1 Similarity  25.4%; Pred. No. 0.014;  87; Conservative 70; Mismatches 6  1 CTTCAAGACCATGGGCAAGGAGATCTGTGCTGACC   ::        : :
69.6 69.6 67.4 67.3 67.3 67.3 66.3 1086 66.9 1113 65.2 1113 65.2 1113 65.1 1047 65.2 1113 65.1 1047 65.2 1113 65.3 1047 65.8 55.8 55.8 55.8 55.8 55.8	plication US/ 982 TION: michev, victo michev, victo Tawi, Hatim I Awar, Tsetska Kova, Tsetska Kova, Tsetska AriON: Charge TION: Charge TION: Charge Arion Number: DATE: 2001 Arion Number: Arion Number: Arion version Aricial Seque	>+ 0-0 4-4 2 · 4 m
28 29 31 31 31 31 31 31 31 31 31 31 31 31 31	RESULT 1 US-09-777-430C-72 Sequence 72, Applica Fatent No. 6780992 GENERAL INFORMATION: APPLICANT: Lyamiche APPLICANT: Lyamiche APPLICANT: AAPLICANT: BATZYC APPLICANT: Wayland APPLICANT: Wayland APPLICANT: Wayland APPLICANT: Wayland FILE REFERENCE: FOR CURRENT APPLICATION: FILE REFERENCE: FOR CURRENT APPLICATION SOFTWARE: PALENTIN: SEQ ID NO 72 LENGTH: 647 FYPE: RNA CREATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FEATURE: FE	Query Match Best Local Similarit Matches 87; Conse Oy 1 CTTCAAGA Oy 61 TTCCATGG Oy 61 TTCCATGG Oy 121 NNNNNNN Oy 121 NNNNNNNN Oy 121 NNNNNNNN Oy 121 NNNNNNNN Oy 121 NNNNNNNN Oy 121 NNNNNNNN Oy 121 NNNNNNNN Oy 121 NNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNNN Oy 121 NNNNNNNNNN Oy 121 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN

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Facence No. 1909-109.
FARENT INFORMATION:
APPLICANT: Gallo, Robert C.
APPLICANT: Devico, Anthony L.
APPLICANT: Garzino, Alfedo
TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
FILE REPRENCE: 4115-109 CIP
CURRENT APPLICATION NUMBER: US/09/591,992
CURRENT FILING DATE: 2000-06-12
FRIOR APPLICATION NUMBER: US 60/186,416
FRIOR FILING DATE: 1998-12-11
FRIOR FILING DATE: 1997-12-11
FRIOR FILING DATE: 1997-12-11
SRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin version 3.1
LENGTH: 725
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                                                                                                                                                                                                                            96.9%; Score 157; DB 4; Length 661; 68.2%; Pred. No. 0.014; ive 50; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/09/814,915A
CURRENT FILING DATE: 2002-03-21
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
SEQ ID NO 104
LENGTH: 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 3
US-09-591-992-3
; Sequence 3, Application US/09591992
; Patent No. 6569418
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Best Local Similarity 68.2*
Matches 107; Conservative
Thereto
                                                                                                                                                                                                                                               Best Local Similarity 68.2
Matches 107; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
TITLE OF INVENTION:
                                                                                                                                                                                                US-09-814-915A-104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-591-992-3
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248 CITCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 307
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                                                        APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Stuart
APPLICANT: Officey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSE: INCTF PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                              COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSFFICATION NUMBER:
APPLICATION NUMBER:
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NAME: Zeller, Karen J.
REGISTATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
Sequence 1344, Application US/09023655; Patent No. 6607879; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 25, Application US/07927391
Patent No. 6001649
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECUPACIONE (650) BSS-con-
TELEPHONE (650) 845-4166
INFORMATION FOR SEQ ID NO: 13-
SEQUENCE CHARACTERISTICS:
LENGTH: 725 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (650) 855-0555
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                     CALIFORNIA
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                                                                                                                                                                                                                                                                   CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; LIBRARY: GENB<sup>1</sup>; CLONE: 934513
US-09-023-655-1344
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US-07-927-391-25
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264 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 323
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68.2%; Pred. No. 0.015;
.ive 50; Mismatches 0; Indele
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; Sequence 1. Application US/08437306
; Patent No. 6787645
; GENERAL INFORMATION:
    APPLICANT: Rollins, Barrett J.
    APPLICANT: Rollins, Charles D.
    TITLE OF INVENTION: No. 6787645el Human Cytokine
    NUMBER OF SEQUENCES: 2
    CORRESPONDENCE ADDRESS:
    ADDRESSER: Hamilton, Brook, Smith & Reynolds, P.C.
    STREE: Two Militia Drive
    CITY: Lexingron
    STATE: Massachusetts
    COUNTRY: USA
                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
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FILING DATE: HERENITH (125,025,025)
FILING DATE: APPLICATION:
FILING DATE: CLASSIFICATION:
FILING DATE: CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,011
REFERENCE/DOCKET NUMBER: PA-0001 US
FELECOMMUNICATION INFORMATION:
FELECOMMUNICATION INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 68.2*
Matches 107; Conservative
      CALIFORNIA
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; CLONE: 9187434
US-09-023-655-1165
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                                           USA
                                                                  94304
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                                    COUNTRY:
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                                                     APPLICANT: VITA, Natalio.
TITLE OF INVENTION: Protein having a cytokin type
TITLE OF INVENTION: activity, and recombinant DNA, expression vector and hosts
TITLE OF INVENTION: for its preparation.
NUMBER OF SEQUENCES: 25
CANDRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA
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68.2%; Pred. No. 0.015;
iive 50; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                      CITY:

STATE: VIRCE
COMPUTRY: USA
ZIP: 22313-0299
ZIP: 22313-0299
ZUP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTRE: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
PLING DATE: 1920929
CLASSIFICATION NUMBER: US/07/927,391
FLING DATE: 1920929
CLASSIFICATION S30
ATTORNEY/AGENT INFORMATION:
NAME: SAKE, Bernhard D
REGISTRATION NUMBER: 16781/369
FELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEPHONE: (703) 836-9300
TELEPHONE: (703) 831-4109
TELEPHONE: TOWNER: US/07/SIP
                                                                                                                                                                                                                                                                                 STREET: King Street Station, Suite 500, 1800 Diagonal STREET: Road, PO Box 299 CITY: ALEXANDRIA STATE: VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                384 ACCCAAGAATCTGCAGCTAACTTATTTCCCCTAGCT 420
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Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Offfrey J. Sellhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETR
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
MILOUX, Brigitte
MINTY, Adrian
VITA, Natalio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEX: 899149
INFORMATION FOR SEQ ID NO: 25
SEQUENCE CHARACTERISTICS:
LENGTH: 741 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 68.2
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: CDNA
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R AFFLICATION NUMBER: 60/047,597
R APPLICATION NUMBER: 60/047,597
R FILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,502
R R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,633
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
R FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/043,669
FILING DATE: 1997-04-11
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APPLICATION UNMBER: 60/043,313
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AFFLICATION NUMBER: 60/047,601
APPLICATION NUMBER: 60/047,601
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/043,580
FILING DATE: 1997-04-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 1997-04-11
APPLICATION UNMBER: 60/043,314
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,311
FILING DATE: 1997-04-11
APPLICATION NUMBER: 60/043,671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/047,612
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/047,613
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 60/043,568
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 1997-05-23
APPLICATION UNMBER: 60/047,618
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 60/047,581
FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 60/047,587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,592
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1997-05-23
APPLICATION NUMBER: 60/047,492
                                                                                         PILING DATE: 1997-03-07
APPLICATION NUMBER: 60/040,163
FILING DATE: 1997-03-07
APPLICATION NUMBER: 60/047,615
FILING DATE: 1997-05-23
                                                                                                                                                                                                             APPLICATION NUMBER: 60/047,600
                                                                           APPLICATION NUMBER: 60/040,336
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96.9%; Score 157; DB 4; Length 772;
Best Local Similarity 68.2%; Pred. No. 0.015;
Matches 107; Conservative 50; Mismatches 0; Indels
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SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/437,306
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TITLE OF INVENTION: 70 Human Secreted Proteins
FILE REFERENCE: PZ001P1
CURRENT APPLICATION NUMBER: US/09/148,545
CURRENT FILING DATE: 1998-09-04
EARLIER FEDINGLON NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
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EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/040,333
EARLIER APPLICATION NUMBER: 60/040,161
EARLIER APPLICATION NUMBER: 60/040,161
                                        CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/437,306
FILING DATE: 09-MAY-1995
CLASSTFICATION TAIS:
APPLICATION NUMBER: US 08/228,931
FILING DAPE: 13-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/003,136
FILING DATE: 13-APR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,515
FILING DATE: L3-MAY-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/701,515
FILING DATE: 12-MAY-1991
FILING DATE: 12-MAY-1991
APPLICATION NUMBER: US 07/351,008
FILING DATE: 12-MAY-1991
APPLICATION NUMBER: US 07/351,008
FILING DATE: 12-MAY-1991
ATCHENTALION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 22,592
REFERENCE/DOCKET NUMBER: 22,592
REFERENCE/OCKET NUMBER: 22,592
REFERENCE/OCKET NUMBER: 21,592
TELEGOMONICATION INFORMATION:
TELEGAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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Patent No. 6590075
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 772 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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US-09-148-545-106
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, LOCATION:
US-08-437-306-1
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R FILING DATE: 1997-06-06
R APPLICATION NUMBER: 60/056,886
R RAPLICATION NUMBER: 60/056,886
R RAPLICATION NUMBER: 60/056,877
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,899
RR APPLICATION NUMBER: 60/056,899
R FILING DATE: 1997-08-22
R RAPLICATION NUMBER: 60/056,830
R FILING DATE: 1997-08-22
R RAPLICATION NUMBER: 60/056,630
RR RILING DATE: 1997-08-22
RR PELICATION NUMBER: 60/056,652
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R FILING DATE: 1997-08-22
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,845
R FILING DATE: 1997-08-22
R PRING DATE: 1997-08-22
R PRING DATE: 1997-08-22
R PILING DATE: 1997-08-22
R PILING DATE: 1997-05-23
R APPLICATION NUMBER: 60/047,595
R PILING DATE: 05-869-1997
R APPLICATION NUMBER: 60/057,761
R APPLICATION NUMBER: 60/047,599
R FILING DATE: 1997-05-29
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R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,880
R APPLICATION NUMBER: 60/056,894
R FILING DATE: 1997-08-22
R APPLICATION NUMBER: 60/056,911
R APPLICATION NUMBER: 60/056,911
R APPLICATION NUMBER: 60/056,616
R APPLICATION NUMBER: 60/056,616
R APPLICATION NUMBER: 60/056,616
R FILING DATE: 1997-08-22
  APPLICATION NUMBER: 60/043,315
FILING DATE: 1997-04-11
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APPLICATION NUMBER: 60/056,888
FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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APPLICATION NUMBER: 60/047,614
FILING DATE: 1997-05-23
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FILING DATE: 1997-08-22
APPLICATION NUMBER: 60/056,903
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FILING DATE: 1997-08-22
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FILING DATE: 1997-08-22
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FILING DATE: 1997-05-23
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APPLICATION NUMBER: 60/047,594
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APPLICATION NUMBER: 60/047,589
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1184 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 1243
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68.2%; Pred. No. 0.025;
iive 50; Mismatches 0; Indels
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CURRENT FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: PCT/US98/04482
EARLIER FILING DATE: 1998-03-06
EARLIER APPLICATION NUMBER: 60/040,162
EARLIER FILING DATE: 1997-03-07
EARLIER PILING DATE: 1997-03-07
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER APPLICATION NUMBER: 60/038,621
EARLIER FILING DATE: 1997-03-07
EARLIER FILING DATE: 1997-04-11
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EARLIER FILING DATE: 1997-04-12
EARLIER FILING DATE: 1997-04-13
EARLIER FILING DATE: 1997-04-13
EARLIER APPLICATION NUMBER: 60/043,670
EARLIER APPLICATION NUMBER: 60/056,632
EARLIER APPLICATION NUMBER: 60/056,641
EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-22
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EARLIER PILING DATE: 1997-08-22
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EARLIER FILING DATE: 1997-08-05
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EARLIER APPLICATION NUMBER: 60/055,884
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EARLIER FILING DATE: 1997-08-22
NUMBER OF SEQ ID NOS: 280
SOFTWARE: PAREATING DATE: 1997-08-22
SOFTWARE: PAREATING DATE: 1997-08-22
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Patent No. 6590075
GENERAL INFORMATION:
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Best Local Similarity
Matches 107; Conserv
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APPLICATION NUMBER: 60/040,161

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DATE:	PPLICATION	PPLICATION	ILING DATE: PPLICATION	FILING DATE: APPLICATION D	LING DATE	NG DATE:	ATION DATE:	PPLICATION	PPLICATION	DATE:	ILING DATE:	APPLICATION 1	PPLICATION	FILING DATE: APPLICATION 1	G DATE:	DATE:	TION DATE:		TION	DATE:	DATE:	LICATION	TION	DATE: TION	DATE:	FILING DATE:	APPLICATION PILING DATE	APPLICATION	FILING DATE: APPLICATION	FILING DATE:	FILING	APPLICATION FILING DATE:	APPLICATION	APPLICA	FILING D	FILING	APPLICA	APPLICATION	FILING DATE	FILING DATE	APPLICATION BILLING DATE	APPLICATION	FILING DATE APPLICATION	FILING DATE	FILING
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EARLIER APPLICATION NUMBER: 60/043,135
ERRITER FILING DATE: 1997-04-11
EARLIER FILING DATE: 1997-04-13
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EARLIER FILING DATE: 1997-04-13
EARLIER FILING DATE: 1997-06-22
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EARLIER APPLICATION NUMBER: 60/056,893
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EARLIER PLING DATE: 1997-08-22
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EARLIER PLING DATE: 1997-08-22
EARLIER PLING DATE: 1997-08-23
CCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 326
                                                                                                  267 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 326
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Patent No. 6500938
GENERAL INFORMATION:
APPLICANT: Janice Au-Young
APPLICANT: Jointee Au-Young
APPLICANT: OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
TITLE OF INVENTION: PATHWAY GENE EXPRESSION
NUMBER OF SEQUENCES: 1490
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
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                                                                                                                                                                                                                                                             RESULT 11
5212073-1
; Patent No. 5212073
APPLICANT: ROLLINS, BARRETT:STILES, CHARLES; WONG, GORDON G.
TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

86.4%; Score 140; DB 6; Length 752;
Best Local Similarity 61.5%; Pred. No. 0.32;
Matches 96; Conservative 50; Mismatches 10; Indels
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
                                                                                                                                                                                   387 CTGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGA 422
                                                                                                                                                     CTGCAGCTAACTTATTTTCCCCTAGCTTTCCCCAGA 422
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                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/07/351,008
FILING DATE:12-MAY-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/09/016,434
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: HEREWITH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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CLASSIFICATION:
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TITLE OF INVENTION: PROCESS FOR PRODUCING HUMAN JE CYTOKINE
NUMBER OF SEQUENCES: 1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/351,008
FILING DATE:12-MAY-1989
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EARLIER APPLICATION NUMBER: 60/048,964
EARLIER FILING DATE: 1997-06-66
EARLIER FILING DATE: 1997-09-05
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER APPLICATION NUMBER: 60/056,884
EARLIER FILING DATE: 1997-09-05
NUMBER OF SEQ ID NOS: 280
                ER APPLICATION NUMBER: 60/043,578
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
ER FILING DATE: 1997-04-11
ER APPLICATION NUMBER: 60/043,576
ER PILING DATE: 1997-05-33
ER APPLICATION NUMBER: 60/043,670
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,632
ER PLING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,816
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,816
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,816
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ER APPLICATION NUMBER: 60/056,816
ER FILING DATE: 1997-08-22
ER APPLICATION NUMBER: 60/056,909
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Best Local Similarity 68.2
Matches 107; Conservative
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LENGTH: 1822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: FOLEY & LARDNER STREET: King Street Station, Suite 500, 1800 Diagonal STREET: Road, PO Box 299 CITY: ALEXANDRIA
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CURRENT APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:

FILING DATE:

APPLICATION S30

ATTORNEY/AGENT INFORMATION:

NAME: SAXE, BETHANDER:

REGISTRATION NUMBER: 16,781/369

REGISTRATION NUMBER: 16781/369

TELEFENCE/DOCKET NUMBER: 16781/369

TELEFENCE/DOCKET NUMBER: 16781/369

TELEFENCE/OMUNICATION INFORMATION:

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                                      385 ACTGAAAACAAGCCATGACTTGAGAAACAAATTTG 422
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58.2%; Pred. No. 1.3;
Live 50; Mismatches
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                        Sequence 15, Application US/07927391; Patent No. 6001649; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                     APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: MILOUX, Brigitte
APPLICANT: MINTY, Adrian
APPLICANT: VITA, Natalio
APPLICANT: VITA, Natalio
TITLE OF INVENTION: Protein he
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TITLE OF INVENTION: for its pi
TITLE OF INVENTION: for its pi
TITLE OF INVENTION: for its pi
TITLE OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
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INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 814 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: VIRGINIA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 814 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
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Best Local Similarity 58.2
Matches 92; Conservative
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OPERATING SYSTEM:
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, LOCATION:
US-07-927-391-15
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LOCATION:
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Sequence 3840, Application US/09949016

Patent NO. 6812339

GENERAL INFORMATION:
PAPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOOGL307

CURRENT PELLING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FeatSEQ for Windows Version 4.0

SEQ ID NO 3840
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; Pred. No. 1.3;
50; Mismatches 16;
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NAWE: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REPERENCE DOCKET NUMBER: PA-007
TELECOMUNICATION INFORMATION:
TELEPHONE: (650) 845-0555
TELEPHONE: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1273: SEQUENCE CHARACTERISTICS:
LENOTH: 810 base pairs
LENOTH: 810 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
STRANDEDNESS: single
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STRANDEDNESS: SINGLE
LIBRARY: GENBANK
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Best Local Similarity
Matches 92; Conserv
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ORGANISM: Human
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Gaps

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APPLICANT: URBYTER, J. Craig et al.
APPLICANT: URBYTER, J. Craig et al.
APPLICANT: URBYTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT BILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastESEQ For Windows Version 4.0
LENGTH: 6022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3477 CTTCAAGACCAAACTGGACAAGGAGATCTGTGCTGACCCCACACAGAAGTGGGTCCAGGA 3536
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81.7%; Score 132.4; DB 4; Length 6022;
Best Local Similarity 58.2%; Pred. No. 4.6;
Matches 92; Conservative 50; Mismatches 16; Indels 0;
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Search completed: August 4, 2005, 17:40:05
Job time : 84 secs
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                                                                                                               RESULT 15
US-09-949-016-15582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15582
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August 4, 2005, 16:50:19; Search time 332 Seconds (without alignments) 3163.062 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7297361 segs, 3241162794 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                     OM nucleic - nucleic search, using sw model
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162
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

|            | Description          | Seguence 5454, Ap    | Sequence 2123, Ap  | Sequence 3105, Ap  | Sequence 262, App | Sequence 97, Appl | Sequence 72, Appl | Sequence 72, Appl |
|------------|----------------------|----------------------|--------------------|--------------------|-------------------|-------------------|-------------------|-------------------|
| SUMMARIES  | ID                   | 9 US-09-864-761-5454 | US-10-060-036-2123 | US-10-060-036-3105 | US-10-717-597-262 | US-10-283-975A-97 | US-09-777-430A-72 | US-10-875-094-72  |
| ;          | BB :                 | 0                    | 74                 | 14                 | 13                | 13                | 6                 |                   |
| •          | Length               | 360                  | 473                | 475                | 478               | 482               | 647               | 647               |
| *<br>Query | e Match Length DB ID | 96.9                 | 96.9               | 96.9               | 6.96              | 96.9              | 96.9              | 6.96              |
| ,          | Score                | 157                  | 157                | 157                | 157               | 157               | 157               | 157               |
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| Result     | ~ ;                  | U                    |                    | υ                  |                   |                   |                   |                   |

| Sequence 104, App<br>Sequence 66, Appl<br>Sequence 1344, Ap<br>Sequence 58, Appl<br>Sequence 17, Appl<br>Sequence 3, Appli  | Sequence 46, Appl Sequence 66, Appl Sequence 66, Appl Sequence 819, App Sequence 819, App Sequence 96, Appl Sequence 15, Appl Sequence 165, Appl Sequence 1165, Appl Sequence 2, Appl Sequence 2, Appl Sequence 1165, Appl Sequence 1165, Appl Sequence 1165, Appl Sequence 1165, Appl Sequence 1165, Appl Sequence 1165, Appl Sequence 1165, Appl Sequence 1165, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 117, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl Sequence 1177, Appl S |                                                                 | 5                                                                                                                                                            |
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| 19 US-10-776-827-104 16 US-10-210-120-66 18 US-10-641-643-1344 19 US-10-28-975A-58 19 US-10-764-649-17 19 US-10-445-735A-46 | US-10-852<br>US-10-852<br>US-10-909<br>US-10-172<br>US-10-473<br>US-10-278<br>US-10-278<br>US-10-685<br>US-10-685<br>US-10-685<br>US-10-685                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |                                                                 | 10 US-09-148-545-105<br>22 US-10-833-656-2<br>19 US-10-685-705-4<br>8 US-08-927-939-76<br>9 US-09-792-793A-54<br>17 US-10-375-209A-54<br>9 US-09-792-793A-52 |
| 661<br>725<br>725<br>725<br>725<br>725                                                                                      | 725<br>725<br>739<br>739<br>739<br>741<br>756                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 757<br>757<br>783<br>804<br>804<br>1102<br>1112<br>1712<br>1822 | 1822<br>2776<br>11793<br>685<br>999<br>999                                                                                                                   |
| 00000000000000000000000000000000000000                                                                                      | , , , , , , , , , , , , , , , , , , ,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |                                                                 | 96.9<br>96.9<br>96.9<br>9.4.0<br>93.0                                                                                                                        |
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| 8 9 10 11 12 12 13 14 14 14 14 14 14 14 14 14 14 14 14 14                                                                   | 221<br>221<br>232<br>24<br>254<br>264<br>264                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 0<br>8 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                    | 0 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4                                                                                                                      |

## ALIGNMENTS

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US-09-664-761-5454/c

Sequence 5454, Application US/09864761

Sequence 9454, Application US/09864761

Sequence 9454, Application US/09864761

Settent No. US20020040763A1

GENERAL INFORMATION:

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Rank, David R.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR TITLE OF INVENTION WHBER: US/09/864,761

CURRENT APPLICATION NUMBER: US 60/180,312

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR PRILNG DATE: 2000-06-26

PRIOR PELING DATE: 2000-06-36

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2000-09-27

PRIOR PELING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30

PRIOR FILING DATE: 2001-01-30
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| Sequence 2123, Application US/10060036
| Publication No. US20030073144A1
| GENERAL INFORMATION:
| APPLICANT: Benson, Darin R. |
| APPLICANT: Lodes, Michael D. |
| APPLICANT: Persing, Michael J. |
| APPLICANT: Persing, David H. |
| APPLICANT: Persing, David H. |
| APPLICANT: Persing, David H. |
| APPLICANT: Persing, David H. |
| APPLICANT: Persing Discrepance Compositions and Merhods FOR THE THERAPY TITLE OF INVENTION: COMPOSITIONS AND DIAGNOSIS OF PANCREATIC CANCER FILE REFERENCE: 210121.566 |
| CURRENT APPLICATION NUMBER: US/10/060,036 |
| CURRENT FILING DATE: 2002-01-30 |
| NUMBER OF SEQ ID NOS: 4560 |
| SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 96.9%; Score 157; DB 9; Length 360; Best Local Similarity 68.2%; Pred. No. 1.7; Matches 107; Conservative 50; Mismatches 0; Indels
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OTHER INFORMATION: EXPRESSED IN LING, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN BONE MARKOW, SIGNAL = 2.4

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.5

OTHER INFORMATION: EXPRESSED IN HEACTIVAR, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.9

OTHER INFORMATION: EXPRESSED IN HERAL, SIGNAL = 2.6

OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN BETAL LIVER, SIGNAL = 3.7
PRIOR APPLICATION NUMBER: PCT/USO1/00669
PRIOR FILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PLING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00663
PRIOR APPLICATION NUMBER: PCT/USO1/00662
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR APPLICATION NUMBER: PCT/USO1/00670
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2001-01-30
PRIOR PILING DATE: 2000-09-21
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-06-30
PRIOR PILING DATE: 2000-01-29
NUMBER OF SEQ ID NOS: 49117
SEQ ID NO SEQ ID NOS: 49117
SEQ ID NO SEQ ID NOS: 49117
SEQ ID NO SEQ ID NOS: 49117
SEQ ID NO SEQ ID NOS: 49117
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ORGANISM: Homo sapiens
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                                                                                                                                              DB 14; Length 473;
1.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3105, Application US/10060036
; Sequence 3105, Application US/10060036
; Publication No. US20030073144A1
; GENERAL INFORMATION:
; APPLICANT: Endes, Michael D.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Hepler, William T.
; APPLICANT: Jiang, Yuqiu
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAP:
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER
; TITLE REPERENCE: 210121.566
; CURRENT APPLICANTON NUMBER: US/10/060,036
; CURRENT FILING DATE: 2002-01-30
; NUMBER OF SEQ ID NOS: 4560
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 3105
; LENGTH: 475
; LENGTH: 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                315 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 351
                                                                                                                                              Query Match 96.9%; Score 157; DB Best Local Similarity 68.2%; Pred. No. 1.8; Matches 107; Conservative 50; Mismatches
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APPLICANT: Wyeth
APPLICANT: Burczynski, Michael B.; APPLICANT: Twine, Natalie C.; APPLICANT: Dorner, Andrew J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 68.2%
Matches 107; Conservative
; SEQ ID NO 2123
; LENGTH: 473
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-060-036-2123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
CORGANISM: Homo sapiens
US-10-060-036-3105
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US-10-717-597-262
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TYPE: RNA
ORGANISM: Artificial Sequence
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                APPLICANT: Slorim, Donna K.
APPLICANT: Slorim, Donna K.
TITLE OF INVENTION: METHODS FOR DIAGNOSING RCC AND OTHER SOLID TUMORS
FILE REFERENCE: AM101080L
CURRENT APPLICATION NUMBER: US,10/717,597
CURRENT FILING DATE: 2003-11-21
PRIOR PRILOR FILING DATE: 2003-14-21
PRIOR FILING DATE: 2003-04-03
PRIOR FILING DATE: 2002-11-21
NUMBER OF SEQ ID NOS: 4904
SOCTYARE: Datentin Version 3.2
LENGTHAR: 478
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; Publication No. US20040110792A1
; Publication No. US20040110792A1
; Publication No. US20040110792A1
; GENERAL INFORMATION:
; APPLICANT: Ortho-Clinical Diagnostics, Inc.
; TITLE OF INVENTION: Methods For Assessing and Treating Leukemia
; FILE REFERENCE: CDS 293 FCT
; CURRENT APPLICATION NUMBER: US/10/283, 975A
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: 60/340, 938
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR FILING DATE: 2001-10-30
; PRIOR PILING DATE: 2001-10-30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
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96.9%; Score 157; DB 19; Length 478;
Best Local Similarity 68.2%; Pred. No. 1.8;
Matches 107; Conservative 50; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Trepicchio, William L.
                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-717-597-262
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APPLICANT:
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US-10-875-094-72

US-10-875-094-72

Sequence 72, Application US/10875094

Publication No. US20050130179A1

GENERAL INFORMATION.

APPLICANT: Lyamichev, Victor

APPLICANT: Allawi, Hatim T.

APPLICANT: Takova, Tsetska

APPLICANT: Neri, Bruce P.

APPLICANT: Neri, Bruce P.

APPLICANT: Neri, Bruce P.

APPLICANT: Neri, Bruce P.

APPLICANT: Neri, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Bruce P.

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APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Bruce P.

APPLICANT: Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser Nori, Ser 
                                                                                                                                                                                                                                                                                                Sequence 72, Application US/09777430A

Sequence 72, Application US/09777430A

Patent No. US2002012465A1

GENERAL INFORMATION:

APPLICANT: Lyanichev, Victor

APPLICANT: Allawi, Hatim T.

APPLICANT: Mayland, Sarah R.

APPLICANT: Mayland, Sarah R.

APPLICANT: Mayland, Sarah R.

APPLICANT: Mayland, Sarah R.

APPLICANT: Mayland, Sarah R.

APPLICANT: Nair, Bruce P.

TITLE OF INVENTION: Charge Tags and the Separation of Nucleic Acid Molecules

FILE REFERENCE: FORS-04912

CURRENT APPLICATION NUMBER: US/09/777,430A

CURRENT FILING DATE: 2001-02-06

NUMBER OF SEQ ID NOS: 85

SOFTWARE: PatentIn version 3.1

SEQ ID NO 72

LENGTH: 647
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Pred. No. 1.9;
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                                                       126 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 162
315 ACCCAAGAAUCUGCAGCUAAUUUUCCCCUAGCU 351
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; OTHER INFORMATION: Synthetic US-09-777-430A-72
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248 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 307
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Jeffrey J. Seilhamer
Jeffrey J. Scilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL
GENE EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                          Length 725;
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
SURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
CLASSPICATION: UNKNOWN>
APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSER: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PA-0001 US
                                        60/334,468
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ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 1344, Application US/10641643 Publication No. US20040077003A1 GENERAL INFORMATION: GOCKS, Benjamin G. APPLICANT: Cocks, Benjamin G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       845-4166
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TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 1344:
SEQUENCE CHARACTERISTICS:
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: US 60/.
NUMBER OF SEQ ID NOS: 123
SOFTWARE: Patentin version 3.2
SEQ ID NO 66
LENGTH: 725
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COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STATE: CALIFORNIA COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                     ; ORGANISM: Homo sapiens
US-10-210-120-66
                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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Best Local
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Sublication No. US20040132086A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TAPLICANT: Howitz, Kathryn
APPLICANT: Howitz, Kathryn
APPLICANT: Richer, Jennifer
TITLE OF INVENTION: Thereto
FILE REFERENCE: 2848-39
CURRENT APPLICATION NUMBER: US/10/776,827
CURRENT FILING DATE: 2004-02-10
PRIOR FILING DATE: 2002-03-21
PRIOR FILING DATE: 2000-06-28
NUMBER OF SEQ ID NOS: 108
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patentin version 3.1
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                                                                          Query Match 96.9%; Score 157; DB 22; Length 647; Best Local Similarity 55.4%; Pred. No. 1.9; Matches 87; Conservative 70; Mismatches 0; Indels 0
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Publication No. US20030175736A1
Publication No. US20030175736A1
APPLICANT: INFORMATION: Arul M.
APPLICANT: Rubin, Mark A.
APPLICANT: Sreekumar, Arun
TITLE OF INVENTION: Expression Profile of Prostate Cancer
FILE REFERENCE: UM-07221
CURRENT FAPILCATION NUMBER: US/10/210,120
CURRENT FILING DATE: 2002-08-01
PRIOR APPLICATION NUMBER: US 60/309,581
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
US-10-776-827-104
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                    US-10-875-094-72
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LENGTH: 661
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APPLICANT: Device, Anthony L.
APPLICANT: Device, Anthony L.
APPLICANT: Garzino, Alfedo
TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
TITLE OF INVENTION: Immuno-Modulating Effects of Chemokines in DNA Vaccination
TITLE OF INVENTION: UNMBER: US/10/445,790
CURRENT APPLICATION NUMBER: US/10/445,790
CURRENT FILING DATE: 2003-05-27
PRIOR FILING DATE: 1998-12-11
PRIOR FILING DATE: 1998-12-11
PRIOR APPLICATION NUMBER: US 60/186,416
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: 2000-03-02
PRIOR FILING DATE: US 60/069,281
PRIOR FILING DATE: US 60/069,281
                     INFLAMMATORY PROTEINS IN THE DIAGNOSIS AND TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     248 CTTCAAGACCATTGTGGCCAAGGAGATCTGTGCTGACCCCAAGCAGAAGTGGGTTCAGGA 307
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               TITLE OF INVENTION: INFLAMMATORY PROTEINS IN TITLE OF INVENTION: METABOLIC DISORDERS FILE REFERENCE: MPISON3-025PRINM; CURRENT PEPLICATION NUMBER: US/10/764,649; CURRENT FILING DATE: 2004-01-26; PRIOR APPLICATION NUMBER: 60/446041; PRIOR FILING DATE: 2003-02-07; NUMBER OF SEQ ID NOS: 20 SOFTWARE: FastSEQ for Windows Version 4.0; SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/10445790
; Publication No. US20040197305A1
; GENERAL INFORMATION:
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
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Best Local Similarity 68.2%
Matches 107; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-445-790-3
                                                                                                                                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (54)...(353)
US-10-764-649-17
                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: human
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Sequence 58, Application US/10283975A

Publication No. US20040110792A1

GENERAL INFORMATION:

APPLICANT: Ortho-Clinical Diagnostics, Inc.

TITLE OF INVENTION: Methods For Assessing and Treating Leukemia FILE REFERENCE: CDS 293 PCT

CURRENT APPLICATION NUMBER: US/10/283,975A

CURRENT FILING DATE: 2002-10-30

PRIOR FILING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

PRIOR PLING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 900

SOFTWARE: PatentIn version 3.1

SEQ ID NO 58

LENGTH: 725
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                                                                                                    Query Match
96.9%; Score 157; DB 18; Length 725;
Best Local Similarity 68.2%; Pred. No. 1.9;
Matches 107; Conservative 50; Mismatches 0; Indels
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Publication No. US20040157253A1
GENERAL INFORMATION:
APPLICANT: Xu, Haiyan
APPLICANT: Chong
APPLICANT: Barnes, Glenn
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR USE OF
                                                                                                                                                                                                                                                                                                                                                       368 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 404
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CLONE: 934513
; SEQUENCE DESCRIPTION: SEQ ID NO: 1344 :
US-10-641-643-1344
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96.9%; Score 157; DB
Best Local Similarity 68.2%; Pred. No. 1.9;
Matches 107; Conservative 50; Mismatches
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ORGANISM: HUMAN
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US-10-283-975A-58
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US-10-852-335A-54
; Sequence 54, Application US/10852335A
; Publication No. US20050112129A1
; GENERAL INFORMATION:
; TITLE OF INVENTION: Compositions and Methods for the Diagnosis and
; TITLE OF INVENTION: Treatment of Tumors of Glial Origin
; TITLE OF INVENTION: Treatment of Tumors of Glial Origin
; TITLE OF INVENTION: UNBER: US/10/852,335A
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US 60/548,299
; PRIOR APPLICATION NUMBER: US 60/548,299
; PRIOR PILING DATE: 2004-02-27
; PRIOR APPLICATION NUMBER: US 60/473,238
                                                                                                                                         US-10-852-335A-46

//S Sequence 46, Application US/10852335A

//S Publication No. US20050112129A1

//S Publication No. US20050112129A1

//S Publication No. US20050112129A1

//S PUBLICANT: HEIDI S. PHILLIPS

//TILE OF INVENTION: Compositions and Methods for the Diagnosis and

//TILE REPRENCE: P5103R1-US

//CURRENT APPLICATION UNMBER: US/10/852,335A

//CURRENT FILING DATE: 2004-05-24

//PRIOR APPLICATION NUMBER: US 60/548,299

//PRIOR FILING DATE: 2004-02-27

//PRIOR PILING DATE: 2003-05-23

//WHER OF SEQ ID NOS: 190

//S SEQ ID NO 46
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              368 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 404
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ORGANISM: Homo sapiens
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LENGTH: 725
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368 ACCCAAGAATCTGCAGCTAACTTATTTTCCCCTAGCT 404
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Job time : 334 secs
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